

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:31:28 ; Search time 44.2069 Seconds
(without alignments)
2301.535 Million cell updates/sec

Title: US-09-538-106-13

Perfect score: 3405

Sequence: 1 MSQSTQNEFLSPVEFQHIW.....FNFDARNRNKKQRIKEDGE 641

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_19Jun03.*
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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3405	100.0	641	20	AAV45247
2	3405	100.0	641	20	AAV05953
3	3405	100.0	641	22	AAAB2129
4	3405	100.0	641	23	ABG95142
5	3401	99.9	641	21	AAAB1358
6	3401	99.9	641	23	ABG95128
7	3401	99.9	641	23	ABG95136
8	3401	99.9	641	23	ABP61910
9	3401	99.9	641	23	ABP74990

10	3397	99.8	680	21	AAAB1361	Human p53 protein
11	3397	99.8	680	21	AAV50997	Human KET protein.
12	3387	99.8	680	23	ABP61913	Human lung cancer
13	3387	99.8	680	23	ABP74993	Human p53 homologue
14	3353	98.5	680	20	AAV05958	Human cell regulat
15	3353	98.5	680	21	AAV50998	Rat KET protein.
16	3033	89.1	586	20	AAV05956	Human cell regulat
17	3033	89.1	586	23	ABG95140	Human oncogene p53
18	3029	89.0	586	23	ABG95132	Human oncogene p51
19	3016	88.6	586	21	AAAB1357	Human p53 protein
20	3016	88.6	586	23	ABP61909	Human lung cancer
21	3016	88.6	586	20	ABP74989	Human p53 homologue
22	3009	88.4	586	23	AAV41032	Human lung tumor a
23	3009	88.4	586	21	AAAB1317	Human lung cancer-
24	3009	88.4	586	23	ABP61869	Human lung cancer
25	3009	88.4	586	23	ABP74949	Human lung tumour
26	2995	88.0	586	20	AAV05962	Mouse cell regulat
27	2722	79.9	516	20	AAV05954	Human cell regulat
28	2722	79.9	516	21	AAAB1363	Human p53 protein
29	2722	79.9	516	23	ABG95135	Human oncogene p51
30	2722	79.9	516	23	ABG95141	Human oncogene p53
31	2722	79.9	516	23	ABP61915	Human lung cancer
32	2722	79.9	516	23	ABP74995	Human p53 homologue
33	2449	71.9	471	23	ABG95129	Human oncogene p51
34	2449	71.9	471	23	ABG95134	Human oncogene p51
35	2350	69.0	461	21	AAAB1362	Human p53 protein
36	2350	69.0	461	23	ABG95131	Human oncogene p51
37	2350	69.0	461	23	ABG95138	Human oncogene p53
38	2350	69.0	461	23	ABP61914	Human lung cancer
39	2350	69.0	461	23	ABP74994	Human p53 homologue
40	2327	68.3	461	20	AAV05965	Mouse cell regulat
41	2185	64.2	448	20	AAV45246	Human p51 protein
42	2185	64.2	448	20	AAV05955	Human cell regulat
43	2185	64.2	448	21	AAAB1359	Human p53 protein
44	2185	64.2	448	22	AAAB8128	Human protein #1 u
45	2185	64.2	448	23	ABG95127	Human oncogene p51

ALIGNMENTS

RESULT 1	
AAV45247	
ID	AAV45247 standard; Protein; 641 AA.
XX	
AC	AAV45247;
XX	
DT	07-JAN-2000 (first entry)
XX	
DE	Human p51 protein B.
XX	
KW	Human; p51, p53 related gene; cell proliferation; regulation; cancer;
KW	tumour suppression; diagnosis.
XX	
OS	Homo sapiens.
XX	
FH	
FT	key
FT	Domain
FT	Location/Qualifiers
FT	1..59
FT	/label= transactivation_domain
FT	142..321
FT	/label= DNA_binding_domain
FT	353..397
FT	/label= oligomerisation_domain
XX	
PN	WO9950412-A1.
XX	
PD	07-OCT-1999.
XX	
PF	24-MAR-1999; 99WO-JP01512.
XX	
PR	27-MAR-1998; 98JP-0100467.
XX	
PA	(SAKA) OTSUKA PHARM CO LTD.

PA (IKAW/) IKAWA Y.
 XX
 PI Ikawa Y, Ikawa S, Obinata M;
 XX
 DR WPI: 1999-591318/50.
 DR N-PSDB; AAZ25771.
 XX
 PI New p53 related human gene p51, useful for diagnosis, investigation and
 PI treatment of cancers and screening for potential cell proliferation
 PI agents -
 XX
 PS Example 1: Page 152-154; 163pp. Japanese.
 XX
 CC The present sequence represents a human p51 protein, which is related to
 CC p53 and has cell proliferation regulation and tumour suppression
 CC activity. The p51 gene can be used in the investigation, diagnosis and
 CC treatment of diseases such as cancer, with which the p53 family cell
 CC proliferation regulation is associated. The p51 protein may be used for
 CC screening potential agonists and antagonists of its regulatory function,
 CC for use as drugs,
 CC
 XX
 SQ Sequence 641 AA;

Query Match 100.0% Score 3405; DB 20; Length 641;
 Best Local Similarity 100.0%; Pred. No. 2,4e-273;
 Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MSQSTQTNNEFLSPEVFOHIMDFLEQPICSVOPIDLFVDESEDEGATNKIEISMDCIMQ 60
DB 1 MSQSTQTNNEFLSPEVFOHIMDFLEQPICSVOPIDLFVDESEDEGATNKIEISMDCIMQ 60
OY 61 DSDLSDDPMWQYNTNGLNLSMDQIQNGSSSTSPYNTHAQNSVAPSPYAPSPSTFAL 120
DB 61 DSDLSDDPMWQYNTNGLNLSMDQIQNGSSSTSPYNTHAQNSVAPSPYAPSPSTFAL 120
OY 121 SPSPALPSTNDYPGHSPFDSVFOQSSSTAKSATWTSTELKLYCOIATCPQIOWMP 180
DB 121 SPSPALPSTNDYPGHSPFDSVFOQSSSTAKSATWTSTELKLYCOIATCPQIOWMP 180
OY 121 SPSPALPSTNDYPGHSPFDSVFOQSSSTAKSATWTSTELKLYCOIATCPQIOWMP 180
DB 121 SPSPALPSTNDYPGHSPFDSVFOQSSSTAKSATWTSTELKLYCOIATCPQIOWMP 180
OY 181 POGAVIRAMPYKKAHEVTEVKKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
DB 181 POGAVIRAMPYKKAHEVTEVKKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
OY 181 POGAVIRAMPYKKAHEVTEVKKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
DB 181 POGAVIRAMPYKKAHEVTEVKKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
OY 241 ITGROSVALYEPPEVGTETFTVLYNEMCNSSCVGAMRRPILLIVTLETBDGYLGRR 300
DB 241 ITGROSVALYEPPEVGTETFTVLYNEMCNSSCVGAMRRPILLIVTLETBDGYLGRR 300
OY 241 ITGROSVALYEPPEVGTETFTVLYNEMCNSSCVGAMRRPILLIVTLETBDGYLGRR 300
DB 241 ITGROSVALYEPPEVGTETFTVLYNEMCNSSCVGAMRRPILLIVTLETBDGYLGRR 300
OY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIOMTSIKRRSPDE 360
DB 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIOMTSIKRRSPDE 360
OY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIOMTSIKRRSPDE 360
DB 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIOMTSIKRRSPDE 360
OY 361 LLIYPVGRRETYEMILTKESLELMQYLPQHTIETRYROOQOQOHOHLQOKTISQSPSSY 420
DB 361 LLIYPVGRRETYEMILTKESLELMQYLPQHTIETRYROOQOQOHOHLQOKTISQSPSSY 420
OY 361 LLIYPVGRRETYEMILTKESLELMQYLPQHTIETRYROOQOQOHOHLQOKTISQSPSSY 420
DB 361 LLIYPVGRRETYEMILTKESLELMQYLPQHTIETRYROOQOQOHOHLQOKTISQSPSSY 420
OY 421 GNSSPPLKKNMSMKLPVSQOLINPOORNALPTTIPGMCAMNIPMGTHMPMGDMNGL 480
DB 421 GNSSPPLKKNMSMKLPVSQOLINPOORNALPTTIPGMCAMNIPMGTHMPMGDMNGL 480
OY 421 GNSSPPLKKNMSMKLPVSQOLINPOORNALPTTIPGMCAMNIPMGTHMPMGDMNGL 480
DB 421 GNSSPPLKKNMSMKLPVSQOLINPOORNALPTTIPGMCAMNIPMGTHMPMGDMNGL 480
OY 481 SPYQALPPLSPMSTSHCTPPPYPTDCSIVSFLARLGCCSSCLDFTTQGGITTIQIHY 540
DB 481 SPYQALPPLSPMSTSHCTPPPYPTDCSIVSFLARLGCCSSCLDFTTQGGITTIQIHY 540
OY 481 SPYQALPPLSPMSTSHCTPPPYPTDCSIVSFLARLGCCSSCLDFTTQGGITTIQIHY 540
DB 481 SPYQALPPLSPMSTSHCTPPPYPTDCSIVSFLARLGCCSSCLDFTTQGGITTIQIHY 540
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DB 541 SMDLASKIPRORRAIWKILDRQLHERSSPSHLIRTPSSASTVSSSETRGERVI 600
OY 541 SMDLASKIPRORRAIWKILDRQLHERSSPSHLIRTPSSASTVSSSETRGERVI 600
DB 541 SMDLASKIPRORRAIWKILDRQLHERSSPSHLIRTPSSASTVSSSETRGERVI 600
OY 601 DAVRETLROTISPPPEDEMNDFNDMDARRNKKOORKEGE 641
DB 601 DAVRETLROTISPPPEDEMNDFNDMDARRNKKOORKEGE 641
OY 601 DAVRETLROTISPPPEDEMNDFNDMDARRNKKOORKEGE 641
DB 601 DAVRETLROTISPPPEDEMNDFNDMDARRNKKOORKEGE 641

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RESULT 2

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AA05953
ID AA05953 standard; Protein; 641 AA.
XX
AC AA05953;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cell regulatory protein p63, isoform hTAP63 alpha.
XX
KW Cell regulatory protein; p63; hTAP63 alpha; TAP63 alpha; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy.
XX
OS Homo sapiens.
XX
PN W0919357-A2.
XX
PD 22-APR-1999.
XX
PF 02-OCT-1998; 98WO-US21992.
XX
PR 29-MAY-1998; 98US-0087216.
PR 15-OCT-1997; 97US-0062076.
PA (HARD ) HARVARD COLLEGE.
PA
PI McKeon F, Yang A;
PI
DR WPI: 1999-277595/23.
DR N-PSDB; AAX58572.
XX
PT New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
XX
PS Claim 23; Fig 9; 161pp; English.
XX
CC The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. It has been observed that the
CC intron-exon organisation is conserved between p73 and p53, and from
CC known exon and intron sizes for these 2 genes, it was possible to
CC identify new members of this gene family using a PCR-based strategy
CC of amplifying 2 exons in a conserved domain and their intervening
CC intron. The human p53 gene was localised to chromosomal position
CC 3q27-29. At least 6 different isoforms exist. Splice variants
CC differing at the C-terminus have been designated as alpha, beta and
CC gamma forms, while p63 members differing in the N-terminus are
CC designated as delta and TA forms, where the delta form lacks the
CC transactivation domain. The present sequence represents human
CC p63 isoform TAP63 alpha. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. Delta isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AA05953-64), polynucleotides (see
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.
XX
SQ Sequence 641 AA;

```

Query Match 100.0% Score 3405; DB 20; Length 641;
 Best Local Similarity 100.0%; Pred. No. 2,4e-273;
 Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MSQSTQTNNEFLSPEVFOHIMDFLEQPICSVOPIDLFVDESEDEGATNKIEISMDCIMQ 60

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Db 1 MSOSTQTNELSPFVQHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
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 Db 61 DSDLSPPMPPQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSSSTFDAL 120
 QY 121 SPSPALPSNTDYPGPHSPFVDFQOOSTASATWTYSTELKLYCQIAKTCPIQIKWTPP 180
 Db 121 SPSPALPSNTDYPGPHSPFVDFQOOSTASATWTYSTELKLYCQIAKTCPIQIKWTPP 180
 QY 181 POGAVIRAMPVYKKAHTEVYKRCNHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
 Db 181 POGAVIRAMPVYKKAHTEVYKRCNHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
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 Db 241 ITGROSVLVPEPPQVTEFTTYLVNFMCNSSCVGGMNRRPILITYLETRDQVIGRRC 300
 QY 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTNRPPQNTNGIOMTSIKRRSPDDE 360
 Db 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTNRPPQNTNGIOMTSIKRRSPDDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYRQOQOQOHOHLQKOTSIQSPSSY 420
 Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYRQOQOQOHOHLQKOTSIQSPSSY 420
 QY 421 GNSSPPLNKMSNKLPSVSQILNPOQRNALPTTIPDGGANIPMGTMPMAGDMNGL 480
 Db 421 GNSSPPLNKMSNKLPSVSQILNPOQRNALPTTIPDGGANIPMGTMPMAGDMNGL 480
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 Db 481 SPQALPPLSMSTSHCTPPPYPTDCISIVSFLARIGCSSCLDYFTTQGLTIYQIEHY 540
 QY 541 SMDOLASLKIPEQFRAIMKGLIDHRLHEFSSPSHLIRPSSASIVSVSSSTRGERVY 600
 Db 541 SMDOLASLKIPEQFRAIMKGLIDHRLHEFSSPSHLIRPSSASIVSVSSSTRGERVY 600
 QY 601 DAVRFTLRQTISSPPRDENWDFNFDARANKQORIKEGE 641
 Db 601 DAVRFTLRQTISSPPRDENWDFNFDARANKQORIKEGE 641

RESULT 3
 AAB82129 standard; protein; 641 AA.
 XX AAB82129;
 AC 03-AUG-2001 (first entry)
 DT Human protein #2 used to produce a chimeric p53 protein.
 DE Human; cytostatic; gene therapy; p53; human tumour.
 XX Homo sapiens.
 OS
 XX
 FH Key location/Qualifiers
 FT Domain 1..59
 FT /label= Transactivation_domain
 FT Domain 142..321
 FT /label= DNA_binding_domain
 FT Domain 353..397
 FT /label= Oligomerisation_domain
 XX
 PN JP2000354488-A.
 PD 26-DEC-2000.
 XX
 PF 09-APR-1999; 99JP-0139034.
 XX
 PR 09-APR-1999; 99JP-0139034.
 XX

PA (IKAW/) IKAWA H.
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX
 DR WPI: 2001-268293/28.
 DR N-PSDB; AAF86589.
 XX
 PT Chimeric gene of the p53 family, useful for gene therapy, and treatment
 PT of cancer, comprises a transcription activating region and a DNA
 PT binding region -
 XX
 PS Example 1; Page 37-40; 57pp; Japanese.
 XX
 CC The present invention relates to a chimera gene of p53 family encoding a
 CC transcription activating region, a DNA binding region, and an oligomer
 CC formation region of different p53 family proteins. The chimeric gene can
 CC be used for gene therapy of p53 variant human tumours, and analysis of
 CC the function of the p53 family gene. The present sequence was used in the
 CC present invention.
 XX
 SQ Sequence 641 AA;
 Query Match 100.0%; Score 3405; DB 22; Length 641;
 Best Local Similarity 100.0%; Pred. No. 2,4e-273;
 Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNELSPFVQHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 Db 1 MSOSTQTNELSPFVQHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
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 Db 61 DSDLSPPMPPQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSSSTFDAL 120
 QY 121 SPSPALPSNTDYPGPHSPFVDFQOOSTASATWTYSTELKLYCQIAKTCPIQIKWTPP 180
 Db 121 SPSPALPSNTDYPGPHSPFVDFQOOSTASATWTYSTELKLYCQIAKTCPIQIKWTPP 180
 QY 181 POGAVIRAMPVYKKAHTEVYKRCNHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
 Db 181 POGAVIRAMPVYKKAHTEVYKRCNHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
 QY 241 ITGROSVLVPEPPQVTEFTTYLVNFMCNSSCVGGMNRRPILITYLETRDQVIGRRC 300
 Db 241 ITGROSVLVPEPPQVTEFTTYLVNFMCNSSCVGGMNRRPILITYLETRDQVIGRRC 300
 QY 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTNRPPQNTNGIOMTSIKRRSPDDE 360
 Db 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTNRPPQNTNGIOMTSIKRRSPDDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYRQOQOQOHOHLQKOTSIQSPSSY 420
 Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYRQOQOQOHOHLQKOTSIQSPSSY 420
 QY 421 GNSSPPLNKMSNKLPSVSQILNPOQRNALPTTIPDGGANIPMGTMPMAGDMNGL 480
 Db 421 GNSSPPLNKMSNKLPSVSQILNPOQRNALPTTIPDGGANIPMGTMPMAGDMNGL 480
 QY 481 SPQALPPLSMSTSHCTPPPYPTDCISIVSFLARIGCSSCLDYFTTQGLTIYQIEHY 540
 Db 481 SPQALPPLSMSTSHCTPPPYPTDCISIVSFLARIGCSSCLDYFTTQGLTIYQIEHY 540
 QY 541 SMDOLASLKIPEQFRAIMKGLIDHRLHEFSSPSHLIRPSSASIVSVSSSTRGERVY 600
 Db 541 SMDOLASLKIPEQFRAIMKGLIDHRLHEFSSPSHLIRPSSASIVSVSSSTRGERVY 600
 QY 601 DAVRFTLRQTISSPPRDENWDFNFDARANKQORIKEGE 641
 Db 601 DAVRFTLRQTISSPPRDENWDFNFDARANKQORIKEGE 641

RESULT 4
 AAG95142 standard; Protein; 641 AA.
 ID AAG95142

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XX AC ABG95142;
XX 04-DEC-2002 (first entry)
XX DE Human oncogene p63 isoform TA p63 alpha.
XX XX
XX XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
XX XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX XX rhabdomyosarcoma; synovial sarcoma; viral infection.
XX OS Homo sapiens.
XX PN WO200269900-A2.
XX PD 12-SEP-2002.
XX XX
XX PF 01-MAR-2002; 2002WO-US06518.
XX PR 01-MAR-2001; 2001US-272751P.
XX XX
XX PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX PI Filtz LC, Burrows FJ;
XX XX
XX DR WPI: 2002-698710/75.
XX DR N-PSDB; ABS73334.
XX PT
XX PT Treating genetically-defined disease associated with chromosomal
XX PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX PT diseases, involves administering an inhibitor of heat shock protein 90
XX PT
XX PS Disclosure: Page 352-354; 369pp; English.
XX XX
XX CC The invention describes a method of treating genetically-defined disease
XX CC associated with chromosomal aberrations yielding oncogenic fusion
XX CC proteins (I), treating cancerous cells containing (II) in a heterogeneous
XX CC cell population, treating proliferative diseases associated with mutant
XX CC protein or cellular protein isoforms (II) dependent on heat shock
XX CC protein (HSP)-90, or selectively treating cells expressing (II)
XX CC involving administering HSP90-inhibitor. The method is useful for
XX CC treating genetically-defined disease with chromosomal aberration yielding
XX CC oncogenic fusion protein, treating cancerous cells containing fusion
XX CC protein in heterogeneous cell population, treating proliferative disease
XX CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX CC p53), or selectively treating cells expressing mutant protein or cellular
XX CC protein isoform in a patient heterozygous for (II). The method is useful
XX CC for treating a disease e.g. haematopoietic disorder such as T or B cell
XX CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
XX CC or a disease characterised by a solid tumour such as papillary thyroid
XX CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX CC synovial sarcoma. The method is also useful for treating viral
XX CC infections. This is the amino acid sequence of a human oncogenic protein.
XX XX
XX SQ Sequence 641 AA:
XX
XX Query Match 100.0%; Score 3405; DB 23; Length 641;
XX Best Local Similarity 100.0%; Pred. No. 2,4e-273;
XX Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MSOSTQNEFLSPVFGHIMDFLEQPTCSVQPIDINFEVDEPSEGCANKIKETISMDICRMQ 60
XX DB 1 MSOSTQNEFLSPVFGHIMDFLEQPTCSVQPIDINFEVDEPSEGCANKIKETISMDICRMQ 60
XX QY 61 DSDLSDPMPWQYTNLGLNSMDQIQNGSSSTSPNTDHAQNSVTAPEYAPQSSSTFPAI 120
XX DB 61 DSDLSDPMPWQYTNLGLNSMDQIQNGSSSTSPNTDHAQNSVTAPEYAPQSSSTFPAI 120

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DB 61 DSDLSDPMPWQYTNLGLNSMDQIQNGSSSTSPNTDHAQNSVTAPEYAPQSSSTFPAI 120
QY 121 SPSPALPSMTDVGPHSPFVSFOOSTSAKATWYSTELKTKYCOIATKCPQIOIWMPP 180
DB 121 SPSPALPSMTDVGPHSPFVSFOOSTSAKATWYSTELKTKYCOIATKCPQIOIWMPP 180
QY 181 PGAVIIRAMPVYKKAHEVTEYVRCRNHLSHEFNQGLAPPSHLLIRVGNSHAQYVEDP 240
DB 181 PGAVIIRAMPVYKKAHEVTEYVRCRNHLSHEFNQGLAPPSHLLIRVGNSHAQYVEDP 240
QY 241 ITGRQSVLVPPYPPVQVGEFTTVLYNPFMCNCSVCGMNRRPLLIVTLETGRQVLYGRRC 300
DB 241 ITGRQSVLVPPYPPVQVGEFTTVLYNPFMCNCSVCGMNRRPLLIVTLETGRQVLYGRRC 300
QY 301 FEARICACGPRRKADDEDSIRKQVSDSTKNDGTRKPRFQNTHTGIOMTSIKRRSPDE 360
DB 301 FEARICACGPRRKADDEDSIRKQVSDSTKNDGTRKPRFQNTHTGIOMTSIKRRSPDE 360
QY 361 ILIYLVGRREYEMLKIKESLELMQVLPQHTIETVYRQOQOQHLLQKOTSIOSPSY 420
DB 361 ILIYLVGRREYEMLKIKESLELMQVLPQHTIETVYRQOQOQHLLQKOTSIOSPSY 420
QY 421 GNSSPPLNKMNSMNLKPSVQLINPOORNALPPTIIPGMGANIPMGTHMPMAGDMGL 480
DB 421 GNSSPPLNKMNSMNLKPSVQLINPOORNALPPTIIPGMGANIPMGTHMPMAGDMGL 480
QY 481 SPTQALPPLSPMSTSHCTPPPPYPTDCSIVSFLARLCCSSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPTQALPPLSPMSTSHCTPPPPYPTDCSIVSFLARLCCSSCLDYFTTQGLTTIYQIEHY 540
QY 541 SMDDLASLKIPQGFHAIWKGLDHRQJLHEFSSPHLLRTPSASTVSGSEETGERVI 600
DB 541 SMDDLASLKIPQGFHAIWKGLDHRQJLHEFSSPHLLRTPSASTVSGSEETGERVI 600
QY 601 DAVRFTLQTIISFPREDMNFMDMDARRNKQKIKKEGE 641
DB 601 DAVRFTLQTIISFPREDMNFMDMDARRNKQKIKKEGE 641

RESULT 5
AAB11358
ID AAB11358 standard; Protein; 641 AA.
XX AC AAB11358;
XX XX
XX DT 21-FEB-2001 (first entry)
XX DE Human p63 protein isoform #2.
XX KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
XX KW vaccine; detection.
XX OS Homo sapiens.
XX PN WO200061612-A2.
XX PD 19-OCT-2000.
XX PF 03-APR-2000; 2000WO-US08896.
XX PR 02-APR-1999; 99US-0285479.
XX PR 17-DEC-1999; 99US-0466396.
XX PR 30-DEC-1999; 99US-0476496.
XX PR 10-JAN-2000; 2000US-0480884.
XX PR 22-FEB-2000; 2000US-0510376.
XX PA (CORI-) CORIXA CORP..
XX XX
XX PI Wang T, Fan L;
XX XX
XX DR WPI: 2000-628399/60.
XX DR N-PSDB; AAC66028.
XX XX

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PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
 PT protein is used for detecting and monitoring progression of lung cancer
 in a patient

PS Disclosure: Page 245-247; 261pp; English.

CC This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.

SO Sequence 641 AA:

Query Match 99.9%; Score 3401; DB 23; Length 641;
 Best Local Similarity 99.8%; Pred. No. 5.1e-273;
 Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTQTNFELSPVEFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 DB 1 MSOSTQTNFELSPVEFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 QY 61 DSDLSDPMPQYTNGLINSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSSSTFDAL 120
 DB 61 DSDLSDPMPQYTNGLINSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSSSTFDAL 120
 QY 121 SPSPALPSNDYPPPHSFVSFOOSSTAKSATWTYSTELKLYCOIACTCPQIQRKMP 180
 DB 121 SPSPALPSNDYPPPHSFVSFOOSSTAKSATWTYSTELKLYCOIACTCPQIQRKMP 180
 QY 181 POGAVIRAMPYKKAHEVTEYKRCNHELSREFNEGAIAPSHLIRVGNASHAQYVDP 240
 DB 181 POGAVIRAMPYKKAHEVTEYKRCNHELSREFNEGAIAPSHLIRVGNASHAQYVDP 240
 QY 241 ITGROSLVPEPPQVSTETTVLYNFCNCSGCGMMRRITLITVLETFDGOVLGRRC 300
 DB 241 ITGROSLVPEPPQVSTETTVLYNFCNCSGCGMMRRITLITVLETFDGOVLGRRC 300
 QY 301 FEARICACPRGRADSDSTRKQOVSSTKNGDGTFRFRONTGIOMTSIKRRSPDE 360
 DB 301 FEARICACPRGRADSDSTRKQOVSSTKNGDGTFRFRONTGIOMTSIKRRSPDE 360
 QY 361 LVLVPRGRETYEMLKIKESLELMOYLPOHTTETTYQOQOQOHLQKOTSIOSSSY 420
 DB 361 LVLVPRGRETYEMLKIKESLELMOYLPOHTTETTYQOQOQOHLQKOTSIOSSSY 420
 QY 421 GNSSPPLKNKSNKLPVSQILNPOQRNALTPPTIPDGAGANIPMGITMPMAGDNGL 480
 DB 421 GNSSPPLKNKSNKLPVSQILNPOQRNALTPPTIPDGAGANIPMGITMPMAGDNGL 480
 QY 481 SPFOALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSCLDYFTTQGLTIYQIEHY 540
 DB 481 SPFOALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSCLDYFTTQGLTIYQIEHY 540
 QY 541 SMDLALSLKIEPQFRAIKGILDHQLEHFSFSSHLKTPSSASTVSGSSETRGRVI 600
 DB 541 SMDLALSLKIEPQFRAIKGILDHQLEHFSFSSHLKTPSSASTVSGSSETRGRVI 600
 QY 601 DAVRFTLRQTISSPPDENWDFNDADARRNKOARIKEGE 641
 DB 601 DAVRFTLRQTISSPPDENWDFNDADARRNKOARIKEGE 641

RESULT 6
 ABG95128
 ID ABG95128 standard; Protein; 641 AA.
 XX

AC ABG95128;
 XX 04-DEC-2002 (first entry)
 DT
 XX Human oncogene p5B.
 DE

XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW Proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 KW
 OS Homo sapiens.
 XX

PN WO200269900-A2.

PD 12-SEP-2002.

PF 01-MAR-2002; 2002WO-US06518.

PR 01-MAR-2001; 2001US-272751P.

PA (CONF-) CONFORMA THERAPEUTICS CORP.

PI Fritz LC, Burrows FJ;

PP WPI; 2002-698710/75.

DR N-PSDB; ABS73328.

PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90

Disclosure: Paeg 322-324; 389pp; English.

CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock
 CC protein (HSP)-90, or selectively treating cells expressing (II)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.

SO Sequence 641 AA:

Query Match 99.9%; Score 3401; DB 23; Length 641;
 Best Local Similarity 99.8%; Pred. No. 5.1e-273;
 Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTQTNFELSPVEFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 DB 1 MSOSTQTNFELSPVEFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 QY 61 DSDLSDPMPQYTNGLINSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSSSTFDAL 120
 DB 61 DSDLSDPMPQYTNGLINSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSSSTFDAL 120

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QY 121 SPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
DB 121 SPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
QY 181 PGAVIRAMPYKKAHEVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 181 PGAVIRAMPYKKAHEVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITGRQSVLYPEPPVPGTEFTVLYNFMCNSSCVGMMRRPILITVLETRDGOYLGRRC 300
DB 241 ITGRQSVLYPEPPVPGTEFTVLYNFMCNSSCVGMMRRPILITVLETRDGOYLGRRC 300
QY 301 FEARICACPGDRKADSDIRKQOVSSTKNGDGTAKRPFRONTGCIOMTSIKRRSPDDE 360
DB 301 FEARICACPGDRKADSDIRKQOVSSTKNGDGTAKRPFRONTGCIOMTSIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLIKESLELMOYLPHQTIETTYRQOQOQHLLQKOTSIOSSPSY 420
DB 361 LLYLPVGRRETYEMLLIKESLELMOYLPHQTIETTYRQOQOQHLLQKOTSIOSSPSY 420
QY 421 GNSSPPLKNNMKNKLSVSOQLNPQORNALPTTIDGMCANIPMMGTHMPMAGDMNGL 480
DB 421 GNSSPPLKNNMKNKLSVSOQLNPQORNALPTTIDGMCANIPMMGTHMPMAGDMNGL 480
QY 481 SPTQALPPLPSMPTSHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPTQALPPLPSMPTSHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
QY 541 SMDDLASLKIPEQFRHAIWKGLDHRQHLHESFSSHLRTSSASTVSGSSETRGERYI 600
DB 541 SMDDLASLKIPEQFRHAIWKGLDHRQHLHESFSSHLRTSSASTVSGSSETRGERYI 600
QY 601 DAVRFTLRQTISSPPRDEMNFNDMARKNKQORKEE 641
DB 601 DAVRFTLRQTISSPPRDEMNFNDMARKNKQORKEE 641

RESULT 7
ABG95136
ID ABG95136 standard; Protein; 641 AA.
AC ABG95136;
DT 04-DEC-2002 (first entry)
DE Human oncogene p51 isoform Tap63alpha.
XX
XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX thadomyosarcoma; synovial sarcoma; viral infection.
XX
XX Homo sapiens.
XX
XX WO200269900-A2.
XX
XX 12-SEP-2002.
XX
XX 01-MAR-2002; 2002WO-US06518.
XX
XX 01-MAR-2001; 2001US-272751P.
XX
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX
XX Fritz LC, Burrows PJ;
XX
XX WPI; 2002-698710/75.
XX

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PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90
PT
PS Disclosure; Page 338-340; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock
XX protein (HSP)-90, or selectively treating cells expressing (II)
XX involving administering HSP90-inhibitor. The method is useful for
XX treating genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This is the amino acid sequence of a human oncogenic protein.
XX
XX Sequence 641 AA:
XX
XX Query Match 99.9%; Score 3401; DB 23; Length 641;
XX Best Local Similarity 99.8%; Pred. No. 5.1e-273;
XX Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSOSTQTNELFSPVFOHIMDFLEQPCISVQPIDLNFVDESESGATNKIEISMDCTIRMQ 60
DB 1 MSOSTQTNELFSPVFOHIMDFLEQPCISVQPIDLNFVDESESGATNKIEISMDCTIRMQ 60
QY 61 DSDLSDPWMPQYTNGLINSMDQOIQNGSSSTSYNTDHAQNSYTAAPSVPQSSSTDAL 120
DB 61 DSDLSDPWMPQYTNGLINSMDQOIQNGSSSTSYNTDHAQNSYTAAPSVPQSSSTDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
DB 121 SPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
QY 181 PGAVIRAMPYKKAHEVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 181 PGAVIRAMPYKKAHEVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITGRQSVLYPEPPVPGTEFTVLYNFMCNSSCVGMMRRPILITVLETRDGOYLGRRC 300
DB 241 ITGRQSVLYPEPPVPGTEFTVLYNFMCNSSCVGMMRRPILITVLETRDGOYLGRRC 300
QY 301 FEARICACPGDRKADSDIRKQOVSSTKNGDGTAKRPFRONTGCIOMTSIKRRSPDDE 360
DB 301 FEARICACPGDRKADSDIRKQOVSSTKNGDGTAKRPFRONTGCIOMTSIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLIKESLELMOYLPHQTIETTYRQOQOQHLLQKOTSIOSSPSY 420
DB 361 LLYLPVGRRETYEMLLIKESLELMOYLPHQTIETTYRQOQOQHLLQKOTSIOSSPSY 420
QY 421 GNSSPPLKNNMKNKLSVSOQLNPQORNALPTTIDGMCANIPMMGTHMPMAGDMNGL 480
DB 421 GNSSPPLKNNMKNKLSVSOQLNPQORNALPTTIDGMCANIPMMGTHMPMAGDMNGL 480
QY 481 SPTQALPPLPSMPTSHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPTQALPPLPSMPTSHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
QY 541 SMDDLASLKIPEQFRHAIWKGLDHRQHLHESFSSHLRTSSASTVSGSSETRGERYI 600
DB 541 SMDDLASLKIPEQFRHAIWKGLDHRQHLHESFSSHLRTSSASTVSGSSETRGERYI 600

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OY	601 DAVRFTLRQTSFPPDEWMDNPNMDARRKNOQRIKEEGE	641
Dd	601 DAVRFTLRQTSFPPDEWMDNPNMDARRKNOQRIKEEGE	641
RESULT 8		
ID	ABP61910 standard; Protein: 641 AA.	
XX	ABP61910;	
AC	ABP61910;	
XX	07-OCT-2002 (first entry)	
DT		
XX	Human lung cancer associated protein sequence SEQ ID NO:339.	
DE		
KM	Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.	
XX	Homo sapiens.	
OS		
PX	WO200247534-A2.	
PN		
PD	20-JUN-2002.	
XX		
PF	30-NOV-2001; 2001WO-US47576.	
PR	12-DEC-2000; 2000US-0735705.	
PR	07-MAY-2001; 2001US-0850716.	
XX	28-JUN-2001; 2001US-0897778.	
PA	(CORI-) CORIXA CORP.	
PI	Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA,	
PI	McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;	
PI	Catter D, Matanabe Y, Peckham DW, Cai F, Foy IW;	
XX	WI; 2002-583465/62.	
DR	N-PSDB; ABQ92433.	
PT		
PT	Novel lung carcinoma polynucleotide sequences and polypeptides encoded	
PT	by the polynucleotides, useful in pharmaceutical compositions such as	
XX	vaccines and as markers to indicate the presence of lung cancer	
XX		
XX	Example 2; Page 328-329; 381pp; English.	
CC	The present invention describes isolated human lung carcinoma	
CC	polynucleotides (I) and polypeptides (II). (I) and (II) have cytosstatic	
CC	activity, and can be used in gene therapy and in vaccines. Compositions	
CC	comprising (I) or (II) can be used for stimulating an immune response in	
CC	a patient and for treating lung cancer in a patient. Oligonucleotides of	
CC	(I) can be used for detecting the presence of a cancer in a patient, by	
CC	obtaining a biological sample from the patient, contacting the	
CC	biological sample with the oligonucleotide, detecting in the sample, an	
CC	amount of polynucleotide that hybridises to the oligonucleotide and	
CC	computing the amount of polynucleotide that hybridises to the	
CC	oligonucleotide to a predetermined cut-off value, and determining the	
CC	presence of a cancer in the patient. (I) and (II) are useful in	
CC	pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to	
CC	indicate the presence or absence of a cancer such as lung cancer.	
CC	ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used	
CC	in the exemplification of the present invention.	
XX		
SQ	Sequence 641 AA:	
Query Match	99.9%; Score 3401; DB 23; Length 641;	
Best Local Similarity	99.8%; Pred. No. 5.1e-273;	
Matches 640; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
OY	1 MSOSTGRNEFSPEYFOHIMPLEDPCISVOPIDLFNFDSESDATNKRTISMDCIRMO	60
Dd	1 MSOSTGRNEFSPEYFOHIMPLEDPCISVOPIDLFNFDSESDATNKRTISMDCIRMO	60
61	DSLDLSDPMWPQTYNLGLNSMDQOIQNGSSSTSPYNTHAONSVAAPSYAOPSSTFDAL	120

Db	61	DSLDSDPMPPQYTNIGLNSMDQQLONGSSSTSPYNTDAQNSVTPSPYAPQSSFTFDL	120
Qy	121	SPSPAIPSNSTDYPGHSHFDVSPFOQSSSTAKSATWTYSTELKYLCOIAKTCPIQIKWTPP	180
Db	121	SPSPAIPSNSTDYPGHSHFDVSPFOQSSSTAKSATWTYSTELKYLCOIAKTCPIQIKWTPP	180
Qy	181	POGAITRAMPYKKKEHTEYVKRCRNHELSNEFNEGQIAPSSHILRVGNSHAQVDEP	240
Db	181	POGAITRAMPYKKKEHTEYVKRCRNHELSNEFNEGQIAPSSHILRVGNSHAQVDEP	240
Qy	241	ITGRQSVLVPEPPOVGTETFTVLVYNFMCNSSCVCGMNRPLILIVTLETBDQOVLGRRC	300
Db	241	ITGRQSVLVPEPPOVGTETFTVLVYNFMCNSSCVCGMNRPLILIVTLETBDQOVLGRRC	300
Qy	301	FEARICACPGRDKRDEDSIRKQOYSDSTKNDDGTRKRPROMTHGIQMTSIRKRRSPDE	360
Db	301	FEARICACPGRDKRDEDSIRKQOYSDSTKNDDGTRKRPROMTHGIQMTSIRKRRSPDE	360
Qy	361	LLYLEPVRGRETEYEMLKIKESLELMQVLPQHTLETRYRQOQOOOHLLQKOTSIOGSSSY	420
Db	361	LLYLEPVRGRETEYEMLKIKESLELMQVLPQHTLETRYRQOQOOOHLLQKOTSIOGSSSY	420
Qy	421	GNSSPPLKMKNSMKNKLPSVSQILINPOQRNALPTPTIPDGMGANIPMGTHMPAGDMGL	480
Db	421	GNSSPPLKMKNSMKNKLPSVSQILINPOQRNALPTPTIPDGMGANIPMGTHMPAGDMGL	480
Qy	481	SPTQALPPLPMPSSTSHCTPPPPYPTDCISVGFRLARGSSCLDFTTGGITTYQIEHY	540
Db	481	SPTQALPPLPMPSSTSHCTPPPPYPTDCISVGFRLARGSSCLDFTTGGITTYQIEHY	540
Qy	541	SMDDLASLIKPEQGFHAIWKGIILDRQLHEFSSPSHLTPSSASTVSAGSSETRGERVY	600
Db	541	SMDDLASLIKPEQGFHAIWKGIILDRQLHEFSSPSHLTPSSASTVSAGSSETRGERVY	600
Qy	601	DAVRTTLRQTIISFPPEDEWDPNFPMDARRNMQQRKEGE	641
Db	601	DAVRTTLRQTIISFPPEDEWDPNFPMDARRNMQQRKEGE	641
RESULT 9			
ABBT4990			
ID	ABBT4990	standard; Protein; 641 AA.	
XX	AC	ABBT4990;	
XX	DT	01-MAY-2002 (first entry)	
XX	DE	Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:339.	
XX	XX	Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;	
XX	KW	Immune response.	
XX	OS	Homo sapiens.	
XX	PN	WO200200174-A2.	
XX	PD	03-JAN-2002.	
XX	PF	28-JUN-2001; 2001WO-US21065.	
XX	PR	28-JUN-2000; 2000US-0606421.	
XX	PR	02-AUG-2000; 2000US-0630940.	
XX	PR	21-AUG-2000; 2000US-0643597.	
XX	PR	15-SEP-2000; 2000US-0662786.	
XX	PR	09-OCT-2000; 2000US-0685696.	
XX	PR	12-DEC-2000; 2000US-0735705.	
XX	PR	07-MAY-2001; 2001US-0850716.	
XX	PA	(CORI-) CORIXA CORP.	
XX	XX	Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;	
PI	McNeill PD, Fanger N, Retter MW, Warnerakis M, Fanger GR;		

PI Vedic TS, Carter D, Watanabe Y, Peckham DW;
XX WPI, 2002-090513/12.
DR N-PSDB; ABL49247.
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX Example 2; Page 321-322; 374pp; English.
PS The present invention describes human lung tumor proteins. Human lung
XX tumor proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumor proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumor proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABL4946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention.
XX
XX Sequence 641 AA:
SQ
Query Match 99.9%; Score 3401; DB 23; Length 641;
Best Local Similarity 99.8%; Pred. No. 5.1e-273;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSOSTQTEHFLSPEVFOHIMFLEOPICSVOPIDINFYDEPSEDGATNKIEISMCIIMQ 60
DB 1 MSOSTQTEHFLSPEVFOHIMFLEOPICSVOPIDINFYDEPSEDGATNKIEISMCIIMQ 60
QY 61 DSDLSDPMPQYNTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSTPDAL 120
DB 61 DSDLSDPMPQYNTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSTPDAL 120
QY 121 SPSPAIPTNTDYPGHSFSDVSFOQSTAKSATWTSTELKIKLYCOIAKTCPIQIKVMP 180
DB 121 SPSPAIPTNTDYPGHSFSDVSFOQSTAKSATWTSTELKIKLYCOIAKTCPIQIKVMP 180
QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVDP 240
DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVDP 240
QY 241 ITGRSVLVYEPPEVGTETTVLYNFMCNSSCVGMMNRPLLIIVTLETGRGOVLGRRC 300
DB 241 ITGRSVLVYEPPEVGTETTVLYNFMCNSSCVGMMNRPLLIIVTLETGRGOVLGRRC 300
QY 301 FEARICACPRGRKADDESIKROQVSDSTKNGDGRPRRONTHTGIOMTSIKRRSPDE 360
DB 301 FEARICACPRGRKADDESIKROQVSDSTKNGDGRPRRONTHTGIOMTSIKRRSPDE 360
QY 361 LLYLVGRRETYEMLLIKESLELMQYLPHHTIETTYRQOOQOHOHLLOKOTSISPSY 420
DB 361 LLYLVGRRETYEMLLIKESLELMQYLPHHTIETTYRQOOQOHOHLLOKOTSISPSY 420
QY 421 GNSSPPLKKNMNNLPSVSQILNPOQRNALPTTIPDGMGNTIMKGTMMADMMGL 480
DB 421 GNSSPPLKKNMNNLPSVSQILNPOQRNALPTTIPDGMGNTIMKGTMMADMMGL 480
QY 481 SPTQALPPPLSMPSHCTPPPPYPTDCSIYFGLARLGSSCLDYFTTQGLTTIOIEHY 540
DB 481 SPTQALPPPLSMPSHCTPPPPYPTDCSIYFGLARLGSSCLDYFTTQGLTTIOIEHY 540
QY 541 SMDIASLAKIEQFRAHAIWKGLDHRQLHEFSSPSHLRLTPSSASTVSVGSSETERGY 600
DB 541 SMDIASLAKIEQFRAHAIWKGLDHRQLHEFSSPSHLRLTPSSASTVSVGSSETERGY 600
QY 601 DAVRFTLRQTSIFPRDEMDNFEMDARKKQOIKEGE 641
DB 601 DAVRFTLRQTSIFPRDEMDNFEMDARKKQOIKEGE 641
RESULT 10
AAB11361

ID AAB11361 standard; Protein; 680 AA.
XX AC AAB11361;
XX 21-FEB-2001 (first entry)
XX Human p63 protein isoform #5.
XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
XX vaccine; detection.
XX Homo sapiens.
XX WO20061612-A2.
XX 19-OCT-2000.
XX 03-APR-2000; 2000WO-US08896.
XX 02-APR-1999; 99US-0285479.
XX 17-DEC-1999; 99US-0466396.
XX 30-DEC-1999; 99US-0476496.
XX 10-JAN-2000; 2000US-0480884.
XX 22-FEB-2000; 2000US-0510376.
XX (CORI-) CORIXA CORP.
XX Wang T, Fan L;
XX WPI, 2000-628399/60.
XX N-PSDB; AAC66031.
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
XX protein is used for detecting and monitoring progression of lung cancer
XX in a patient -
XX Disclosure; Page 250-253; 261pp; English.
XX
XX This invention describes a novel isolated polypeptide (I) which
XX comprising an immunogenic portion of a lung tumor protein or variant (P2)
XX which have cytostatic activity. The polypeptides and polynucleotides are
XX used in compositions and vaccines to inhibit the development of cancer,
XX especially lung cancer, in a patient. Methods described in the invention
XX can be used to monitor the progression of a cancer by carrying out the
XX detection at subsequent time points and comparing the results from the
XX different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
XX are treated with P2, polynucleotides encoding P2 or antigen presenting
XX cells expressing P2 and then administered to the patient to inhibit
XX development of cancer.
XX
XX Sequence 680 AA:
SQ
Query Match 99.8%; Score 3397; DB 21; Length 680;
Best Local Similarity 99.8%; Pred. No. 1.2e-272;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSOSTQTEHFLSPEVFOHIMFLEOPICSVOPIDINFYDEPSEDGATNKIEISMCIIMQ 60
DB 1 MSOSTQTEHFLSPEVFOHIMFLEOPICSVOPIDINFYDEPSEDGATNKIEISMCIIMQ 60
QY 40 MSOSTQTEHFLSPEVFOHIMFLEOPICSVOPIDINFYDEPSEDGATNKIEISMCIIMQ 99
DB 40 MSOSTQTEHFLSPEVFOHIMFLEOPICSVOPIDINFYDEPSEDGATNKIEISMCIIMQ 99
QY 61 DSDLSDPMPQYNTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSTPDAL 120
DB 61 DSDLSDPMPQYNTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSTPDAL 120
QY 100 DSDLSDPMPQYNTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSTPDAL 159
DB 100 DSDLSDPMPQYNTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSTPDAL 159
QY 121 SPSPAIPTNTDYPGHSFSDVSFOQSTAKSATWTSTELKIKLYCOIAKTCPIQIKVMP 180
DB 121 SPSPAIPTNTDYPGHSFSDVSFOQSTAKSATWTSTELKIKLYCOIAKTCPIQIKVMP 180
QY 160 SPSPAIPTNTDYPGHSFSDVSFOQSTAKSATWTSTELKIKLYCOIAKTCPIQIKVMP 219
DB 160 SPSPAIPTNTDYPGHSFSDVSFOQSTAKSATWTSTELKIKLYCOIAKTCPIQIKVMP 219
QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVDP 240
DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVDP 240
QY 220 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVDP 279
DB 220 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVDP 279
QY 241 ITGRSVLVYEPPEVGTETTVLYNFMCNSSCVGMMNRPLLIIVTLETGRGOVLGRRC 300

```

DB      280  ITGRGSVLVYEPPOVGETFTTVLYNFMNCSVCVGAMNRRPILIIYTLERDQVIGRRC 339
QY      301  FEARICACGRDRKKADESDIRKQVSDSTRKNGCTRPFRONTHGIOMTSIKRRSPDDE 360
DB      340  FEARICACGRDRKKADESDIRKQVSDSTRKNGCTRPFRONTHGIOMTSIKRRSPDDE 399
QY      361  LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYROOQOOHQLKQTSIQSPSSY 420
DB      400  LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYROOQOOHQLKQTSIQSPSSY 459
QY      421  GNSSPPLNKMNSMKNKLPSVSQLINPOQRNALPTTIPDGMGANIPMGTHMPAGMNGI 480
DB      460  GNSSPPLNKMNSMKNKLPSVSQLINPOQRNALPTTIPDGMGANIPMGTHMPAGMNGI 519
QY      481  SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYTTGGLTTIYQIEHY 540
DB      520  SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYTTGGLTTIYQIEHY 579
QY      541  SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSVGSSSTRGERVY 600
DB      580  SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSVGSSSTRGERVY 639
QY      601  DAVRFTLRQTISEPPRDEWDFMDARNRKQORIKEGE 641
DB      640  DAVRFTLRQTISEPPRDEWDFMDARNRKQORIKEGE 680

```

RESULT 11

AA50997
ID AA50997 standard; Protein; 680 AA.

AA50997;

14-MAR-2000 (first entry)

Human KET protein.

KET; anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;
p53 family; angiogenic; cytotoxic; cancer; human.

Homo sapiens.

WO9961610-A2.

02-DEC-1999.

25-MAY-1999; 99WO-DE01557.

25-MAY-1998; 98DE-1022985.

(FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

Paul D, Augustin M, Schmale H, Bamberger C;

WPI: 2000-062710/05.

N-PSDB: AA43913.

New KET-encoding nucleic acid and related proteins, for diagnosis and
treatment of tumors

Claim 7; Page 26-28; 28pp; German.

This invention describes a novel KET-encoding nucleic acid (I) and its
fragments, variants and mutants which has anticancer activity. (I)
encodes a protein, (II), involved in control of the cell cycle and
apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the
p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to
detect (I) in biological samples, specifically angiogenic tumor tissue,
including (I) sequences that have a homozygotic deletion and (b) to
detect presence or absence of human chromosome 3q27 or murine chromosome
16, or their fragments, by hybridization. Also, (I) is used as a tumor
suppressor, particularly in tumors where an alteration in the wild-type

CC p53 allele has not been identified. (I) and (II) may also be used for
CC development of specific cytotoxic agents and for predicting the risk of
CC developing cancer. This sequence represents the human KET protein
CC described in the method of the invention.

SO Sequence 680 AA;

Query Match 99.88; Score 3397; DB 21; Length 680;
Best Local Similarity 99.88; Pred. No. 1,2e-272;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      1  MSQSTQNEELSPSEVEFOHIMDFLEQPICSVQPIDLNFVDEPSDGAATNKIEIMDCIRMO 60
DB      40  MSQSTQNEELSPSEVEFOHIMDFLEQPICSVQPIDLNFVDEPSDGAATNKIEIMDCIRMO 99
QY      61  DSDLSPPMFWQYTNGLLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPDSSTFDAL 120
DB      100  DSDLSPPMFWQYTNGLLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPDSSTFDAL 159
QY      121  SPSPALPSMTDYPGPHSFQVSPQSSSTAKSATWTYSTEKLKCYQIAKCPQIQKWTTP 180
DB      160  SPSPALPSMTDYPGPHSFQVSPQSSSTAKSATWTYSTEKLKCYQIAKCPQIQKWTTP 219
QY      181  PGGAIVRAMPVYKKAHEVTEVVKRCPNHLSREFNQGQIAPSHLIRVEGNSHAQYVEDP 240
DB      220  PGGAIVRAMPVYKKAHEVTEVVKRCPNHLSREFNQGQIAPSHLIRVEGNSHAQYVEDP 279
QY      241  ITGRGSVLVYEPPOVGETFTTVLYNFMNCSVCVGAMNRRPILIIYTLERDQVIGRRC 300
DB      280  ITGRGSVLVYEPPOVGETFTTVLYNFMNCSVCVGAMNRRPILIIYTLERDQVIGRRC 339
QY      301  FEARICACGRDRKKADESDIRKQVSDSTRKNGCTRPFRONTHGIOMTSIKRRSPDDE 360
DB      340  FEARICACGRDRKKADESDIRKQVSDSTRKNGCTRPFRONTHGIOMTSIKRRSPDDE 399
QY      361  LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYROOQOOHQLKQTSIQSPSSY 420
DB      400  LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYROOQOOHQLKQTSIQSPSSY 459
QY      421  GNSSPPLNKMNSMKNKLPSVSQLINPOQRNALPTTIPDGMGANIPMGTHMPAGMNGI 480
DB      460  GNSSPPLNKMNSMKNKLPSVSQLINPOQRNALPTTIPDGMGANIPMGTHMPAGMNGI 519
QY      481  SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYTTGGLTTIYQIEHY 540
DB      520  SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYTTGGLTTIYQIEHY 579
QY      541  SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSVGSSSTRGERVY 600
DB      580  SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSVGSSSTRGERVY 639
QY      601  DAVRFTLRQTISEPPRDEWDFMDARNRKQORIKEGE 641
DB      640  DAVRFTLRQTISEPPRDEWDFMDARNRKQORIKEGE 680

```

RESULT 12

ABP61913
ID ABP61913 standard; Protein; 680 AA.

ABP61913;

07-OCT-2002 (first entry)

Human lung cancer associated protein sequence SEQ ID NO:342.

Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.

Homo sapiens.

WO200247534-A2.

20-JUN-2002.


```

XX 30-NOV-2001: 2001WO-US47576.
PF
XX
PR 12-DEC-2000: 2000US-0735705.
PR 07-MAY-2001: 2001US-0850716.
PR 28-JUN-2001: 2001US-0897778.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
XX
DR WPI: 2002-583465/62.
DR N-PSDB: AB092436.
XX
PT Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT by the polynucleotides, useful in pharmaceutical compositions such as
PT vaccines and as markers to indicate the presence of lung cancer
XX
PS Example 2: Page 331-333; 381pp; English.
XX
CC The present invention describes isolated human lung carcinoma
CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC activity, and can be used in gene therapy and in vaccines. Compositions
CC comprising (I) or (II) can be used for stimulating an immune response in
CC a patient and for treating lung cancer in a patient. Oligonucleotides of
CC (I) can be used for detecting the presence of a cancer in a patient, by
CC obtaining a biological sample from the patient, contacting the
CC biological sample with the oligonucleotide, detecting in the sample, an
CC amount of polynucleotide that hybridises to the oligonucleotide and
CC comparing the amount of polynucleotide that hybridises to the
CC oligonucleotide to a predetermined cut-off value, and determining the
CC presence of a cancer in the patient. (I) and (II) are useful in
CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
CC indicate the presence or absence of a cancer such as lung cancer.
CC AB092145 to AB092486 and ABP61866 to ABP61992 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 680 AA:

```

```

QY 421 GNSPPLKMNKMSNKLPSVSQLINPQORNALPTTIPDGMANIPMGTHMPMAGDMNGL 480
DB 460 GNSPPLKMNKMSNKLPSVSQLINPQORNALPTTIPDGMANIPMGTHMPMAGDMNGL 519
QY 481 SPTQALPPLPLMSPSTSHCTPPPPYPTDCSYSLFARLCCSSLDYFTTQGLTTIQIEHY 540
DB 520 SPTQALPPLPLMSPSTSHCTPPPPYPTDCSYSLFARLCCSSLDYFTTQGLTTIQIEHY 579
QY 541 SMDDLASLKIPEQFHAHAIWKGLIDHROLHEFSSPSHLRTFSSASTVSAGSSETRGERVI 600
DB 580 SMDDLASLKIPEQFHAHAIWKGLIDHROLHEFSSPSHLRTFSSASTVSAGSSETRGERVI 639
QY 601 DAVFRTLQRTISFPPEDEWDFNFDMDARRNKQRIKEGE 641
DB 640 DAVFRTLQRTISFPPEDEWDFNFDMDARRNKQRIKEGE 680

RESULT 13
ABB74993
ID ABB74993 standard; Protein; 680 AA.
AC
XX ABB74993;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:342.
XX
KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW immune response.
XX
OS Homo sapiens.
XX
PN WO200200174-A2.
XX
PD 03-JAN-2002.
XX
PF 28-JUN-2001: 2001WO-US21065.
XX
PR 28-JUN-2000: 2000US-0606421.
PR 02-AUG-2000: 2000US-0630940.
PR 21-AUG-2000: 2000US-0643597.
PR 15-SEP-2000: 2000US-0662786.
PR 09-OCT-2000: 2000US-0685696.
PR 12-DEC-2000: 2000US-0735705.
PR 07-MAY-2001: 2001US-0850716.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX
DR WPI: 2002-090513/12.
DR N-PSDB: ABL49250.
XX
PT Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response
XX
PS Example 2: Page 324-326; 374pp; English.
XX
CC The present invention describes human lung tumor proteins. Human lung
CC tumor proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumor proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumor proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL4959 to ABL49300 and ABB74946 to
CC ABB75070 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 680 AA:

```

Query Match 99.8%; Score 3397; DB 23; Length 680;

Db 400 LLYLPRGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSMSQSSY 459
 Qy 421 GNSSEPLKNNMKNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMGL 480
 Db 460 GNSSEPLKNNMKNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMGL 519
 Qy 481 SPTQALPPLSMPSSTSHCTPPPPYPTDCSIYSFLARLCCSCLDYFTTQGLTTIYQIEHY 540
 Db 520 SPTQALPPLSMPSSTSHCTPPPPYPTDCSIYSFLARLCCSCLDYFTTQGLTTIYQIEHY 579
 Qy 541 SMDPLASLKIPQEFHAIWKGLDHRQLHDFSSPHLLRTPSGASTVSGSSETRGERVI 600
 Db 580 SMDPLASLKIPQEFHAIWKGLDHRQLHDFSSPHLLRTPSGASTVSGSSETRGERVI 639
 Qy 601 DAVRETLRQTLISFPPEDEMDNFEDMDARNNKQRIKEGE 641
 Db 640 DAVRETLRQTLISFPPEDEMDNFEDMDARNNKQRIKEGE 680

RESULT 15

AAV50998 ID AAV50998 standard; Protein; 680 AA.
 AC AAV50998;

DT 14-MAR-2000 (first entry)
 DE Rat KET protein.

KW KET: antitumor; cell cycle; apoptosis; tumor suppressor; p53 family;
 KM p53 family; angiogenic; cytotoxic; cancer; rat.

OS Rattus sp.

PN MO9961610-A2.

PD 02-DEC-1999.

PF 25-MAY-1999; 99WO-DE01557.

PR 25-MAY-1998; 98DE-1022985.

PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

PI Paul D, Augustin M, Schmale H, Bamberger C;

DR WPI: 2000-062710/05.

PT New KET-encoding nucleic acid and related proteins, for diagnosis and
 treatment of tumors

PS Disclosure; Fig 1; 28pp; German.

CC This invention describes a novel KET-encoding nucleic acid (I) and its
 fragments, variants and mutants which has antitumor activity. (I)
 encodes a protein, (II), involved in control of the cell cycle and
 apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the
 p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to
 detect (I) in biological samples, specifically angiogenic tumor tissue,
 including (I) sequences that have a homozygotic deletion and (b) to
 detect presence or absence of human chromosome 3q27 or murine chromosome
 16, or their fragments, by hybridization. Also, (I) is used as a tumor
 suppressor, particularly in tumors where an alteration in the wild-type
 p53 allele has not been identified. (I) and (II) may also be used for
 development of specific cytotoxic agents and for predicting the risk of
 developing cancer. This sequence represents the rat KET protein described
 in the method of the invention.

XX Sequence 680 AA;

Query Match 98.5%; Score 3353; DB 21; Length 680;
 Best Local Similarity 98.1%; Pred. No. 5.3e-269;
 Matches 629; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSQSTQINFLSPVEVQHIWDFLEOPICSVOPIDLNFDVDESEDAINKIEISMDCIHQ 60
 Db 40 MSQSTQINFLSPVEVQHIWDFLEOPICSVOPIDLNFDVDESEDAINKIEISMDCIHQ 99
 Qy 61 DSDLSDPMPQYTNGLNSMDQIQONSSSTSPNTHAQNSVTAPEPIQPSSTFAL 120
 Db 100 DSDLSDPMPQYTNGLNSMDQIQONSSSTSPNTHAQNSVTAPEPIQPSSTFAL 159
 Qy 121 SPSPAIPNTQYPGHSPDVSFOOSTKATWYSTELKLYCOIATCPQIKVMP 180
 Db 160 SPSPAIPNTQYPGHSPDVSFOOSTKATWYSTELKLYCOIATCPQIKVMP 219
 Qy 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQYEDP 240
 Db 220 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQYEDP 279
 Qy 241 ITGRQSVLVPEPPQVGEFTTLYLYNFCNSSCVGAMRRPILLIYLETBDGQVLRRC 300
 Db 280 ITGRQSVLVPEPPQVGEFTTLYLYNFCNSSCVGAMRRPILLIYLETBDGQVLRRC 339
 Qy 301 FEARICACPGDRKADSDSIRKQVSDSTKNKNGDGTKRPPRONTGICQTSIKRRSPDE 360
 Db 340 FEARICACPGDRKADSDSIRKQVSDSTKNKNGDGTKRPPRONTGICQTSIKRRSPDE 399
 Qy 361 LLYLPRGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSMSQSSY 420
 Db 400 LLYLPRGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSMSQSSY 459
 Qy 421 GNSSEPLKNNMKNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMGL 480
 Db 460 GNSSEPLKNNMKNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMGL 519
 Qy 481 SPTQALPPLSMPSSTSHCTPPPPYPTDCSIYSFLARLCCSCLDYFTTQGLTTIYQIEHY 540
 Db 520 SPTQALPPLSMPSSTSHCTPPPPYPTDCSIYSFLARLCCSCLDYFTTQGLTTIYQIEHY 579
 Qy 541 SMDPLASLKIPQEFHAIWKGLDHRQLHDFSSPHLLRTPSGASTVSGSSETRGERVI 600
 Db 580 SMDPLASLKIPQEFHAIWKGLDHRQLHDFSSPHLLRTPSGASTVSGSSETRGERVI 639
 Qy 601 DAVRETLRQTLISFPPEDEMDNFEDMDARNNKQRIKEGE 641
 Db 640 DAVRETLRQTLISFPPEDEMDNFEDMDARNNKQRIKEGE 680

Search completed: August 7, 2003, 09:46:21
 Job time : 46.2069 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:54 : Search time 17.6828 Seconds
(without alignments)
1533.769 Million cell updates/sec

Title: US-09-538-106-13

Perfect score: 3405

Sequence: 1 MSOSTQTNEFLSPVEFQHIV.....FNEDMDARRNKQRIKEGE 641

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
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6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3401	99.9	641	US-09-643-597-339	Sequence 339, App
2	3401	99.9	641	US-09-542-615A-339	Sequence 339, App
3	3401	99.9	641	US-09-606-421B-339	Sequence 339, App
4	3397	99.8	680	US-09-643-597-342	Sequence 342, App
5	3397	99.8	680	US-09-542-615A-342	Sequence 342, App
6	3397	99.8	680	US-09-606-421B-342	Sequence 342, App
7	3016	88.6	586	US-09-643-597-338	Sequence 338, App
8	3016	88.6	586	US-09-542-615A-338	Sequence 338, App
9	3016	88.6	586	US-09-606-421B-338	Sequence 338, App
10	3009	88.4	586	US-09-643-597-152	Sequence 152, App
11	3009	88.4	586	US-09-480-884A-152	Sequence 152, App
12	3009	88.4	586	US-09-542-615A-152	Sequence 152, App
13	3009	88.4	586	US-09-606-421B-152	Sequence 152, App
14	2722	79.9	516	US-09-643-597-344	Sequence 344, App
15	2722	79.9	516	US-09-542-615A-344	Sequence 344, App
16	2722	79.9	516	US-09-606-421B-344	Sequence 344, App
17	2350	69.0	461	US-09-643-597-343	Sequence 343, App
18	2350	69.0	461	US-09-542-615A-343	Sequence 343, App
19	2350	69.0	461	US-09-606-421B-343	Sequence 343, App
20	2222	65.3	426	US-09-277-196-19	Sequence 19, Appl
21	2185	64.2	448	US-09-643-597-340	Sequence 340, App
22	2185	64.2	448	US-09-542-615A-340	Sequence 340, App
23	2185	64.2	448	US-09-606-421B-340	Sequence 340, App
24	1801	52.9	356	US-09-643-597-341	Sequence 341, App
25	1801	52.9	356	US-09-277-196-2	Sequence 2, Appl
26	1801	52.9	356	US-09-542-615A-341	Sequence 341, App
27	1801	52.9	356	US-09-606-421B-341	Sequence 341, App

ALIGNMENTS

RESULT 1									
US-09-643-597-339									
Sequence 339, Application US/09643597									
Patent No. 6426072									
GENERAL INFORMATION:									
APPLICANT: Wang, Tonglong									
APPLICANT: Fan, Liqun									
APPLICANT: Kalos, Michael D.									
APPLICANT: Bangur, Chaitanya S.									
APPLICANT: Hosken, Nancy									
APPLICANT: Fanger, Gary R.									
APPLICANT: Li, Samuel X.									
APPLICANT: Wang, Yajun									
APPLICANT: Skeiky, Yasir A.W.									
APPLICANT: Henderson, Robert A.									
APPLICANT: McNeill, Patricia D.									
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY									
FILE REFERENCE: AND DIAGNOSIS OF LUNG CANCER									
CURRENT APPLICATION NUMBER: US/09/643,597									
CURRENT FILING DATE: 2000-08-21									
NUMBER OF SEQ ID NOS: 369									
SOFTWARE: FastSeq for Windows Version 3.0									
SEQ ID NO 339									
LENGTH: 641									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-09-643-597-339									
Query Match									
Best Local Similarity 99.9%; Score 3401; DB 4; Length 641;									
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	1	MSOSTQTNEFLSPVEFQHIVDFEOPICSVQPIDLNFVDEPSDGAATNKLEIMDCIRMG	60						
DB	1	MSOSTQTNEFLSPVEFQHIVDFEOPICSVQPIDLNFVDEPSDGAATNKLEIMDCIRMG	60						
QY	61	DSLSLSPMMQYVNLILNSMDQIQNGSSSTPYNTDHAQNSVTAAPSPAPQSSSTFDAL	120						
DB	61	DSLSLSPMMQYVNLILNSMDQIQNGSSSTPYNTDHAQNSVTAAPSPAPQSSSTFDAL	120						
QY	121	SPSPALPSNTDYGPSPFDVSPFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKWTPP	180						
DB	121	SPSPALPSNTDYGPSPFDVSPFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKWTPP	180						
QY	181	PGCAVIRAMPVYKKAHVYVRCRPNHLSREFNGQIAPSHLIRVBSNSAOVVEOP	240						
DB	181	PGCAVIRAMPVYKKAHVYVRCRPNHLSREFNGQIAPSHLIRVBSNSAOVVEOP	240						
QY	241	ITRGQSVLYPEPPQVGTETFTVLYNFMNCSGVGMNRRLIIVTLERDQVYLGRRRC	300						
DB	241	ITRGQSVLYPEPPQVGTETFTVLYNFMNCSGVGMNRRLIIVTLERDQVYLGRRRC	300						

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Db 241 ITGRQSVLVPYPPVGGTEFTVLNFMKNSSCVGMNRPILLIVTLETGRGOYLGRRC 300
OY 301 FEARICACGRRKRDDEDSIRKQOYSDSTKNKGDTKRPRRONTGHIOMTSIKRRSPDDE 360
Db 301 FEARICACGRRKRDDEDSIRKQOYSDSTKNKGDTKRPRRONTGHIOMTSIKRRSPDDE 360
OY 361 LLYLVPRGRETEYEMLLIKESLELMQYLPQHTIETRYROOOOHOHLLQKOTSISPSY 420
Db 361 LLYLVPRGRETEYEMLLIKESLELMQYLPQHTIETRYROOOOHOHLLQKOTSISPSY 420
OY 421 GNSSPPLKMNMSNKLPSVQLINPQORNALPTTIPGKGANITPMGTHMPMAGDMNGL 480
Db 421 GNSSPPLKMNMSNKLPSVQLINPQORNALPTTIPGKGANITPMGTHMPMAGDMNGL 480
OY 481 SPTQALPPLSMPSHCTPPPPYPTDCSIVSFARLGSSCLDYFTTQGLTTIYQIEHY 540
Db 481 SPTQALPPLSMPSHCTPPPPYPTDCSIVSFARLGSSCLDYFTTQGLTTIYQIEHY 540
OY 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHESSPSHLLRTPSASTVSIGSSETGERVI 600
Db 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHESSPSHLLRTPSASTVSIGSSETGERVI 600
OY 601 DAVRETLROTISFPPEDEMDNPFMDARNRKQRIKEGE 641
Db 601 DAVRETLROTISFPPEDEMDNPFMDARNRKQRIKEGE 641
```

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RESULT 2
US-09-542-615A-339
; Sequence 339, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-339
```

```
Query Match 99.9%; Score 3401; DB 4; Length 641;
Best Local Similarity 99.8%; Pred. No. 2.9e-304;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 MSQSTQNEFLSPEYFOHIMDFLEOPICSVOPIDINFVDESEDAATKIEISMDCIRMQ 60
Db 1 MSQSTQNEFLSPEYFOHIMDFLEOPICSVOPIDINFVDESEDAATKIEISMDCIRMQ 60
OY 61 DSDLSDPMPQYTNGLINSMDOQIONGSSSTSPYNTHAQNSVAPSPYQOPSSTFAL 120
Db 61 DSDLSDPMPQYTNGLINSMDOQIONGSSSTSPYNTHAQNSVAPSPYQOPSSTFAL 120
OY 121 SPSPAIPESTNDYPGHSHFDVSFOQSSSTAKSATWTYSTELKLYCOIACTCPQIKVMTP 180
Db 121 SPSPAIPESTNDYPGHSHFDVSFOQSSSTAKSATWTYSTELKLYCOIACTCPQIKVMTP 180
OY 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQYVDP 240
Db 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQYVDP 240
OY 241 ITGQSVLVPYPPVGGTEFTVLNFMKNSSCVGMNRPILLIVTLETGRGOYLGRRC 300
```

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Db 241 ITGRQSVLVPYPPVGGTEFTVLNFMKNSSCVGMNRPILLIVTLETGRGOYLGRRC 300
OY 301 FEARICACGRRKRDDEDSIRKQOYSDSTKNKGDTKRPRRONTGHIOMTSIKRRSPDDE 360
Db 301 FEARICACGRRKRDDEDSIRKQOYSDSTKNKGDTKRPRRONTGHIOMTSIKRRSPDDE 360
OY 361 LLYLVPRGRETEYEMLLIKESLELMQYLPQHTIETRYROOOOHOHLLQKOTSISPSY 420
Db 361 LLYLVPRGRETEYEMLLIKESLELMQYLPQHTIETRYROOOOHOHLLQKOTSISPSY 420
OY 421 GNSSPPLKMNMSNKLPSVQLINPQORNALPTTIPGKGANITPMGTHMPMAGDMNGL 480
Db 421 GNSSPPLKMNMSNKLPSVQLINPQORNALPTTIPGKGANITPMGTHMPMAGDMNGL 480
OY 481 SPTQALPPLSMPSHCTPPPPYPTDCSIVSFARLGSSCLDYFTTQGLTTIYQIEHY 540
Db 481 SPTQALPPLSMPSHCTPPPPYPTDCSIVSFARLGSSCLDYFTTQGLTTIYQIEHY 540
OY 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHESSPSHLLRTPSASTVSIGSSETGERVI 600
Db 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHESSPSHLLRTPSASTVSIGSSETGERVI 600
OY 601 DAVRETLROTISFPPEDEMDNPFMDARNRKQRIKEGE 641
Db 601 DAVRETLROTISFPPEDEMDNPFMDARNRKQRIKEGE 641
```

```
RESULT 3
US-09-606-421B-339
; Sequence 339, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-339
```

```
Query Match 99.9%; Score 3401; DB 4; Length 641;
Best Local Similarity 99.8%; Pred. No. 2.9e-304;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 MSQSTQNEFLSPEYFOHIMDFLEOPICSVOPIDINFVDESEDAATKIEISMDCIRMQ 60
Db 1 MSQSTQNEFLSPEYFOHIMDFLEOPICSVOPIDINFVDESEDAATKIEISMDCIRMQ 60
OY 61 DSDLSDPMPQYTNGLINSMDOQIONGSSSTSPYNTHAQNSVAPSPYQOPSSTFAL 120
Db 61 DSDLSDPMPQYTNGLINSMDOQIONGSSSTSPYNTHAQNSVAPSPYQOPSSTFAL 120
OY 121 SPSPAIPESTNDYPGHSHFDVSFOQSSSTAKSATWTYSTELKLYCOIACTCPQIKVMTP 180
Db 121 SPSPAIPESTNDYPGHSHFDVSFOQSSSTAKSATWTYSTELKLYCOIACTCPQIKVMTP 180
OY 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQYVDP 240
Db 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQYVDP 240
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Db 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGQIAPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSVLVYEPPOVGTETFTVLYNFMCNSSCVGGMNRPILIIYTLERDQOYIGRRC 300
Db 241 ITGROSVLVYEPPOVGTETFTVLYNFMCNSSCVGGMNRPILIIYTLERDQOYIGRRC 300
QY 301 FEARICACPRDRKKADEDSIRKQOVSSTKNGDGTFRPFQNTNGIOMTSIKRRSPDDE 360
Db 301 FEARICACPRDRKKADEDSIRKQOVSSTKNGDGTFRPFQNTNGIOMTSIKRRSPDDE 360
QY 361 LLYLVRGRETYEMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSIOSSSY 420
Db 361 LLYLVRGRETYEMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSIOSSSY 420
QY 421 GNSSPPLNKMNSMKNKLPVSQILNPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGL 480
Db 421 GNSSPPLNKMNSMKNKLPVSQILNPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGL 480
QY 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTIYQIEHY 540
Db 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTIYQIEHY 540
QY 541 SMDDLASLKIPEQFRHAIWKGLIDHRLHEFSSPSHLRTPSSASTVSVSSSETRGERVI 600
Db 541 SMDDLASLKIPEQFRHAIWKGLIDHRLHEFSSPSHLRTPSSASTVSVSSSETRGERVI 600
QY 601 DAVFTLROTISPPRDENMFNDMDARANKOORKEGE 641
Db 601 DAVFTLROTISPPRDENMFNDMDARANKOORKEGE 641

RESULT 4
US-09-643-597-342
; Sequence 342; Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-643-597-342

Query Match 99.8%; Score 3397; DB 4; Length 680;
Best local similarity 99.8%; Pred. No. 7.4e-304;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTQTNELFSEVFOHIMDFLEQIPICSVQPIDLNFVDEPSEDEGATNKIEISMDCIRMQ 60
Db 40 MSOSTQTNELFSEVFOHIMDFLEQIPICSVQPIDLNFVDEPSEDEGATNKIEISMDCIRMQ 99
QY 61 DSDLSPPMPOYNTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQSSSTFDAL 120
Db 100 DSDLSPPMPOYNTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQSSSTFDAL 159
QY 121 SPSPALPSNTDYGPHSFVDSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTTP 180

Db 160 SPSPALPSNTDYGPHSFVDSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTTP 219
QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGQIAPSHLIRVEGNSHAQYVEDP 240
Db 220 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGQIAPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGROSVLVYEPPOVGTETFTVLYNFMCNSSCVGGMNRPILIIYTLERDQOYIGRRC 300
Db 280 ITGROSVLVYEPPOVGTETFTVLYNFMCNSSCVGGMNRPILIIYTLERDQOYIGRRC 339
QY 301 FEARICACPRDRKKADEDSIRKQOVSSTKNGDGTFRPFQNTNGIOMTSIKRRSPDDE 360
Db 340 FEARICACPRDRKKADEDSIRKQOVSSTKNGDGTFRPFQNTNGIOMTSIKRRSPDDE 399
QY 361 LLYLVRGRETYEMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSIOSSSY 420
Db 400 LLYLVRGRETYEMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSIOSSSY 459
QY 421 GNSSPPLNKMNSMKNKLPVSQILNPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGL 480
Db 460 GNSSPPLNKMNSMKNKLPVSQILNPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGL 519
QY 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTIYQIEHY 540
Db 520 SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTIYQIEHY 579
QY 541 SMDDLASLKIPEQFRHAIWKGLIDHRLHEFSSPSHLRTPSSASTVSVSSSETRGERVI 600
Db 580 SMDDLASLKIPEQFRHAIWKGLIDHRLHEFSSPSHLRTPSSASTVSVSSSETRGERVI 639
QY 601 DAVFTLROTISPPRDENMFNDMDARANKOORKEGE 641
Db 640 DAVFTLROTISPPRDENMFNDMDARANKOORKEGE 680

RESULT 5
US-09-542-615A-342
; Sequence 342; Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-542-615A-342

Query Match 99.8%; Score 3397; DB 4; Length 680;
Best local similarity 99.8%; Pred. No. 7.4e-304;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTQTNELFSEVFOHIMDFLEQIPICSVQPIDLNFVDEPSEDEGATNKIEISMDCIRMQ 60
Db 40 MSOSTQTNELFSEVFOHIMDFLEQIPICSVQPIDLNFVDEPSEDEGATNKIEISMDCIRMQ 99
QY 61 DSDLSPPMPOYNTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQSSSTFDAL 120
Db 100 DSDLSPPMPOYNTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQSSSTFDAL 159
QY 121 SPSPALPSNTDYGPHSFVDSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTTP 180

Db 160 SPSPAIPISTNTDYPGSHSDVSPFOOSSTAKSATWTSTELKLYCOIATCPLOIIVMTMP 219
OY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOLAPPSHLIRVEGNSHAQYVBDP 240
Db 220 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOLAPPSHLIRVEGNSHAQYVBDP 279
OY 241 ITGRQSVLVPEPPVGTETFTVLVNFMCNSSCVGMMRRPILLIIVTLETBDGVLGRRC 300
Db 280 ITGRQSVLVPEPPVGTETFTVLVNFMCNSSCVGMMRRPILLIIVTLETBDGVLGRRC 339
OY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDKRFRONTHTGIOMTSIKRRSPDDE 360
Db 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDKRFRONTHTGIOMTSIKRRSPDDE 399
OY 361 LLYLVRGRRETYEMLLKIKESLELMQYLPQHTIETTYRQOQOQHLLQKOTSIOSSPSY 420
Db 400 LLYLVRGRRETYEMLLKIKESLELMQYLPQHTIETTYRQOQOQHLLQKOTSIOSSPSY 459
OY 421 GNSSPPLKMSMNKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
Db 460 GNSSPPLKMSMNKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 519
OY 481 SPTQALPPPLSMPSISGCTPPPPYPTDCSIVSFLARLCCSCLDYFTTQGLTTIYQIEHY 540
Db 520 SPTQALPPPLSMPSISGCTPPPPYPTDCSIVSFLARLCCSCLDYFTTQGLTTIYQIEHY 579
OY 541 SMDDLASLKIPQGFHAIWKGLDHRQLHEFSSPSHLRTPSASTVSGSSETGERVI 600
Db 580 SMDDLASLKIPQGFHAIWKGLDHRQLHEFSSPSHLRTPSASTVSGSSETGERVI 639
OY 601 DAVRETLRQTIISFPPEDEWDFNFDMDARRNKQRIKEGE 641
Db 640 DAVRETLRQTIISFPPEDEWDFNFDMDARRNKQRIKEGE 680

RESULT 6
US-09-606-421B-342
; Sequence 342, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Baogur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-342

Query Match 99.8%; Score 3397; DB 4; Length 680;
Best Local Similarity 99.8%; Pred. No. 7,4e-304;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSQSTQTNELSPVEYFOHIMDFLEQPICSVQPIDINFEVDESEDAATNKIEISMDCIRMQ 60
Db 40 MSQSTQTNELSPVEYFOHIMDFLEQPICSVQPIDINFEVDESEDAATNKIEISMDCIRMQ 99
OY 61 DSDLDPMWPOYTNGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL 120

Db 100 DSDLDPMWPOYTNGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL 159
OY 121 SPSPAIPISTNTDYPGSHSDVSPFOOSSTAKSATWTSTELKLYCOIATCPLOIIVMTMP 180
Db 160 SPSPAIPISTNTDYPGSHSDVSPFOOSSTAKSATWTSTELKLYCOIATCPLOIIVMTMP 219
OY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOLAPPSHLIRVEGNSHAQYVBDP 240
Db 220 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOLAPPSHLIRVEGNSHAQYVBDP 279
OY 241 ITGRQSVLVPEPPVGTETFTVLVNFMCNSSCVGMMRRPILLIIVTLETBDGVLGRRC 300
Db 280 ITGRQSVLVPEPPVGTETFTVLVNFMCNSSCVGMMRRPILLIIVTLETBDGVLGRRC 339
OY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDKRFRONTHTGIOMTSIKRRSPDDE 360
Db 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDKRFRONTHTGIOMTSIKRRSPDDE 399
OY 361 LLYLVRGRRETYEMLLKIKESLELMQYLPQHTIETTYRQOQOQHLLQKOTSIOSSPSY 420
Db 400 LLYLVRGRRETYEMLLKIKESLELMQYLPQHTIETTYRQOQOQHLLQKOTSIOSSPSY 459
OY 421 GNSSPPLKMSMNKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
Db 460 GNSSPPLKMSMNKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 519
OY 481 SPTQALPPPLSMPSISGCTPPPPYPTDCSIVSFLARLCCSCLDYFTTQGLTTIYQIEHY 540
Db 520 SPTQALPPPLSMPSISGCTPPPPYPTDCSIVSFLARLCCSCLDYFTTQGLTTIYQIEHY 579
OY 541 SMDDLASLKIPQGFHAIWKGLDHRQLHEFSSPSHLRTPSASTVSGSSETGERVI 600
Db 580 SMDDLASLKIPQGFHAIWKGLDHRQLHEFSSPSHLRTPSASTVSGSSETGERVI 639
OY 601 DAVRETLRQTIISFPPEDEWDFNFDMDARRNKQRIKEGE 641
Db 640 DAVRETLRQTIISFPPEDEWDFNFDMDARRNKQRIKEGE 680

RESULT 7
US-09-643-597-338
; Sequence 338, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Baogur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-338

Query Match 88.6%; Score 3016; DB 4; Length 586;
Best Local Similarity 99.5%; Pred. No. 6,9e-269;
Matches 569; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 70 POYTNGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDALSPSPAIPISN 129

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Db 15 PNTNGLNSMDQOIRNGSSSTSPYNTDHAQNSVTAAPSPYAOPTFDALSPSPAIPSN 74
QY 130 TDYGPSPDVSFOOSSTAKSATWTYSTELKRLKYLCOIAKTCPIQIKVMTPPPOGAVIRAM 189
Db 75 TDYGPSPDVSFOOSSTAKSATWTYSTELKRLKYLCOIAKTCPIQIKVMTPPPOGAVIRAM 134
QY 190 PYKKAHEHTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
Db 135 PYKKAHEHTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGEFTTLYNFMCNSSCVGGMNRPLILIVTLETRDGOVLGRRCFEARICACP 309
Db 195 PYEPPOVGEFTTLYNFMCNSSCVGGMNRPLILIVTLETRDGOVLGRRCFEARICACP 254
QY 310 GDRKADSDSIRKQOVSSTKNGDKTRPFRONTGHIOMTSIKRRSPDDELLYLPRGR 369
Db 255 GDRKADSDSIRKQOVSSTKNGDKTRPFRONTGHIOMTSIKRRSPDDELLYLPRGR 314
QY 370 EYEMMLKIKESLELMQYLPQHTIETYROOQOOHQHLLQKOTSISPSYSGNSPPLNK 429
Db 315 EYEMMLKIKESLELMQYLPQHTIETYROOQOOHQHLLQKOTSISPSYSGNSPPLNK 374
QY 430 NMSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
Db 375 NMSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
QY 490 LSMPTSHCTPPPPPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 549
Db 435 LSMPTSHCTPPPPPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
QY 550 IPEQFRHAIWKGLDHRQLHEFSSPHLRTSPSASTVSAGSETERGERVIDAVRFTLQ 609
Db 495 IPEQFRHAIWKGLDHRQLHEFSSPHLRTSPSASTVSAGSETERGERVIDAVRFTLQ 554
QY 610 TISFPRDEMDNFMDARRNKQORIKEGE 641
Db 555 TISFPRDEMDNFMDARRNKQORIKEGE 586

RESULT 8
US-09-542-615A-338
: Sequence 338, Application US/09542615A
: Patent No. 6518256
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C8
: CURRENT APPLICATION NUMBER: US/09/542,615A
: CURRENT FILING DATE: 2000-04-14
: NUMBER OF SEQ ID NOS: 350
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 338
: LENGTH: 586
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-542-615A-338

Query Match 88.6%; Score 3016; DB 4; Length 586;
Best Local Similarity 99.5%; Pred. No. 6,9e-269;
Matches 569; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

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|||||
Db 75 TDYGPSPDVSFOOSSTAKSATWTYSTELKRLKYLCOIAKTCPIQIKVMTPPPOGAVIRAM 134
QY 190 PYKKAHEHTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
Db 135 PYKKAHEHTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGEFTTLYNFMCNSSCVGGMNRPLILIVTLETRDGOVLGRRCFEARICACP 309
Db 195 PYEPPOVGEFTTLYNFMCNSSCVGGMNRPLILIVTLETRDGOVLGRRCFEARICACP 254
QY 310 GDRKADSDSIRKQOVSSTKNGDKTRPFRONTGHIOMTSIKRRSPDDELLYLPRGR 369
Db 255 GDRKADSDSIRKQOVSSTKNGDKTRPFRONTGHIOMTSIKRRSPDDELLYLPRGR 314
QY 370 EYEMMLKIKESLELMQYLPQHTIETYROOQOOHQHLLQKOTSISPSYSGNSPPLNK 429
Db 315 EYEMMLKIKESLELMQYLPQHTIETYROOQOOHQHLLQKOTSISPSYSGNSPPLNK 374
QY 430 NMSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
Db 375 NMSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
QY 490 LSMPTSHCTPPPPPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 549
Db 435 LSMPTSHCTPPPPPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
QY 550 IPEQFRHAIWKGLDHRQLHEFSSPHLRTSPSASTVSAGSETERGERVIDAVRFTLQ 609
Db 495 IPEQFRHAIWKGLDHRQLHEFSSPHLRTSPSASTVSAGSETERGERVIDAVRFTLQ 554
QY 610 TISFPRDEMDNFMDARRNKQORIKEGE 641
Db 555 TISFPRDEMDNFMDARRNKQORIKEGE 586

RESULT 9
US-09-606-421B-338
: Sequence 338, Application US/09606421B
: Patent No. 6531315
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Wang, Aijun
: APPLICANT: Li, Samuel X.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C9
: CURRENT APPLICATION NUMBER: US/09/606,421B
: CURRENT FILING DATE: 2000-06-28
: NUMBER OF SEQ ID NOS: 358
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 338
: LENGTH: 586
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-606-421B-338

Query Match 88.6%; Score 3016; DB 4; Length 586;
Best Local Similarity 99.5%; Pred. No. 6,9e-269;
Matches 569; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```



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Db 75 TDYGPBHSFVDSFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVTPPGQAVIRAM 134
Qy 190 PYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPTTGROSLV 249
Db 135 PYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPTTGROSLV 194
Qy 250 PYEPVOGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOVLGRCFEARIACAP 309
Db 195 PYEPVOGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOVLGRCFEARIACAP 254
Qy 310 GRDRKADSDIRKQOVSSTKNGDGTAKPPFRONTHGICOMTSIKRRSPDDELIVLPVGR 369
Db 255 GRDRKADSDIRKQOVSSTKNGDGTAKPPFRONTHGICOMTSIKRRSPDDELIVLPVGR 314
Qy 370 EYEMLVKIKESLELMOYLPOHTIETRYQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 EYEMLVKIKESLELMOYLPOHTIETRYQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Qy 430 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPP 489
Db 375 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPP 434
Qy 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGSCCLDYFTTQGLTITTYQIEHYSMDLASK 549
Db 435 LSMSTSHCTPPPPYPTDCSIVSFLARLGSCCLDYFTTQGLTITTYQIEHYSMDLASK 494
Qy 550 IPEOFRAIMKGIIDHROLHEFSSPSHLRTPPSSASTVSSETRGERVIDAVFTLRQ 609
Db 495 IPEOFRAIMKGIIDHROLHEFSSPSHLRTPPSSASTVSSETRGERVIDAVFTLRQ 554
Qy 610 TISEPPRDEWDFNFMMDARRNKOORKEGE 641
Db 555 TISEPPRDEWDFNFMMDARRNKOORKEGE 586
```

```
RESULT 10
US-09-643-597-152
; Sequence 152, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-643-597-152
```

```
Query Match 88.4%; Score 3009; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-268;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 70 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDALSPSPALPSN 129
Db 15 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDALSPSPALPSN 74
Qy 130 TDYGPBHSFVDSFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVTPPGQAVIRAM 189
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Db 75 TDYGPBHSFVDSFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVTPPGQAVIRAM 134
Qy 190 PYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPTTGROSLV 249
Db 135 PYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPTTGROSLV 194
Qy 250 PYEPVOGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOVLGRCFEARIACAP 309
Db 195 PYEPVOGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOVLGRCFEARIACAP 254
Qy 310 GRDRKADSDIRKQOVSSTKNGDGTAKPPFRONTHGICOMTSIKRRSPDDELIVLPVGR 369
Db 255 GRDRKADSDIRKQOVSSTKNGDGTAKPPFRONTHGICOMTSIKRRSPDDELIVLPVGR 314
Qy 370 EYEMLVKIKESLELMOYLPOHTIETRYQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 EYEMLVKIKESLELMOYLPOHTIETRYQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Qy 430 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPP 489
Db 375 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPP 434
Qy 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGSCCLDYFTTQGLTITTYQIEHYSMDLASK 549
Db 435 LSMSTSHCTPPPPYPTDCSIVSFLARLGSCCLDYFTTQGLTITTYQIEHYSMDLASK 494
Qy 550 IPEOFRAIMKGIIDHROLHEFSSPSHLRTPPSSASTVSSETRGERVIDAVFTLRQ 609
Db 495 IPEOFRAIMKGIIDHROLHEFSSPSHLRTPPSSASTVSSETRGERVIDAVFTLRQ 554
Qy 610 TISEPPRDEWDFNFMMDARRNKOORKEGE 641
Db 555 TISEPPRDEWDFNFMMDARRNKOORKEGE 586
```

```
RESULT 11
US-09-480-884A-152
; Sequence 152, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480.884A
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-480-884A-152
```

```
Query Match 88.4%; Score 3009; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-268;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Qy 70 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDALSPSPALPSN 129
Db 15 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDALSPSPALPSN 74
Qy 130 TDYGPBHSFVDSFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVTPPGQAVIRAM 189
Db 75 TDYGPBHSFVDSFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVTPPGQAVIRAM 134
Qy 190 PYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPTTGROSLV 249
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```

Db      135  PYKKAHEVTEVVKRCPNHELSEFNEGOIAPSSHLIRVEGNSHAQYVEDPITGRQSVLY 194
QY      250  PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIYVLETRDGOVYLGRRCFEARIACAP 309
Db      195  PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIYVLETRDGOVYLGRRCFEARIACAP 254
QY      310  GDRKRADEDSIRKQOVSSTKNGDGTRKPRRONTHTGIOMTSIKRRSPDELLYLPRGR 369
Db      255  GDRKRADEDSIRKQOVSSTKNGDGTRKPRRONTHTGIOMTSIKRRSPDELLYLPRGR 314
QY      370  EYEMILKIKESLELMQYLPQHTIERYRQOQOQHLLQKOTSIOSSPSYGNSSPPLNK 429
Db      315  EYEMILKIKESLELMQYLPQHTIERYRQOQOQHLLQKOTSIOSSPSYGNSSPPLNK 374
QY      430  MNSMKNLPVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
Db      375  MNSMKNLPVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
QY      490  LSMPTSHCTPPPPYPTDCSIVFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 549
Db      435  LSMPTSHCTPPPPYPTDCSIVFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
QY      550  IPEQFHAIWKGLIDHROLHEFSSPSHLRTPSASTSVSGSSETRGERVIDAVRFTLRQ 609
Db      495  IPEQFHAIWKGLIDHROLHEFSSPSHLRTPSASTSVSGSSETRGERVIDAVRFTLRQ 554
QY      610  TISFPPRDEWDFNFDMDARRNKQORIKEGE 641
Db      555  TISFPPRDEWDFNFDMDARRNKQORIKEGE 586

```

RESULT 12
US-09-542-615A-152
Sequence 152, Application US/09542615A
Patent No. 6518256

```

GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-542-615A-152

```

Query Match 88.4%; Score 3009; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-268;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

QY      70  PQTNLGLINSDMOQIIONGSSSTSPYNTDHAQNSVTAAPSYPAPSSSTFDALSPSPAIPSN 129
Db      15  PQTNLGLINSDMOQIIONGSSSTSPYNTDHAQNSVTAAPSYPAPSSSTFDALSPSPAIPSN 74
QY      130  TDYPGHSDVDFSOOSSTAKSATWTYSTELKLYCOIATCPQIKVMPPPGAVIRAM 189
Db      75  TDYPGHSDVDFSOOSSTAKSATWTYSTELKLYCOIATCPQIKVMPPPGAVIRAM 134
QY      190  PYKKAHEVTEVVKRCPNHELSEFNEGOIAPSSHLIRVEGNSHAQYVEDPITGRQSVLY 249
Db      135  PYKKAHEVTEVVKRCPNHELSEFNEGOIAPSSHLIRVEGNSHAQYVEDPITGRQSVLY 194
QY      250  PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIYVLETRDGOVYLGRRCFEARIACAP 309

```

```

Db      195  PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIYVLETRDGOVYLGRRCFEARIACAP 254
QY      310  GDRKRADEDSIRKQOVSSTKNGDGTRKPRRONTHTGIOMTSIKRRSPDELLYLPRGR 369
Db      255  GDRKRADEDSIRKQOVSSTKNGDGTRKPRRONTHTGIOMTSIKRRSPDELLYLPRGR 314
QY      370  EYEMILKIKESLELMQYLPQHTIERYRQOQOQHLLQKOTSIOSSPSYGNSSPPLNK 429
Db      315  EYEMILKIKESLELMQYLPQHTIERYRQOQOQHLLQKOTSIOSSPSYGNSSPPLNK 374
QY      430  MNSMKNLPVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
Db      375  MNSMKNLPVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
QY      490  LSMPTSHCTPPPPYPTDCSIVFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 549
Db      435  LSMPTSHCTPPPPYPTDCSIVFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
QY      550  IPEQFHAIWKGLIDHROLHEFSSPSHLRTPSASTSVSGSSETRGERVIDAVRFTLRQ 609
Db      495  IPEQFHAIWKGLIDHROLHEFSSPSHLRTPSASTSVSGSSETRGERVIDAVRFTLRQ 554
QY      610  TISFPPRDEWDFNFDMDARRNKQORIKEGE 641
Db      555  TISFPPRDEWDFNFDMDARRNKQORIKEGE 586

```

RESULT 13
US-09-606-421B-152
Sequence 152, Application US/09606421B
Patent No. 6531315

```

GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-606-421B-152

```

Query Match 88.4%; Score 3009; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-268;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

QY      70  PQTNLGLINSDMOQIIONGSSSTSPYNTDHAQNSVTAAPSYPAPSSSTFDALSPSPAIPSN 129
Db      15  PQTNLGLINSDMOQIIONGSSSTSPYNTDHAQNSVTAAPSYPAPSSSTFDALSPSPAIPSN 74
QY      130  TDYPGHSDVDFSOOSSTAKSATWTYSTELKLYCOIATCPQIKVMPPPGAVIRAM 189
Db      75  TDYPGHSDVDFSOOSSTAKSATWTYSTELKLYCOIATCPQIKVMPPPGAVIRAM 134
QY      190  PYKKAHEVTEVVKRCPNHELSEFNEGOIAPSSHLIRVEGNSHAQYVEDPITGRQSVLY 249
Db      135  PYKKAHEVTEVVKRCPNHELSEFNEGOIAPSSHLIRVEGNSHAQYVEDPITGRQSVLY 194
QY      250  PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIYVLETRDGOVYLGRRCFEARIACAP 309
Db      195  PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIYVLETRDGOVYLGRRCFEARIACAP 254

```

QY 310 GDRKADEDSIRKQOVSDSTKNGDGTKRPFRONTGIGIOMTSIKRRSPDDELLYPVGR 369
DB 255 GDRKADEDSIRKQOVSDSTKNGDGTKRPFRONTGIGIOMTSIKRRSPDDELLYPVGR 314
QY 370 ETEMLIKESLEMOYLPOHTIETTYROOOOQHLLQKOTSIOSSPSSTGNSPPLNK 429
DB 315 ETEMLIKESLEMOYLPOHTIETTYROOOOQHLLQKOTSIOSSPSSTGNSPPLNK 374
QY 430 MNSMKLPSVSLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPP 489
DB 375 MNSMKLPSVSLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPP 434
QY 490 LSPSTHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHNSMDLASLK 549
DB 435 LSPSTHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHNSMDLASLK 494
QY 550 IPEORRAIWKIILDRHOLHESSPSHLRTPSSASIVSVSSSETRGERVIDAVFTLRQ 609
DB 495 IPEORRAIWKIILDRHOLHESSPSHLRTPSSASIVSVSSSETRGERVIDAVFTLRQ 554
QY 610 TISPPRDEWMDNFMDARRNKKOORKEEGE 641
DB 555 TISPPRDEWMDNFMDARRNKKOORKEEGE 586

RESULT 14

US-09-643-597-344
; Sequence 344, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-344

Query Match 79.9%; Score 2722; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 6.5e-242;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTOTNEFLSPEVFOHIMDFLEQIPICSVQPIDLNFYDEPSEDEGATNKIETSMDCIRMQ 60
DB 1 MSOSTOTNEFLSPEVFOHIMDFLEQIPICSVQPIDLNFYDEPSEDEGATNKIETSMDCIRMQ 60
QY 61 DSDLSDPMPQYNTNIGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMPQYNTNIGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIISNTDYPGHSPFVSFOQSSSTAKSATWTYSTELKLYCOIACTCPIQIKVMP 180
DB 121 SPSPAIISNTDYPGHSPFVSFOQSSSTAKSATWTYSTELKLYCOIACTCPIQIKVMP 180
QY 181 POGAVIRAMPYKKAHEHTEVVKRCRNHELREFFNEGIIAPPSHLIRVEGNSHAQYVDP 240
DB 181 POGAVIRAMPYKKAHEHTEVVKRCRNHELREFFNEGIIAPPSHLIRVEGNSHAQYVDP 240

DB 181 POGAVIRAMPYKKAHEHTEVVKRCRNHELREFFNEGIIAPPSHLIRVEGNSHAQYVDP 240
QY 241 ITGRQSVLVPEPPVGTETFTVLVNFMCNSSCVGAMRRPILITVLETRDGOVLGRRC 300
DB 241 ITGRQSVLVPEPPVGTETFTVLVNFMCNSSCVGAMRRPILITVLETRDGOVLGRRC 300
QY 301 FEARICACPGDRKADEDSIRKQOVSDSTKNGDGTKRPFRONTGIGIOMTSIKRRSPDE 360
DB 301 FEARICACPGDRKADEDSIRKQOVSDSTKNGDGTKRPFRONTGIGIOMTSIKRRSPDE 360
QY 361 LLYLPVGRRETEYEMLIKESLEMOYLPOHTIETTYROOOOQHLLQKOTSIOSSPSY 420
DB 361 LLYLPVGRRETEYEMLIKESLEMOYLPOHTIETTYROOOOQHLLQKOTSIOSSPSY 420
QY 421 GNSPPLKMSMNKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGL 480
DB 421 GNSPPLKMSMNKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGL 480
QY 481 SPTQALPPPLSPSTHCTPPPPYPTDCSIV 511
DB 481 SPTQALPPPLSPSTHCTPPPPYPTDCSIV 511

RESULT 15

US-09-542-615A-344
; Sequence 344, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-344

Query Match 79.9%; Score 2722; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 6.5e-242;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTOTNEFLSPEVFOHIMDFLEQIPICSVQPIDLNFYDEPSEDEGATNKIETSMDCIRMQ 60
DB 1 MSOSTOTNEFLSPEVFOHIMDFLEQIPICSVQPIDLNFYDEPSEDEGATNKIETSMDCIRMQ 60
QY 61 DSDLSDPMPQYNTNIGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMPQYNTNIGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIISNTDYPGHSPFVSFOQSSSTAKSATWTYSTELKLYCOIACTCPIQIKVMP 180
DB 121 SPSPAIISNTDYPGHSPFVSFOQSSSTAKSATWTYSTELKLYCOIACTCPIQIKVMP 180
QY 181 POGAVIRAMPYKKAHEHTEVVKRCRNHELREFFNEGIIAPPSHLIRVEGNSHAQYVDP 240
DB 181 POGAVIRAMPYKKAHEHTEVVKRCRNHELREFFNEGIIAPPSHLIRVEGNSHAQYVDP 240
QY 241 ITGRQSVLVPEPPVGTETFTVLVNFMCNSSCVGAMRRPILITVLETRDGOVLGRRC 300
DB 241 ITGRQSVLVPEPPVGTETFTVLVNFMCNSSCVGAMRRPILITVLETRDGOVLGRRC 300
QY 301 FEARICACPGDRKADEDSIRKQOVSDSTKNGDGTKRPFRONTGIGIOMTSIKRRSPDE 360
DB 301 FEARICACPGDRKADEDSIRKQOVSDSTKNGDGTKRPFRONTGIGIOMTSIKRRSPDE 360

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Db      301 FEARICACPGDRKADEDSIRKQOYSDSTKNGDGTKRPFRONTGHIQMTSIRKKRSPDDE 360
QY      361 LLYPVGRREYEMLIKIKESLEMOYLPQHTIETPYROOOOHOHLQKOTSIOSSSY 420
        |||||||
Db      361 LLYPVGRREYEMLIKIKESLEMOYLPQHTIETPYROOOOHOHLQKOTSIOSSSY 420
QY      421 GNSSPPLKMSMKNLPSVSQLINPQORALPTTIPDGMGANIPMGTMPMAGDMNGL 480
        |||||||
Db      421 GNSSPPLKMSMKNLPSVSQLINPQORALPTTIPDGMGANIPMGTMPMAGDMNGL 480
QY      481 SPTQALPPPLSMPTSHCTPPPPPTDCSIV 511
        |||||||
Db      481 SPTQALPPPLSMPTSHCTPPPPPTDCSIV 511

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Search completed: August 7, 2003, 09:54:49
 Job time : 19.6828 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	3401	99.9	641	9	US-09-735-705-339		Sequence 339, App
2	3401	99.9	641	10	US-09-850-716A-339		Sequence 339, App
3	3401	99.9	641	10	US-09-897-778-339		Sequence 339, App
4	3397	99.8	680	9	US-09-735-705-342		Sequence 342, App
5	3397	99.8	680	10	US-09-850-716A-342		Sequence 342, App
6	3397	99.8	680	10	US-09-897-778-342		Sequence 342, App
7	3016	88.6	586	9	US-09-735-705-338		Sequence 338, App
8	3016	88.6	586	10	US-09-850-716A-338		Sequence 338, App
9	3016	88.6	586	10	US-09-897-778-338		Sequence 338, App
10	3009	88.4	586	9	US-09-735-705-152		Sequence 152, App
11	3009	88.4	586	10	US-09-850-716A-152		Sequence 152, App
12	3009	88.4	586	10	US-09-897-778-152		Sequence 152, App
13	3009	88.4	586	11	US-09-466-396A-152		Sequence 152, App
14	2722	79.9	516	9	US-09-735-705-344		Sequence 344, App
15	2722	79.9	516	10	US-09-850-716A-344		Sequence 344, App

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QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCTPIQIKVMTTP 180
DB 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCTPIQIKVMTTP 180
QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHELREFNEGOIAPPShLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPYKKAHVTEVVKRCPNHELREFNEGOIAPPShLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETDRGQVGLGRR 300
DB 241 ITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETDRGQVGLGRR 300
QY 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTFRFRQNTGHIOMTSIKKRSPDDE 360
DB 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTFRFRQNTGHIOMTSIKKRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLKQKTSIQSPSSY 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLKQKTSIQSPSSY 420
QY 421 GNSPPLNKNMNMKLPVSQOLINPQORNALTPPTIPDGMGANIPMGTHMPMAGDMNGL 480
DB 421 GNSPPLNKNMNMKLPVSQOLINPQORNALTPPTIPDGMGANIPMGTHMPMAGDMNGL 480
QY 481 SPTQALPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPTQALPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSCLDYFTTQGLTTIYQIEHY 540
QY 541 SMDDLASLKIPEQFRHAIWKIGILDHRQLHEFSPPSHLLRTPSSASTVSGSSETRGERVI 600
DB 541 SMDDLASLKIPEQFRHAIWKIGILDHRQLHEFSPPSHLLRTPSSASTVSGSSETRGERVI 600
QY 601 DAVRFTLRQTSIFPPRDEWDFNFDMDARRNKQRIKEEGE 641
DB 601 DAVRFTLRQTSIFPPRDEWDFNFDMDARRNKQRIKEEGE 641
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RESULT 2

US-09-850-716A-339

; Sequence 339, Application US/09850716A

; Patent No. US20020115139A1

; GENERAL INFORMATION:

; APPLICANT: Kalos, Michael D.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Retter, Marc W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C15

; CURRENT APPLICATION NUMBER: US/09/850.716A

; CURRENT FILING DATE: 2001-05-07

; NUMBER OF SEQ ID NOS: 440

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 339

; LENGTH: 641

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-850-716A-339

Query Match 99.9%; Score 3401; DB 10; Length 641;

Best Local Similarity 99.8%; Pred. No. 4.5e-273;

Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQSTQTNNEFLSPVFGHWDLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60

DB 1 MSQSTQTNNEFLSPVFGHWDLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60

QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

DB 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

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QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCTPIQIKVMTTP 180
DB 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCTPIQIKVMTTP 180
QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHELREFNEGOIAPPShLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPYKKAHVTEVVKRCPNHELREFNEGOIAPPShLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETDRGQVGLGRR 300
DB 241 ITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETDRGQVGLGRR 300
QY 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTFRFRQNTGHIOMTSIKKRSPDDE 360
DB 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTFRFRQNTGHIOMTSIKKRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLKQKTSIQSPSSY 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLKQKTSIQSPSSY 420
QY 421 GNSPPLNKNMNMKLPVSQOLINPQORNALTPPTIPDGMGANIPMGTHMPMAGDMNGL 480
DB 421 GNSPPLNKNMNMKLPVSQOLINPQORNALTPPTIPDGMGANIPMGTHMPMAGDMNGL 480
QY 481 SPTQALPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPTQALPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSCLDYFTTQGLTTIYQIEHY 540
QY 541 SMDDLASLKIPEQFRHAIWKIGILDHRQLHEFSPPSHLLRTPSSASTVSGSSETRGERVI 600
DB 541 SMDDLASLKIPEQFRHAIWKIGILDHRQLHEFSPPSHLLRTPSSASTVSGSSETRGERVI 600
QY 601 DAVRFTLRQTSIFPPRDEWDFNFDMDARRNKQRIKEEGE 641
DB 601 DAVRFTLRQTSIFPPRDEWDFNFDMDARRNKQRIKEEGE 641
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RESULT 3

US-09-897-778-339

; Sequence 339, Application US/09897778

; Patent No. US20020147143A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Marnerakis, Margarita

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedrick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Henderson, Robert A.

; APPLICANT: Peckham, David W.

; APPLICANT: Fanger, Neil

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C16

; CURRENT APPLICATION NUMBER: US/09/897,778

; CURRENT FILING DATE: 2001-06-28

; NUMBER OF SEQ ID NOS: 467

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 339

; LENGTH: 641

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-897-778-339

Query Match 99.9%; Score 3401; DB 10; Length 641;

Best Local Similarity 99.8%; Pred. No. 4.5e-273;

Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQSTQTNNEFLSPVFGHWDLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60

DB 1 MSQSTQTNNEFLSPVFGHWDLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60

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QY 61 DSDLDSDPMPMPQYTNLGLNSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
DB 61 DSDLDSDPMPMPQYTNLGLNSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSDVDFVFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 180
DB 121 SPSPALPSNTDYPGPHSDVDFVFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 180
QY 181 POGAVIRAMPYKKAHEHTEVVKRCPNHLSRENEGOIAPSHLIRVGNSHAQYVEP 240
DB 181 POGAVIRAMPYKKAHEHTEVVKRCPNHLSRENEGOIAPSHLIRVGNSHAQYVEP 240
QY 241 ITGRQSVLVPEPPOVGTETTYLVYNFMCNSSCVGMNRRPILIVTLETBDGQVIGRR 300
DB 241 ITGRQSVLVPEPPOVGTETTYLVYNFMCNSSCVGMNRRPILIVTLETBDGQVIGRR 300
QY 301 FEARICACPGDRKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRRSPDE 360
DB 301 FEARICACPGDRKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRRSPDE 360
QY 361 LLYLVRGRETTEMLIKIKESLELMQYLPQHTIETRYQOQOQOHOHLQKQTSIOSPS 420
DB 361 LLYLVRGRETTEMLIKIKESLELMQYLPQHTIETRYQOQOQOHOHLQKQTSIOSPS 420
QY 421 GNSPPLNKNSMKNKLPVSQILNPOQRNALPTTIPDGMCANIPMGTHMPAGDMNGL 480
DB 421 GNSPPLNKNSMKNKLPVSQILNPOQRNALPTTIPDGMCANIPMGTHMPAGDMNGL 480
QY 481 SPQALPPLPSMPSSTHCTPPPPYPTDCSIVSFARLGSSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPQALPPLPSMPSSTHCTPPPPYPTDCSIVSFARLGSSCLDYFTTQGLTTIYQIEHY 540
QY 541 SMDDLASLKIPEQFRAHAIWKGLDHRQLHEFSSPSHLRTPSASSTVSGSSETRGERVI 600
DB 541 SMDDLASLKIPEQFRAHAIWKGLDHRQLHEFSSPSHLRTPSASSTVSGSSETRGERVI 600
QY 601 DAVRFTLRQTIISFPPEDEMDNFMDARNRKQOIRKEGE 641
DB 601 DAVRFTLRQTIISFPPEDEMDNFMDARNRKQOIRKEGE 641

RESULT 4
US-09-735-705-342
; Sequence 342, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-342

Query Match 99.8%; Score 3397; DB 9; Length 680;
Best Local Similarity 99.8%; Pred. No. 1.1e-272;

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Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSOSTQTNELSPPEVFOHIDFLEOPICSVOPIDLANFVDEPSDEGATNKIEISMDCIRMQ 60
DB 40 MSOSTQTNELSPPEVFOHIDFLEOPICSVOPIDLANFVDEPSDEGATNKIEISMDCIRMQ 99
QY 61 DSDLDSDPMPMPQYTNLGLNSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
DB 61 DSDLDSDPMPMPQYTNLGLNSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSDVDFVFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 180
DB 121 SPSPALPSNTDYPGPHSDVDFVFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 180
QY 160 SPSPALPSNTDYPGPHSDVDFVFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 219
DB 160 SPSPALPSNTDYPGPHSDVDFVFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 219
QY 241 ITGRQSVLVPEPPOVGTETTYLVYNFMCNSSCVGMNRRPILIVTLETBDGQVIGRR 300
DB 241 ITGRQSVLVPEPPOVGTETTYLVYNFMCNSSCVGMNRRPILIVTLETBDGQVIGRR 300
QY 301 FEARICACPGDRKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRRSPDE 360
DB 301 FEARICACPGDRKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRRSPDE 360
QY 361 LLYLVRGRETTEMLIKIKESLELMQYLPQHTIETRYQOQOQOHOHLQKQTSIOSPS 420
DB 361 LLYLVRGRETTEMLIKIKESLELMQYLPQHTIETRYQOQOQOHOHLQKQTSIOSPS 420
QY 421 GNSPPLNKNSMKNKLPVSQILNPOQRNALPTTIPDGMCANIPMGTHMPAGDMNGL 480
DB 421 GNSPPLNKNSMKNKLPVSQILNPOQRNALPTTIPDGMCANIPMGTHMPAGDMNGL 480
QY 460 GNSPPLNKNSMKNKLPVSQILNPOQRNALPTTIPDGMCANIPMGTHMPAGDMNGL 519
DB 460 GNSPPLNKNSMKNKLPVSQILNPOQRNALPTTIPDGMCANIPMGTHMPAGDMNGL 519
QY 481 SPQALPPLPSMPSSTHCTPPPPYPTDCSIVSFARLGSSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPQALPPLPSMPSSTHCTPPPPYPTDCSIVSFARLGSSCLDYFTTQGLTTIYQIEHY 540
QY 520 SPQALPPLPSMPSSTHCTPPPPYPTDCSIVSFARLGSSCLDYFTTQGLTTIYQIEHY 579
DB 520 SPQALPPLPSMPSSTHCTPPPPYPTDCSIVSFARLGSSCLDYFTTQGLTTIYQIEHY 579
QY 541 SMDDLASLKIPEQFRAHAIWKGLDHRQLHEFSSPSHLRTPSASSTVSGSSETRGERVI 600
DB 541 SMDDLASLKIPEQFRAHAIWKGLDHRQLHEFSSPSHLRTPSASSTVSGSSETRGERVI 600
QY 601 DAVRFTLRQTIISFPPEDEMDNFMDARNRKQOIRKEGE 641
DB 601 DAVRFTLRQTIISFPPEDEMDNFMDARNRKQOIRKEGE 641

RESULT 5
US-09-850-716A-342
; Sequence 342, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Ketter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-342

Query Match 99.8%; Score 3397; DB 10; Length 680;
Best Local Similarity 99.8%; Pred. No. 1.1e-272;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSOSTQTNELSPPEVFOHIDFLEOPICSVOPIDLANFVDEPSDEGATNKIEISMDCIRMQ 60

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Db 40 MSOSTQINELSPFVQHIDLEPQICSVQPIDLNVDPSEEGANKKEISMDICRMQ 99
QY 61 DSDLDSPMPOYTNIGLINSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSTFDAL 120
Db 100 DSDLDSPMPOYTNIGLINSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSTFDAL 159
QY 121 SPSPALPSNTDYGPHSPFDVSPFOOSSTAKSATWTSTELKLYCOIAKTCPIQIKVMP 180
Db 160 SPSPALPSNTDYGPHSPFDVSPFOOSSTAKSATWTSTELKLYCOIAKTCPIQIKVMP 219
QY 181 PGAVIRAMPYKKAHEVTEVYKRCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
Db 220 PGAVIRAMPYKKAHEVTEVYKRCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYEDP 279
QY 241 ITGROSVLVYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVLRRC 300
Db 280 ITGROSVLVYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVLRRC 339
QY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTFRPFRONTHGQIOMTSIKKRRSPDE 360
Db 340 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTFRPFRONTHGQIOMTSIKKRRSPDE 399
QY 361 LLYLPVGRRETEYEMLLKIKESLELMQYLPQHTIETRYROOQOOQHLLQKOTSIOSSSY 420
Db 400 LLYLPVGRRETEYEMLLKIKESLELMQYLPQHTIETRYROOQOOQHLLQKOTSIOSSSY 459
QY 421 GNSSPPLKNKSNMKNLPVSOLINPOORNALPTTIPDGGMANIPMGTHMPAGDMNGI 480
Db 460 GNSSPPLKNKSNMKNLPVSOLINPOORNALPTTIPDGGMANIPMGTHMPAGDMNGI 519
QY 481 SPFOALPPLSPMSTSHCTPPPPYPTDCSIVSEFLARLGCCSCLDYFTTQGLTTIYOIEHY 540
Db 520 SPFOALPPLSPMSTSHCTPPPPYPTDCSIVSEFLARLGCCSCLDYFTTQGLTTIYOIEHY 579
QY 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHESSPSHLKTRPSSASTVSVGSSETRGERVI 600
Db 580 SMDDLASLKIPEQFRHAIWKGLDHRQLHESSPSHLKTRPSSASTVSVGSSETRGERVI 639
QY 601 DAVRETLKQITISFPPEDEWDFNFDMDARRNKQKRIKEGE 641
Db 640 DAVRETLKQITISFPPEDEWDFNFDMDARRNKQKRIKEGE 680

```

RESULT 6
US-09-897-778-342
Sequence 342, Application US/09897778
Patent No. US20020147143A1

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Mainerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 342
LENGTH: 680
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-342

Query Match 99.8%; Score 3397; DB 10; Length 680;
Best Local Similarity 99.8%; Pred. No. 1,1e-272;

```

Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSOSTQINELSPFVQHIDLEPQICSVQPIDLNVDPSEEGANKKEISMDICRMQ 60
Db 40 MSOSTQINELSPFVQHIDLEPQICSVQPIDLNVDPSEEGANKKEISMDICRMQ 99
QY 61 DSDLDSPMPOYTNIGLINSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSTFDAL 120
Db 100 DSDLDSPMPOYTNIGLINSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSTFDAL 159
QY 121 SPSPALPSNTDYGPHSPFDVSPFOOSSTAKSATWTSTELKLYCOIAKTCPIQIKVMP 180
Db 160 SPSPALPSNTDYGPHSPFDVSPFOOSSTAKSATWTSTELKLYCOIAKTCPIQIKVMP 219
QY 181 PGAVIRAMPYKKAHEVTEVYKRCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
Db 220 PGAVIRAMPYKKAHEVTEVYKRCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYEDP 279
QY 241 ITGROSVLVYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVLRRC 300
Db 280 ITGROSVLVYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVLRRC 339
QY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTFRPFRONTHGQIOMTSIKKRRSPDE 360
Db 340 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTFRPFRONTHGQIOMTSIKKRRSPDE 399
QY 361 LLYLPVGRRETEYEMLLKIKESLELMQYLPQHTIETRYROOQOOQHLLQKOTSIOSSSY 420
Db 400 LLYLPVGRRETEYEMLLKIKESLELMQYLPQHTIETRYROOQOOQHLLQKOTSIOSSSY 459
QY 421 GNSSPPLKNKSNMKNLPVSOLINPOORNALPTTIPDGGMANIPMGTHMPAGDMNGI 480
Db 460 GNSSPPLKNKSNMKNLPVSOLINPOORNALPTTIPDGGMANIPMGTHMPAGDMNGI 519
QY 481 SPFOALPPLSPMSTSHCTPPPPYPTDCSIVSEFLARLGCCSCLDYFTTQGLTTIYOIEHY 540
Db 520 SPFOALPPLSPMSTSHCTPPPPYPTDCSIVSEFLARLGCCSCLDYFTTQGLTTIYOIEHY 579
QY 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHESSPSHLKTRPSSASTVSVGSSETRGERVI 600
Db 580 SMDDLASLKIPEQFRHAIWKGLDHRQLHESSPSHLKTRPSSASTVSVGSSETRGERVI 639
QY 601 DAVRETLKQITISFPPEDEWDFNFDMDARRNKQKRIKEGE 641
Db 640 DAVRETLKQITISFPPEDEWDFNFDMDARRNKQKRIKEGE 680

```

RESULT 7
US-09-735-705-338
Sequence 338, Application US/09735705
Patent No. US20020052329A1

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586

QY 70 PoytNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSTFDALSPSPALPSN 129
DB 15 PoytNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSTFDALSPSPALPSN 74
QY 130 TDYGPSPHSDVSPFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQCAVIRAM 189
DB 75 TDYGPSPHSDVSPFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQCAVIRAM 134
QY 190 PYYKAEHVTEVYKRCPNHLSREFNEQOIAFPSHLIVEGNSHAQYVEDPITGQSVLY 249
DB 135 PYYKAEHVTEVYKRCPNHLSREFNEQOIAFPSHLIVEGNSHAQYVEDPITGQSVLY 194
QY 250 PYYKAEHVTEVYKRCPNHLSREFNEQOIAFPSHLIVEGNSHAQYVEDPITGQSVLY 309
DB 195 PYYKAEHVTEVYKRCPNHLSREFNEQOIAFPSHLIVEGNSHAQYVEDPITGQSVLY 254
QY 310 GRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTGHIOMTSIKRRSPDDELIVYLVGR 369
DB 255 GRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTGHIOMTSIKRRSPDDELIVYLVGR 314
QY 370 EYEMLLKIKESLELMOYLPOHTTETRYQOQOQOHLQKOTSIOSSPSYGNSSPPLNK 429
DB 315 EYEMLLKIKESLELMOYLPOHTTETRYQOQOQOHLQKOTSIOSSPSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQOLINPOORNALTPPTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 489
DB 375 MNSMNLKPSVSQOLINPOORNALTPPTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 434
QY 490 LSPBSTSHCTPPPPYPTDCSIVSFLARLGCCSCDLYFTTQGLTYYQIEHSMDDLAK 549
DB 435 LSPBSTSHCTPPPPYPTDCSIVSFLARLGCCSCDLYFTTQGLTYYQIEHSMDDLAK 494
QY 550 IPEQFRHAIWGIIDHROLHEFSSPSHLLRTPSSASIVSVSSSETRGERVIDAVFTLRQ 609
DB 495 IPEQFRHAIWGIIDHROLHEFSSPSHLLRTPSSASIVSVSSSETRGERVIDAVFTLRQ 554
QY 610 TISFPPRDEWMDNFMDARRNKQORIKEGE 641
DB 555 TISFPPRDEWMDNFMDARRNKQORIKEGE 586

RESULT 10

US-09-735-705-152
; Sequence 152, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-735-705-152

Query Match 88.4%; Score 3009; DB 9; Length 586;
Best Local Similarity 99.3%; Pred. No. 1.2e-240;

Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 70 PoytNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSTFDALSPSPALPSN 129
DB 15 PoytNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSTFDALSPSPALPSN 74
QY 130 TDYGPSPHSDVSPFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQCAVIRAM 189
DB 75 TDYGPSPHSDVSPFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQCAVIRAM 134
QY 190 PYYKAEHVTEVYKRCPNHLSREFNEQOIAFPSHLIVEGNSHAQYVEDPITGQSVLY 249
DB 135 PYYKAEHVTEVYKRCPNHLSREFNEQOIAFPSHLIVEGNSHAQYVEDPITGQSVLY 194
QY 250 PYYKAEHVTEVYKRCPNHLSREFNEQOIAFPSHLIVEGNSHAQYVEDPITGQSVLY 309
DB 195 PYYKAEHVTEVYKRCPNHLSREFNEQOIAFPSHLIVEGNSHAQYVEDPITGQSVLY 254
QY 310 GRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTGHIOMTSIKRRSPDDELIVYLVGR 369
DB 255 GRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTGHIOMTSIKRRSPDDELIVYLVGR 314
QY 370 EYEMLLKIKESLELMOYLPOHTTETRYQOQOQOHLQKOTSIOSSPSYGNSSPPLNK 429
DB 315 EYEMLLKIKESLELMOYLPOHTTETRYQOQOQOHLQKOTSIOSSPSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQOLINPOORNALTPPTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 489
DB 375 MNSMNLKPSVSQOLINPOORNALTPPTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 434
QY 490 LSPBSTSHCTPPPPYPTDCSIVSFLARLGCCSCDLYFTTQGLTYYQIEHSMDDLAK 549
DB 435 LSPBSTSHCTPPPPYPTDCSIVSFLARLGCCSCDLYFTTQGLTYYQIEHSMDDLAK 494
QY 550 IPEQFRHAIWGIIDHROLHEFSSPSHLLRTPSSASIVSVSSSETRGERVIDAVFTLRQ 609
DB 495 IPEQFRHAIWGIIDHROLHEFSSPSHLLRTPSSASIVSVSSSETRGERVIDAVFTLRQ 554
QY 610 TISFPPRDEWMDNFMDARRNKQORIKEGE 641
DB 555 TISFPPRDEWMDNFMDARRNKQORIKEGE 586

RESULT 11

US-09-850-716A-152
; Sequence 152, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-850-716A-152

Query Match 88.4%; Score 3009; DB 10; Length 586;
Best Local Similarity 99.3%; Pred. No. 1.2e-240;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 70 PoytNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSTFDALSPSPALPSN 129
DB 15 PoytNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSTFDALSPSPALPSN 74
QY 130 TDYGPSPHSDVSPFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQCAVIRAM 189

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Db 75 TDYGPBSPDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
QY 190 PYYKKAHEVTEYVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYVDPITGRQSVLY 249
Db 135 PYYKKAHEVTEYVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYVDPITGRQSVLY 194
QY 250 PYEPVOGTEFTTVLYNFMCNSSCVGGMNRRLIIVLTETRDGOVLGRCEARICACP 309
Db 195 PYEPVOGTEFTTVLYNFMCNSSCVGGMNRRLIIVLTETRDGOVLGRCEARICACP 254
QY 310 GDRKADEDISIRKQVSDSTKNGDGTKRPFRONTGHIQMTSIKKRSPDELLYLPRGR 369
Db 255 GDRKADEDISIRKQVSDSTKNGDGTKRPFRONTGHIQMTSIKKRSPDELLYLPRGR 314
QY 370 EYEMLKIKESLELMQYLPQHTIETRYOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 429
Db 315 EYEMLVKIKESLELMQYLOHTIETRYOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
QY 430 MNSMKLPVSQLINPOORNALPTTIPGMCANIPMGTHMPMAGDMNGLSPTQALPP 489
Db 375 MNSMKLPVSQLINPOORNALPTTIPGMCANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSPSTSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 549
Db 435 LSPSTSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
QY 550 IPEQFRAIWKIGILHRQHLHERFSSPSHLRTSSASTVSGSSETRGERIVDAVRETLQ 609
Db 495 IPEQFRAIWKIGILHRQHLHERFSSPSHLRTSSASTVSGSSETRGERIVDAVRETLQ 554
QY 610 TISFPPEMDNPFNDMDARRNKQORIKEGE 641
Db 555 TISFPPEMDNPFNDMDARRNKQORIKEGE 586
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RESULT 12
US-09-897-778-152
; Sequence 152, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnetakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-152
```

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Query Match 88.4%; Score 3009; DB 10: Length 586;
Best Local Similarity 99.3%; Pred. No. 1.2e-240;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 70 PYYNLGLNMDQIQNGSSSTSPYNTDHAONSVTAPSPYQPSSTFDALSPSPAIIPN 129
Db 15 PYYNLGLNMDQIQNGSSSTSPYNTDHAONSVTAPSPYQPSSTFDALSPSPAIIPN 74
QY 130 TDYGPBSPDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
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Db 75 TDYGPBSPDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
QY 190 PYYKKAHEVTEYVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYVDPITGRQSVLY 249
Db 135 PYYKKAHEVTEYVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYVDPITGRQSVLY 194
QY 250 PYEPVOGTEFTTVLYNFMCNSSCVGGMNRRLIIVLTETRDGOVLGRCEARICACP 309
Db 195 PYEPVOGTEFTTVLYNFMCNSSCVGGMNRRLIIVLTETRDGOVLGRCEARICACP 254
QY 310 GDRKADEDISIRKQVSDSTKNGDGTKRPFRONTGHIQMTSIKKRSPDELLYLPRGR 369
Db 255 GDRKADEDISIRKQVSDSTKNGDGTKRPFRONTGHIQMTSIKKRSPDELLYLPRGR 314
QY 370 EYEMLKIKESLELMQYLPQHTIETRYOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 429
Db 315 EYEMLVKIKESLELMQYLOHTIETRYOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
QY 430 MNSMKLPVSQLINPOORNALPTTIPGMCANIPMGTHMPMAGDMNGLSPTQALPP 489
Db 375 MNSMKLPVSQLINPOORNALPTTIPGMCANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSPSTSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 549
Db 435 LSPSTSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
QY 550 IPEQFRAIWKIGILHRQHLHERFSSPSHLRTSSASTVSGSSETRGERIVDAVRETLQ 609
Db 495 IPEQFRAIWKIGILHRQHLHERFSSPSHLRTSSASTVSGSSETRGERIVDAVRETLQ 554
QY 610 TISFPPEMDNPFNDMDARRNKQORIKEGE 641
Db 555 TISFPPEMDNPFNDMDARRNKQORIKEGE 586
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RESULT 13
US-09-466-396A-152
; Sequence 152, Application US/09466396A
; Publication No. US20030119763A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.455C4
; CURRENT APPLICATION NUMBER: US/09/466,396A
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-466-396A-152
```

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Query Match 88.4%; Score 3009; DB 11: Length 586;
Best Local Similarity 99.3%; Pred. No. 1.2e-240;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 70 PYYNLGLNMDQIQNGSSSTSPYNTDHAONSVTAPSPYQPSSTFDALSPSPAIIPN 129
Db 15 PYYNLGLNMDQIQNGSSSTSPYNTDHAONSVTAPSPYQPSSTFDALSPSPAIIPN 74
QY 130 TDYGPBSPDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
Db 75 TDYGPBSPDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
QY 190 PYYKKAHEVTEYVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYVDPITGRQSVLY 249
Db 135 PYYKKAHEVTEYVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYVDPITGRQSVLY 194
QY 250 PYEPVOGTEFTTVLYNFMCNSSCVGGMNRRLIIVLTETRDGOVLGRCEARICACP 309
Db 195 PYEPVOGTEFTTVLYNFMCNSSCVGGMNRRLIIVLTETRDGOVLGRCEARICACP 254
```

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QY 310 GRDKRAEDSIRKQOVSSTKNGDGTKRPFQNTHGIGMTSIRKKRSPDDELLXLPVGR 369
| | | | |
Db 255 GRDKRAEDSIRKQOVSSTKNGDGTKRPFQNTHGIGMTSIRKKRSPDDELLXLPVGR 314
QY 370 ETEMLIKIKESLEMOYLPOHTIETYROOOOQHLLQKOTSIQSSSYGNSPPLNK 429
| | | | |
Db 315 ETEMLIKIKESLEMOYLPOHTIETYROOOOQHLLQKOTSIQSSSYGNSPPLNK 374
QY 430 MNSMNLKPSVSQLINPOQRNALPTTIPDGAGANIPMGTHMPMAGDMNGLSPTQALPP 489
| | | | |
Db 375 MNSMNLKPSVSQLINPOQRNALPTTIPDGAGANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTITTYQIEHYSMDDLASLK 549
| | | | |
Db 435 LSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTITTYQIEHYSMDDLASLK 494
QY 550 IPEQFRAHWGIIDHROHLEFSSSHLPTPSASATSVGSSSEFRGRVDAVAFETLRQ 609
| | | | |
Db 495 IPEQFRAHWGIIDHROHLEFSSSHLPTPSASATSVGSSSEFRGRVDAVAFETLRQ 554
QY 610 TISEPPRDEWDFNEDMDARRNKQORKEGE 641
| | | | |
Db 555 TISEPPRDEWDFNEDMDARRNKQORKEGE 586
```

RESULT 14

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US-09-735-705-344
; Sequence 344, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735.705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-344
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Query Match 79.9%; Score 2722; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 5.8e-217;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSOSTQNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDESEEGATNKIEISMDCI RMQ 60
| | | | |
Db 1 MSOSTQNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDESEEGATNKIEISMDCI RMQ 60
QY 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTYATSPYAQPSSTPDAL 120
| | | | |
Db 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTYATSPYAQPSSTPDAL 120
QY 121 SPSPALPSNTDYEPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWMP 180
| | | | |
Db 121 SPSPALPSNTDYEPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWMP 180
QY 181 PGCAVIRAMPYVYKKAHEVTEVYVRCRNHLSRENEGOIAPPSHLIRVEGNSHAQYEDP 240
```

```
Db 181 PGCAVIRAMPYVYKKAHEVTEVYVRCRNHLSRENEGOIAPPSHLIRVEGNSHAQYEDP 240
| | | | |
QY 241 ITGRQSVLYPEPPQVGTETTYLYNFMCNSSCVGAMRRPILITVLETRDGOYLGRRC 300
| | | | |
Db 241 ITGRQSVLYPEPPQVGTETTYLYNFMCNSSCVGAMRRPILITVLETRDGOYLGRRC 300
QY 301 FEARICACPGDRKRAEDSIRKQOVSSTKNGDGTKRPFQNTHGIGMTSIRKKRSPDDE 360
| | | | |
Db 301 FEARICACPGDRKRAEDSIRKQOVSSTKNGDGTKRPFQNTHGIGMTSIRKKRSPDDE 360
QY 361 ILLYPRRRETEYEMLKIKESLEMOYLPOHTIETYROOOOQHLLQKOTSIQSSSY 420
| | | | |
Db 361 ILLYPRRRETEYEMLKIKESLEMOYLPOHTIETYROOOOQHLLQKOTSIQSSSY 420
QY 421 GNSSPPLKMSMNLKPSVSQLINPOQRNALPTTIPDGAGANIPMGTHMPMAGDMNGL 480
| | | | |
Db 421 GNSSPPLKMSMNLKPSVSQLINPOQRNALPTTIPDGAGANIPMGTHMPMAGDMNGL 480
QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
| | | | |
Db 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
```

RESULT 15

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US-09-850-716A-344
; Sequence 344, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850.716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-344
```

Query Match 79.9%; Score 2722; DB 10; Length 516;
Best Local Similarity 100.0%; Pred. No. 5.8e-217;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MSOSTQNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDESEEGATNKIEISMDCI RMQ 60
| | | | |
Db 1 MSOSTQNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDESEEGATNKIEISMDCI RMQ 60
QY 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTYATSPYAQPSSTPDAL 120
| | | | |
Db 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTYATSPYAQPSSTPDAL 120
QY 121 SPSPALPSNTDYEPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWMP 180
| | | | |
Db 121 SPSPALPSNTDYEPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWMP 180
QY 181 PGCAVIRAMPYVYKKAHEVTEVYVRCRNHLSRENEGOIAPPSHLIRVEGNSHAQYEDP 240
| | | | |
Db 181 PGCAVIRAMPYVYKKAHEVTEVYVRCRNHLSRENEGOIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITGRQSVLYPEPPQVGTETTYLYNFMCNSSCVGAMRRPILITVLETRDGOYLGRRC 300
| | | | |
Db 241 ITGRQSVLYPEPPQVGTETTYLYNFMCNSSCVGAMRRPILITVLETRDGOYLGRRC 300
QY 301 FEARICACPGDRKRAEDSIRKQOVSSTKNGDGTKRPFQNTHGIGMTSIRKKRSPDDE 360
| | | | |
Db 301 FEARICACPGDRKRAEDSIRKQOVSSTKNGDGTKRPFQNTHGIGMTSIRKKRSPDDE 360
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```

QY 361 LLYLPVGRREYEMLIKIKESLELMQYLPQHTTIEFYROOOOOHOLLOKOTSIOPSSY 420
    |||||||
Db 361 LLYLPVGRREYEMLIKIKESLELMQYLPQHTTIEFYROOOOOHOLLOKOTSIOPSSY 420
    |||||||
QY 421 GNSSPPLNKNMSMKLPSYSQLINPOQRNALPPTIPDGMGANIPMGTMPMAGDMNGL 480
    |||||||
Db 421 GNSSPPLNKNMSMKLPSYSQLINPOQRNALPPTIPDGMGANIPMGTMPMAGDMNGL 480
    |||||||
QY 481 SPTQALPPPLSMSTSHCTPPPPPTDCSIV 511
    |||||||
Db 481 SPTQALPPPLSMSTSHCTPPPPPTDCSIV 511
    |||||||

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Search completed: August 7, 2003, 09:57:05
 Job time : 28.3662 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:03 : Search time 20.2089 Seconds
(without alignments)
3050.350 Million cell updates/sec

Title: US-09-538-106-13

Perfect score: 3405

Sequence: 1 MSQSTQTNDFELSPVEVQHIM.....FNFDMDARRNKQRIKEGE 641

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	847.5	24.9	396	1 JH0631	cellular tumor ant
2	777.5	22.8	363	1 A29376	cellular tumor ant
3	764.5	22.5	367	1 S02193	cellular tumor ant
4	740	21.7	386	1 S51648	cellular tumor ant
5	735	21.6	391	1 S02192	cellular tumor ant
6	719	21.1	396	1 JH0633	cellular tumor ant
7	718	21.1	393	1 JH0633	cellular tumor ant
8	717	21.1	390	1 DNMS53	cellular tumor ant
9	714.5	21.0	393	1 S06594	cellular tumor ant
10	703.5	20.7	381	2 S38824	cellular tumor ant
11	693.5	20.7	393	2 JG6176	tumor suppressor p
12	690.5	20.5	391	2 JG6193	tumor suppressor p
13	259.5	7.6	77	2 I46226	cellular tumor ant
14	149.5	4.4	925	2 T19361	hypothetical prote
15	144.5	4.2	1621	2 T15264	hypothetical prote
16	141.5	4.2	1081	2 S66736	transcription acti
17	138	4.1	1520	1 TVEFA	protein-tyrosine k
18	134.5	4.0	901	2 JG6093	dead ringer nuclea
19	134.5	4.0	2578	2 A56922	transcription fact
20	132.5	3.9	2529	2 A56923	transcription fact
21	130.5	3.8	628	2 S19150	hypothetical prote
22	129.5	3.8	1062	2 G86325	hypothetical prote
23	129	3.8	964	2 T41547	hypothetical prote
24	129	3.8	1819	2 T32008	hypothetical prote
25	128.5	3.8	3942	2 T42730	hypothetical prote
26	128	3.8	921	2 A48184	Bassoon protein -
27	128	3.8	921	2 A45183	transcription init
28	127.5	3.7	628	2 S01955	TBP-associated fac
29	127.5	3.7	963	2 T40290	hypothetical prote

30	126.5	3.7	628	2 J00110	hypothetical 69K p
31	126.5	3.7	864	2 H85335	hypothetical prote
32	126.5	3.7	864	2 T04518	hypothetical prote
33	126.5	3.7	1051	2 G59436	KIAA1304 protein l
34	126.5	3.7	1791	2 T24089	hypothetical prote
35	126	3.7	2897	2 B48666	cell proliferation
36	126	3.7	3256	2 A48666	cell proliferation
37	125	3.7	724	2 T47149	hypothetical prote
38	125	3.7	799	2 JH0797	hypothetical prote
39	125	3.7	2342	2 T13412	castor protein - f
40	124.5	3.7	811	2 JG7619	hypothetical prote
41	124.5	3.7	1572	2 S45251	SNF2alpha protein
42	124	3.6	590	2 A44068	cell pattern forma
43	124	3.6	826	2 I38972	hypoxia-inducible
44	124	3.6	2232	2 T34434	hypothetical prote
45	124	3.6	2688	2 I49477	alpha-A-crystallin

ALIGNMENTS

RESULT 1	
JH0631	cellular tumor antigen p53 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)	
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999	
C:Accession: JH0631	
R:de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.	
Gene 112, 241-245, 1992	
A:title: Rainbow trout p53: cDNA cloning and biochemical characterization.	
A:Reference number: JH0631, MWID:92210006, PMID:1339362	
A:Accession: JH0631	
A:Molecule type: mRNA	
A:Residues: 1-396 <DB>	
A:Cross-references: GB:W5145; NID:q213828; PIDN:AAA9605.1; PID:q213829	
A:Experimental source: liver	
C:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive	
C:Superfamily: cellular tumor antigen p53	
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pbc	
F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted	
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted	
Query Match	24.9%; Score 847.5; DB 1; Length 396;
Best Local Similarity	45.4%; Pred. No. 6.1e-51;
Matches	101; Conservative 61; Mismatches 102; Indels 55; Gaps 10;
OY	11 LSPEVQHIMDFLEQPGICSVQPIIDNFVDEPSEDGATNKIEISMDCTRMODSLDPMMP 70
DB	12 LSQSEFEDLM-----KMNILNVAVQPPETE-----SMV 39
OY	71 QYTNGLGLNSMQQIQNGSSSTPYNTDAHONSVTAPSPYAPQS-STFDALS-PSPAIRS 128
DB	40 GYDNF-----MMEAPLD-----VEFDSLFEVSATERPAPQPSISTLDGSPPTSTVP 87
OY	129 NTDPGPHSPDVSFOOSSTAKSATWTSTREKLYOIAKTCPIQIKVMTPPGQAVIRA 188
DB	88 TSDYPALGFOLFLOSSTAKSVTCYSPDLNKLFOIAKTCVQIVVDHPPPGAVNRA 147
OY	189 MPYKKAHVTEVYKRCPNHLSREFNEQIAPSHLIRVGNASHAQVEDPITGRQSVL 248
DB	148 LAIYKRLSDVADVVRRCPPHQSTSENNEGP-APRGHLVREVGQREYMDGWTLRHSVL 206
OY	249 VPEPPQVGTETFTVLYNMCNCSYGVGNRRPILITVILETDGQVLRGCEATICAC 308
DB	207 VPEPPQVSECTVLYNMCNCSYGVGNRRPILITVILETDGQVLRGCEATICAC 266
OY	309 PGDRKKADEDSIRKQO---VSDTKNGDGTRKRFPRQ-NTRGIOMTSTIKKRS----PDE 360
DB	267 PGDRKTEELNKLKQOETILETKPAQGIKRRMKASLAPAPGASKTKSSPAVSDDE 326
OY	361 LYLTPVGRGTEYEMLLKIKESLELMQYLPOHTIETVYRQ 399
DB	327 IYTLQIRGKEKYEMLKKFNDSLELSLVPAADKVRK 365

RESULT 2

A29376

cellular tumor antigen p53 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A29376; S61531; S72313; S15639

R:Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.

Oncogene 1, 71-78, 1987

A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein

A:Reference number: A29376; MUID:86143684; PMID:2830576

A:Accession: A29376

A:Molecule type: mRNA

A:Residues: 1-363 <SO>

A:Cross-references: EMBL:X05191; NID:9649661; PIDN:CAA2882.1; PID:964962

R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montemari, M.; Knoechel, W.

Oncogene 9, 109-120, 1994

A:Title: Overexpression of wild-type p53 interferes with normal development in Xenopus

A:Reference number: 151639; MUID:94134403; PMID:8302570

A:Accession: S61531

A:Molecule type: mRNA

A:Residues: 1-293, 295-363 <HO>

A:Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514

R:Hoever, M.; Clement, J.; Wedlich, D.; Montemari, M.; Knoechel, W.

Submitted to the EMBL Data Library, March 1994

A:Reference number: S72313

A:Accession: S72313

A:Molecule type: mRNA

A:Residues: 1-51, 'S', 53-70, 72-293, 295-363 <HO>

A:Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho

F,150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F,362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 22.8%; Score 777.5; DB 1; Length 363;

Best Local Similarity 42.5%; Pred. No. 3.7e-46;

Matches 171; Conservative 55; Mismatches 95; Indels 81; Gaps 11;

Db 2 SOSTQTNFLEPVEPHQIMDFLEQI-----CSYQPIDLNFVDEPDEGATNKIEISMCI 57

Db 4 SSETGMDFPLSOEFEDLMSLLPDLQVTCRLDMS-EPDPY-----LAADMT 52

QY 58 RMODSDSDPMWPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTE 117

Db 53 VLQF-----GLMGN-----AVPTVT- 67

QY 118 DALSPSPALPSTNDYPGHSEFVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVM 177

Db 68 -----SCAVPSTDYAGKYGLQDLDFQNGSTAKSVCTSPLELNFCOLAKTCPLVRAVE 122

QY 178 TPPOGAVIRAMPYKKAEHYEVKRCPNHELSEFNEGOIAPPSHLIRVGNHAGYV 237

Db 123 SPFRGSLTKATAYKKSEHAEEVKKCPHERSVPEE-DAAPSHLMRVEGNLQAYTM 181

QY 238 EDPIITGRQSVLVPEPPDVGTEFTTVLYNFCNNSCVGMNRRPILITVLETRDGOVLG 297

Db 182 EDVNSGRHSVCVPEPGVGTCTVLYNFCNNSCMGMNRRPILITVLETRDGOVLG 241

QY 298 RRCFEARICACPGDRKRADEDS-TRKQOVSDSTKNGDGTAKPPRONTH-GIQMTSIKR 354

Db 242 RRCFEARICACPGDRKRADEDS-TRKQOVSDSTKNGDGTAKPPRONTH-GIQMTSIKR 354

QY 355 R---SPDDELTYLTVRGRTEYEMLKIKESLELMQYLPQNTI 393

Db 293 LVVVDDEELFTTLTKIKGRSRYEMTKINDALELQESLDQKRV 334

RESULT 3

S02193

cellular tumor antigen p53 - chicken

N:Alternate names: nuclear oncoprotein p53

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S02193

R:Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P.

Nucleic Acids Res. 16, 11383, 1988

A:Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.

A:Reference number: S02193; MUID:89083584; PMID:3060861

A:Accession: S02193

A:Molecule type: mRNA

A:Residues: 1-367 <SO>

A:Cross-references: EMBL:X13057; NID:963740; PIDN:CAA31456.1; PID:963741

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho

F,161,164,224,228/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F,366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 22.5%; Score 764.5; DB 1; Length 367;

Best Local Similarity 44.6%; Pred. No. 2.9e-45;

Matches 169; Conservative 50; Mismatches 105; Indels 55; Gaps 10;

QY 11 LSP-EVPHQIMDFLEQPCISYQPIDLNFVDEPDEGATNKIEISMCI RMODSDSDPMW 69

Db 9 LEPTVEFMDLMSMLPY-----SMOQI-----PLPDSHNMDEL-----PLESDPPPPP 54

QY 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTEFDALSPSPAPISN 129

Db 55 PEPPLPL-----AAAAPPPLNP--TPPRAAPSVIVST 85

QY 130 TDYPGPHSFDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPOGAVIRAM 189

Db 86 EDYGDGDFPFRVGFAGTAKSVTCYSPVLNKKVYRLAKRPPGVQVAVAPPGSSLRVAV 145

QY 190 PYKKAHEHYEVKRCPNHELSEFNEGOIAPPSHLIRVGNHAGYVEDPITGRQSVLY 249

Db 146 AVYKSEHVAEYVKKCPHERKRGCGGTDG-LAQGLILVVEGPPQARHHDDETKRHSAVYV 204

QY 250 PYEPVGTETFTTVLYNFCNNSCVGMNRRPILITVLETRDGOVLGRGFEARICACP 309

Db 205 PYEPVGTETFTTVLYNFCNNSCVGMNRRPILITVLETRDGOVLGRGFEARICACP 264

QY 310 GDRKRAEDSIRKQOVSDSTKNGDG--TRKPPRONTHGIQMTSIKRSPDDELTYLTVR 367

Db 265 GDRKRIEENFRK-----RGAGGVAKRAMSPTEAPEPK-KRVLPNDNEIFLYQVLR 316

QY 368 GREYEMLKIKESLELMQ 386

Db 317 GRRRYEMLKIKESLELMQ 335

RESULT 4

S51648

cellular tumor antigen p53 - bovine

N:Alternate names: tumor-suppressor protein p53

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S51648

R:Dequiedt, F.; Williams, L.; Burny, A.; Kettmann, R.

submitted to the EMBL Data Library, September 1994

A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and it

A:Reference number: S51648

A:Accession: S51648

A:Molecule type: mRNA

A:Status: preliminary

A:Residues: 1-386 <DEQ>

A:Cross-references: EMBL:X81704; NID:9602332; PIDN:CAA57348.1; PID:9602333

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprote

F,168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F,385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.7%; Score 740; DB 1; Length 386;

Best Local Similarity 45.88; Pred. No. 1.5e-43;
Matches 152; Conservative 57; Mismatches 94; Indels 29; Gaps 8;

```

0Y      SPVADPSTFDALSSPP-----IPSNIDPPEHSEDVFSQOSSRAKATWYYSLEL 159
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      APAAPRAT-----PAPATSNPPLSSFFVSQTTYPEONYGFRIGFILOSIGRAKSYTCYSSSL 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      KKYCQIAKTCPIQIKVMTPPPGQAVIRAMPYKKAHEVTEVVKRCPHNELSREPEGOI 219
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      NKLFQIAKTCPIVQIOWMDSPPPPGFRVYRAMAIYKKLEHMETEVVRRCPIHHERSDSDG-L 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      APPSHLIVEENSHAOVEDPITGOSVLAHYEPQVOTEEFTYLYUNMCNSSCGGNRR 279
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      APQGHILRVENLRAEYIEDDKNTFRHSAVYVEESEIDSECTTIYANMCNSSCGGNRR 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      APPSHLIVEENSHAOVEDPITGOSVLAHYEPQVOTEEFTYLYUNMCNSSCGGNRR 279
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      APQGHILRVENLRAEYIEDDKNTFRHSAVYVEESEIDSECTTIYANMCNSSCGGNRR 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      RPILIYVLEFRDQVIGRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRPF 339
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      RPILIYVLESCGMLGRNSEFEVAVCACPDRTREENIRKKQOSCPEPPRSTKRAL 301
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      RQNTHGIDMTSIRKRRSP-DELLIYLPVRGRETYMLLKIKESLEIMQYLPOHNTETFRQ 398
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      PTNT-----SSSPQPKKKRPLDEEYFTLIQIRGRKRYEMFEINDALEL-----KDALDGREP 352
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      QQQQQQH-OHLQKQTSIOSSPSYGNSSPLK 429
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      GSRHSHSLKSK-----KRPSPCSKKKRPMKLR 380
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 5

Cellular tumor antigen p53 - rat
N:Alternate names: gene p53 protein; nuclear oncoprotein p53
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence
C:Accession: S02192; S41149
R:Soussi, T.; de Fromental, C.C.; Breugnot, C.; May, E.
Nucleic Acids Res. 16, 11384, 1988
A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A:Reference number: S02192; MUID:85083585; PMID:3060862
A:Accession: S02192
A:Molecule type: mRNA
A:Residues: 1-391 <SD>
A:Cross-references: EMBL:X13058; NID:g56828; PIDN:CAA31457.1; PID:g56829
R:Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A:Title: Structure of the rat p53 tumor suppressor gene.
A:Reference number: S41149; MUID:93181268; PMID:8441680
A:Accession: S41149
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173, 'W', 175-391 <HUU>
A:Cross-references: EMBL:L07909
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:
A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoblasts; cell division control; DNA binding; homotetramer; nucleus; phospho
E:114,177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
E:330/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

	Query Match	21.6%; Score 735; DB 1; Length 391;
	Best Local Similarity	38.3%; Pred. No.3.5e-43;
	Matches 171; Conservative	72; Mismatches 134; Indels 70; Gaps 13;
QY	2 SOSTOTEEFV-LSPVEFOHIMWPLEQCITCVOPIDILNFVDEPSEDATNKIEISMDCINMQ	60
	: : : :	
Db	4 SQDSMSLEPLSQGTFCSCMKLL--PPDDILP-----TTATGSPSMSE-----	44
QY	61 DSDLSDPMPQPYTNGLINSMDQOIQNGSSSTPYNTDHAONSVAPAYAPQSFTDAL	120
	: : : : :	
Db	45 -----DLFLPDGV-AELLEGPEALQVSAPAAGEGTE-----APAPVAASATPPPL	91
QY	121 SPSPAIISNDIPCPHFDFVSFOQSSSTAASKATWTYSIELKKLYCOIACTCPQIKRVMPR	180

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Db      92  $$$--VP$KTYQ$N$G$H$F$L$G$T$A$K$S$W$M$C$T$S$I$S$L$N$K$L$F$Q$L$K$T$C$P$Y$Q$L$M$W$T$P 149
Qy      181  P$G$A$V$R$A$M$P$Y$K$K$A$E$H$T$E$V$V$K$R$C$P$N$H$E$L$R$E$N$E$G$-I$P$S$H$L$I$R$B$G$N$H$A$O$Y$E$D 239
Db      150  P$C$T$R$V$R$A$M$A$I$Y$K$K$S$O$H$M$T$E$V$V$R$C$P$H$H$E$--R$C$S$D$G$G$L$P$O$H$L$I$R$B$G$N$P$A$E$Y$D$D 206
Qy      240  P$I$G$R$O$S$V$V$P$E$R$P$O$V$G$E$F$E$T$Y$V$N$M$C$N$S$C$G$G$N$R$R$P$I$L$Y$T$E$R$O$Q$V$G$R 299
Db      207  R$O$T$F$R$S$V$V$V$P$E$R$P$O$V$G$D$Y$T$T$H$K$Y$M$C$N$S$C$G$G$N$R$P$I$L$Y$T$E$D$S$S$N$L$G$R$D 266
Qy      300  C$E$P$A$R$I$C$A$P$G$D$R$A$D$E$S$I$R$K$O$O$V$S$D$S$T$K$N$G$D$T$K$R$P$O$N$T$H$G$I$O$M$S$I$K$K$R$S$P$-D 358
Db      267  S$E$F$V$R$V$C$A$P$G$D$R$R$E$E$N$E$F$K$K$E$H$O$C$D$E$L$P$P$S$A$K$A$L$P$T$S$----S$S$P$Q$K$K$P$D 322
Qy      359  D$E$L$L$I$V$P$V$G$R$E$T$E$M$L$K$I$K$E$L$S$E$L$M$O$Y$L$P$O$H$T$E$Y$R$O$O$O$O$H$O$H$L$O$K$O$T$S$I$O$S$P$S 418
Db      323  G$E$F$T$L$K$I$G$R$E$F$E$F$E$F$R$E$L$N$E$A$L$E$L$K$-----D$A$R$A$E$R$S$C$D 359
Qy      419  S$Y$G$N$S$P$L$N$K$--M$N$S$M$K$L$P$S$E$Q$L 442
Db      360  S$R$A$H$S$Y$P$T$K$G$O$S$T$S$R$H$K$K$P$M$I$K$V 386

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RESULT 6

cellular tumor antigen p53 - golden hamster
N:Alternate names: tumor-suppressor protein p53
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH06933
R:Legros, Y.; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992
A:Title: The cDNA cloning and immunological characterization of hamster p53.
A:Reference number: JH06933; MUID:92210007; PMID:1355773
A:Accession: JH06933
A:Molecule type: mRNA
A:Residues: 1-396 <LG>
A:Cross-references: GB:W75144; NID:g191414; PIDN:AAA37085.1; PID:g191415
A:Experimental source: kidney, strain MP1
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
F:179,180,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:335/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

[illegible]

Db 283 RDRTEKNFKGKCELPKSAKRALPTNT---SSSPQPKRKLDEYFTLKINGOE 339
 QY 371 TYEMLTKIKESLEL 384
 Db 340 RPKMFOELNEALEL 353

RESULT 7
 DNH053
 cellular tumor antigen p53 [validated] - human
 M.Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppressor
 C.Species: Homo sapiens (man)
 C.Date: 05-Oct-1988 #sequence-revision 18-Nov-1994 #text-change 15-Sep-2000
 C.Accession: A25224; A43073; J0436; S40773; S42669; A22837; A55060; A25397; S42405; I58354; I78850; I52681; S60153
 R.Lamb, P.; Crawford, L.
 Mol. Cell. Biol. 6, 1379-1385, 1986
 A.Title: Characterization of the human p53 gene.
 A.Reference number: A25224; MUID:87064416; PMID:2946935
 A.Accession: A25224
 A.Molecule type: DNA
 A.Residues: 1-393 <LAM>
 A.Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AA59987.1; PIDN:AA59987.1; Chumakov, P.M.; Nikitina, N.N.; Samarina, O.P.; Georgiev, G.P.
 Gene 70, 245-252, 1988
 A.Title: A variation in the structure of the protein-coding region of the human p53 gene
 A.Reference number: J0436; MUID:89108008; PMID:2905688
 A.Accession: A43073
 A.Molecule type: DNA
 A.Residues: 1-393 <BUC1>
 A.Cross-references: EMBL:M22898; NID:g189474
 A.Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro allele
 A.Accession: J0436
 A.Molecule type: DNA
 A.Residues: 1-71, 'P', '73-393 <BUC2>
 A.Cross-references: EMBL:M22898; NID:g189474; PIDN:AA59988.1; PID:g189476
 R.Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.
 A.Note: this 72-Pro allele was found in both normal and malignant cell lines
 submitted to the EMBL Data Library, August 1990
 A.Reference number: S40773
 A.Accession: S40773
 A.Molecule type: DNA
 A.Residues: 1-393 <CHD>
 A.Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
 R.Matlaasewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, S.
 EMBO J. 3, 3257-3262, 1984
 A.Title: Isolation and characterization of a human p53 cDNA clone: expression of the human p53
 A.Reference number: S42669; MUID:85126934; PMID:6396087
 A.Accession: S42669
 A.Molecule type: mRNA
 A.Residues: 1-393 <MKI1>
 A.Cross-references: EMBL:X01405; NID:g35215; PIDN:CAA25652.1; PID:g642241
 R.Zakut-Houri, R.; Blenz-Padmon, B.; Glivol, D.; Oren, M.
 EMBO J. 4, 1251-1255, 1985
 A.Title: Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.
 A.Reference number: A22837; MUID:85230577; PMID:4006516
 A.Accession: A22837
 A.Molecule type: mRNA
 A.Residues: 1-71, 'P', '73-393 <ZAK>
 A.Cross-references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210
 R.Harlow, E.; Williamson, N.M.; Ralston, R.; Heltman, D.M.; Adams, T.E.
 Mol. Cell. Biol. 5, 1601-1610, 1985
 A.Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tumor antigen p53
 A.Reference number: A55060; MUID:85267676; PMID:3894933
 A.Accession: A55060
 A.Molecule type: mRNA
 A.Residues: 1-71, 'P', '73-393 <HAR>
 A.Cross-references: GB:K03199; NID:g189478; PIDN:AA59989.1; PID:g189479
 R.Harris, N.; Billi, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Rotter, V.
 Mol. Cell. Biol. 6, 4650-4656, 1986
 A.Title: Molecular basis for heterogeneity of the human p53 protein.
 A.Reference number: A93086; MUID:87089826; PMID:3025664

A.Accession: A25397
 A.Molecule type: mRNA
 A.Residues: 1-78, 'T', '80-393 <HAR1>
 A.Cross-references: EMBL:M1694; NID:g339813; PIDN:AA61211.1; PID:g339814
 A.Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
 A.Accession: B25397
 A.Molecule type: mRNA
 A.Residues: 1-71, 'P', '73-78, 'T', '80-393 <HAR2>
 A.Cross-references: EMBL:M1695; NID:g339815; PIDN:AA61212.1; PID:g339816
 A.Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
 R.Matlaasewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
 Mol. Cell. Biol. 7, 961-963, 1987
 A.Title: Primary structure polymorphism at amino acid residue 72 of human p53.
 A.Reference number: S42452; MUID:87144273; PMID:3547088
 A.Accession: S42452
 A.Molecule type: mRNA; DNA
 A.Residues: 66-71, 'P', '73-79 <MKI2>
 A.Experimental source: clone lambda C113
 A.Note: 72-Cys was also found, and appears to represent a polymorphism
 A.Accession: S42453
 A.Molecule type: mRNA; DNA
 A.Residues: 66-79 <MKI3>
 A.Experimental source: clone J6K
 R.Patrelli, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.; Crook, T.
 EMBO J. 10, 2879-2887, 1991
 A.Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
 A.Reference number: I38082; MUID:92007731; PMID:1915267
 A.Accession: I38082
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-189, 'L', '192, 'R', '194-393 <F02>
 A.Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA2625.1; PID:g506433
 A.Note: deletion of a C nucleotide causes a frameshift at position 566
 A.Accession: I38083
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-192, 'R', '194-393 <F02>
 A.Cross-references: EMBL:X60011; NID:g506434; PIDN:CAA2626.1; PID:g506435
 A.Accession: I38084
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-393 <F03>
 A.Cross-references: EMBL:X60012; NID:g506436; PIDN:CAA2627.1; PID:g506437
 A.Accession: I38085
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-245, 'T', '247-393 <F04>
 A.Cross-references: EMBL:X60013; NID:g506438; PIDN:CAA2628.1; PID:g506439
 A.Accession: I38086
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-247, 'Q', '249-393 <F05>
 A.Cross-references: EMBL:X60015; NID:g506442; PIDN:CAA2630.1; PID:g506443
 A.Accession: I38088
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-71, 'P', '73-237, 'Y', '239-393 <F07>
 A.Cross-references: EMBL:X60016; NID:g506444; PIDN:CAA2631.1; PID:g506445
 A.Accession: I38089
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-247, 'Q', '249-393 <F08>
 A.Cross-references: EMBL:X60017; NID:g506446; PIDN:CAA2632.1; PID:g506447
 A.Accession: I38090
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-71, 'P', '73-162, 'H', '164-393 <F09>
 A.Cross-references: EMBL:X60018; NID:g506448; PIDN:CAA2633.1; PID:g506449

A:Accession: I38091
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212, 'Q', 214-393 <F10>
 A:Cross-References: EMBL:X60019; NID:9506450; PIDN:CAA42634.1; PID:9506451
 A:Accession: I38092
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-253, 'D', 255-393 <F11>
 A:Cross-References: EMBL:X60020; NID:9506452; PIDN:CAA42635.1; PID:9506453
 A:Note: all sequences submitted to the EMBL/GenBank/DBJ databases June 1991
 R:Putnal, P.A.; Barrett, J.C.; Wiseman, R.W.
 Nucleic Acids Res. 19, 6977, 1991
 A:Title: An Alu polymorphism intragenic to the TP53 gene.
 A:Reference number: I38093; MUID:92107726; PMID:1762841
 A:Accession: I38093
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-393 <FUT>
 A:Cross-References: EMBL:X54156; NID:935213; PIDN:CAA38095.1; PID:935214
 R:Yamada, Y.; Yoshida, T.; Hayaashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakatani, C.
 Res. 51, 5800-5805, 1991
 A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell line
 A:Reference number: A44905; MUID:92034678; PMID:1933850
 A:Accession: A44905
 A:Molecule type: DNA
 A:Residues: 246-247, 'W', 249-250 <YAM>
 A:Cross-References: GB:S63157; NID:9237829; PIDN:AAB20140.1; PID:9237830
 A:Note: sequence extracted from NCB1 backbone (NCIN:63157, NCBIP:63158)
 A:Note: mutation from a liver metastasis of a gastric cancer
 R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
 Oncogene 6, 1067-1071, 1991
 A:Title: Use of the single strand conformation polymorphism technique and PCR to detect
 A:Reference number: I58354; MUID:91296386; PMID:1648702
 A:Accession: I58354
 A:Molecule type: DNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 244-247, 'W', 249-252 <HEN1>
 A:Cross-References: GB:S41969; NID:91679931; PIDN:AAB19324.1; PID:9232814
 A:Accession: I78850
 A:Molecule type: DNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 274-277, 'S', 279-282 <HEN2>
 A:Cross-References: GB:S41977; NID:91679932; PIDN:AAB19325.1; PID:9232816
 R:Chow, V.T.; Quek, H.H.; Tock, E.P.C.
 Cancer Lett. 73, 141-148, 1993
 A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphoblastoid cell line
 A:Reference number: I52681; MUID:94036762; PMID:8221626
 A:Accession: I52681
 A:Molecule type: mRNA
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 327-331, 'DOTSFQKENC', <CHO>
 A:Cross-References: GB:S6666; NID:9436292; PIDN:AAB28601.1; PID:9436293
 A:Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymphoblastoid cell line
 R:Peterson, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Baurz, E.K.F.
 Mol. Gen. Genet. 249, 425-431, 1995
 A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragments
 A:Reference number: S60151; MUID:96133682; PMID:8552047
 A:Accession: S60151
 A:Molecule type: DNA
 A:Residues: 3-44 <PNT>
 R:Dang, C.V.; Lee, W.M.F.
 J. Biol. Chem. 264, 18019-18023, 1989
 A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, p53, HSP70,
 A:Query Match 21.1%; Score 718; DB 1; Length 393;
 Best Local Similarity 38.4%; Pred. No. 5, 2e-42;
 Matches 163; Conservative 69; Mismatches 132; Indels 60; Gaps 12;
 11 LSPFQHTWDFLEPGICVQPTDLNFVDEPSEDAKTKIEISMCIKMODSDLSPPMP 70
 14 ISOETFSIDWKLLP-----NNVLSPLPSQAMDLMLSPDIEQWFE--DP--- 58

QY 71 QXTNLGLNMDQOIQNGSSSTPYNTDHAQNSVAPSPAPSPFDLSP-----SPA 126
 DB 59 -----GPEAPRMEAPR--VAPAP-AAFTPAAPAPAPSPSSSV 97
 QY 127 PSNTDYPGPHSPDVSFOQSSSTAKSATMTSTELKLYCOIAKTCPIQIIVMTPPGAVI 186
 DB 98 PSQKTYQSGYGRGLGTLGSHGTAQSVCTYSPALNKKFQCLAKCPQLWVDSPPPGTIV 157
 QY 187 RAMPYKKAHEVTEVVKRCPNHELSEFNEGQIAPPSHLIRVGNSHAQVDEPTIGROS 246
 DB 158 RMAITKQSOHMTTEVVRCPNHE--RCSQSDGIAPQOHLIRVGNIRVLEDDRNFRRS 215
 QY 247 VLVPYEPPOVGEFTVLTNFMQNSCVCYGMNRPILITVLTETPDGCVLGRCPFARIC 306
 DB 216 VVPTPEPPEVSDCTITHNYMCNNSCGMNRPLITITLEDSSGNLGRNFEVRVC 275
 QY 307 ACPGRDKADEDSIRKQVSDSTKNGDGTGRPFONTHTGIOMTSIKRRSP--DDELLYLP 365
 DB 276 ACPGRDRREERLEFRKGPBPHHELPGSTKRALPNMT---SSPQPKKKPLDGEVFTIQ 331
 QY 366 VGRREYEMALKESLELMQYLP-----QHT--IEYRQOQOQHHLQKTSIQ 415
 DB 332 IGRERFEMFRELNEALELKDQAGKEPGSGRAHSSHLKSKQSTSRKKLMFK--TE 388
 QY 416 SPSS 419
 DB 389 GPDSS 392
 RESULT 8
 DNMS53
 N:Alternate names: oncoprotein p53
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #ext_change 11-May-2000
 C:Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
 R:Blenz, B.; Zakut-Houri, R.; Gliovol, D.; Oren, M.
 EMBO J. 3, 2179-2183, 1984
 A:Title: Analysis of the gene coding for the murine cellular tumour antigen p53.
 A:Reference number: A22739; MUID:85027173; PMID:6092064
 A:Accession: A22739
 A:Molecule type: DNA
 A:Residues: 1-134, 'V', 136-390 <BIE>
 A:Cross-References: GB:X00876; NID:9871420; PIDN:CAA25420.1; PID:9871421; GB:X01237;
 R:Chumakov, P.M.
 Bioorg. Khim. 13, 1691-1694, 1987
 A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.
 A:Reference number: S06336; MUID:88221682; PMID:3329909
 A:Accession: S06336
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-134, 'V', 136-390 <CHU>
 R:Zakut-Houri, R.; Oren, M.; Blenz, B.; Lavie, V.; Hazum, S.; Gliovol, D.
 Nature 306, 594-597, 1983
 A:Title: A single gene and a pseudogene for the cellular tumour antigen p53.
 A:Reference number: A02684; MUID:84068204; PMID:6646235
 A:Accession: A02684
 A:Molecule type: mRNA
 A:Residues: 1-159, 'H', 161-167, 'G', 169-233, 'T', 235-390 <AK>
 A:Cross-References: GB:X01237; GB:X01700; NID:953375
 R:Rat, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
 Mol. Cell. Biol. 6, 3232-3239, 1986
 A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
 A:Reference number: S38822; MUID:87064640; PMID:3023970
 A:Accession: S38822
 A:Molecule type: mRNA
 A:Residues: 1-390 <ARA1>
 A:Cross-References: EMBL:M13872; NID:9200198; PIDN:AAA39881.1; PID:9200199
 A:Accession: S38823
 A:Molecule type: mRNA
 A:Residues: 1-167, 'G', 169-233, 'T', 235-390 <ARA2>
 A:Cross-References: EMBL:M13873
 R:Rat, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

submitted to the EMBL Data Library, July 1988

A:Reference number: S40014

A:Accession: S40014

A:Molecule type: mRNA

A:Residues: 1-167, 'G', 169-390 <RAA3>

A:Cross-references: EMBL:M1873; NID:g200200; PIDN:AAA39882.1; PID:g200201

R:Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.

Nucleic Acids Res. 12, 5609-5626, 1984

A:Title: Cloning and expression analysis of full length mouse cDNA sequences encoding th

A:Reference number: 148703; MUID:84272240; PMID:6379601

A:Accession: 148703

A:Status: translated from GB/EMBL/DBUT

A:Molecule type: mRNA

A:Residues: 1-47, 'R', 49-78, 'QW', 82-390 <RES>

A:Cross-references: EMBL:X00741; NID:953570; PIDN:CAA25323.1; PID:953571

C:Comment: This DNA-binding protein plays an essential role in the regulation of cell di

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;

F:1-44/Domain: transcription activation #status predicted <TRA>

F:16-26/Region: conserved region I

F:99-289/Domain: DNA-binding core #status predicted <DBC>

F:108-121/Region: L1 loop

F:114-139/Region: conserved region II

F:160-192/Region: L2 loop

F:168-178/Region: conserved region III

F:231-252/Region: conserved region IV

F:233-248/Region: L3 loop

F:267-283/Region: conserved region V

F:313-319/Region: tetramer association

F:319-357/Region: nuclear location signal

F:7-9, 12, 18, 23, 37/Binding site: phosphate (Ser) (covalent) #status predicted

F:173, 176, 235, 239/Binding site: zinc (Cys, His, Cys) #status predicted

F:312/Binding site: phosphate (Ser) (covalent) (by cdcd kinase) #status predicted

F:389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.1%; Score 717; DB 1; Length 390;

Best Local Similarity 38.0%; Pred. No. 6e-42;

Matches 167; Conservative 63; Mismatches 129; Indels 80; Gaps 13;

QY 2 SOSTQTNEF-LSPEVQHIMDFLEQPTCSVQPIDLNFDEPSEDGATNKIISMDICIMQ 60

DB 7 SQSISLEPLRSQETFSIMKLL-----PPED-----ILPSPIC----- 40

QY 61 DSDLSDPMPQYTNILGLINSMDOQIQNGSSSTSPYNTDHAQNSVT-APSPYAOPSSPTDA 119

DB 41 ---MDLLLPQ-----DVEEFEGEPSEALRVSGADPAODPVTEGPAV----- 81

QY 120 LSPSPA-----IPSTWDYPPGPHSPVFSQGSSTASATWYSTEKLKLYCQIAKTC 171

DB 82 --PAPATPWPUSFSVPSQKTYQGNVGFILGFLGSLGTAQSVNCTYSPPLNKLFQCOLAKTCP 139

QY 172 IQIKVMTPPPGAGAVIRAPVYKKAHVTEVVKRCENHLSRENFEGQ-IAPPSHLIRVEG 230

DB 140 VQIWMVSAFPPAGSVRAIAIKKQHMTEVVRCPHNE--RCSGSGGLAPPHILIRVEG 196

QY 231 NSHAQVYEDPITGQSVLVPEPQVQTEFTTVLYNFQCNSSCVGGMRRPILITVLET 290

DB 197 NLPEYLEDROTFHFHSVYVPEPEAGSEYTTIHKKYCNSSCGMRRPILITILED 256

QY 291 RDGQVILGRCPFEARICACPGDRKADDSIRKQOVSDSTKNGDGTKRFRONTGICQMTS 350

DB 257 SSGMLLRDSFEVACACPGDRKTEENFRKKRVLEPDLPGSAKRALPTCT---SASP 313

QY 351 IKRRSPDDELILYPVGARETYEMLKIKESLELMQVLPQRTIE-----TYR 397

DB 314 PQKKRPIDGELYTLKINGRKFEFRLNEALELKD---AAATEBSGDSRAHSYLTKTK 370

QY 398 QQQQOHOHLQKQTSIOS 416

DB 371 GQSTSRHKTKTKVKKVGPDS 389

RESULT 9

S06594

cellular tumor antigen p53 - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S06594

R:Rigaudy, P.; Eckhart, W.

Nucleic Acids Res. 17, 8375, 1989

A:Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p5

A:Reference number: S06594; MUID:90045967; PMID:2530498

A:Accession: S06594

A:Molecule type: mRNA

A:Residues: 1-393 <RID>

A:Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho

F:176, 179, 238, 242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F:392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.0%; Score 714.5; DB 1; Length 393;

Best Local Similarity 41.2%; Pred. No. 9.1e-42;

Matches 156; Conservative 63; Mismatches 113; Indels 47; Gaps 10;

QY 11 LSPEVQHIMDFLEQPTCSVQPIDLNFDEPSEDGATNKIISMDICIMQSDLPMP 70

DB 14 LSETFSDMLKLEP-----NNVLSPLPSQAVDMLSP-----DLA--QW- 53

QY 71 QYTNGLINSMDOQIQNGSSSTSPYNTDHAQNSVAPSPYQPSSTFDALSP---SPAI 126

DB 54 -----LTEDGPPDEAPRMSDAAH--MAFPP-AAFPPAAPAPSPMLSSV 97

QY 127 PSNTDYPGPHSFDVSPQGSSTAKSATWYSTEKLKLYCQIAKTCPIQIKVMTPPGAGAVI 186

DB 98 PSQKTYHGSYGFRLGFLHSGCATSVCTYSPDLNMFQALAKTCVPQLWVSDTPPGSRV 157

QY 187 RAMPYKKAHVTEVVKRCENHLSRENFEGQIAPPSHLIRVEGNSHAQVYEDPITGQOS 246

DB 158 RAMALYKQSQHMTVEVVRCPHNE--RCSDSGLAPPHILIRVEGRLVEYSDDRNTPRHS 215

QY 247 VLVPYEPQVQTEFTTVLYNFQCNSSCVGGMRRPILITVLETFRDGOVLGRCPFEARIC 306

DB 216 VVPEYEPPEVSDCTTHYTNMCNSSCGMRRPILITILEDSSGMLLRNSFEVAVC 275

QY 307 ACPGRKADDSIRKQOVSDSTKNGDGTKRFRONTGICQMTSIRKRSR-DEELVLP 365

DB 276 ACPGRDRTEENFRKKRVLEPDLPGSTKRALPNT-----SSSPQPKKPLDGEYFTLQ 331

QY 366 VGRGTYEMLKIKESLEL 384

DB 332 IRGRREFEFRLNEALEL 350

RESULT 10

S38824

cellular tumor antigen p53, minor splice form - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S38824; S35478

R:Araki, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

MOL. CELL. BIOL. 6, 3232-3229, 1986

A:Title: Immunologically distinct p53 molecules generated by alternative splicing.

A:Reference number: S38822; MUID:87064640; PMID:3023970

A:Accession: S38824

A:Molecule type: mRNA

A:Residues: 1-381 <ARA>

A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203

Nucleic Acids Res. 20, 1979-1981, 1992

A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different t

A:Reference number: S35478; MUID:92253421; PMID:1579500

A:Accession: S35478

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

OY 126 -----IPSTNDYPCGHSFVDSFQSSAKSATWTSTELKLYCQIAKTCPQIKVMPDP 181
Db 90 LSSSPSQKTYHGNYGFLGFLHSGTAKSVCTCTSPCLNFKFCQIAKTCPQLWWDSTPP 149
OY 182 OGAVIRAMPVYKKAHEVYVRCRPNHLSREFNEGOIAPPSHLIRVGNSHAQVDEPI 241
Db 150 PGTIRKAMATYKKSOMHEVYVRCRPNHE--RCSDSDGLAPPOHLIRVGNRAETLDRN 207
OY 242 TGRSVLVPYEPPOVGETTYLVLYNFMCSNCVSGMNRPLIIVTETRDQVYLGRCF 301
Db 208 TFRHSVYVYEPPEVGSCTTIHYNMCSNCSMGMMNRPLITITLEDSSGNLLGRSF 267
OY 302 EARLCACPRGRKADEDSIRKQVSDSTKNGDKTRPRONTHTGIQMTSIRKRSDDDEL 361
Db 268 EVRCACPRGRDRREEMFRKKGEPCDELPPGSSKRALPTT--TDSSPQTKRKLDEY 325
OY 362 LYLPRGRETEMLKIKESDEL 384
Db 326 FILKIRGERFERMELEL 348

RESULT 13

146226

Cellular tumor antigen p53 - dog (fragment)

C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-May-2000
C:Accession: I46226
R:Devilee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, C.
Anticancer Res. 14, 2039-2046, 1994
A:Title: The canine p53 gene is subject to somatic mutations in thyroid carcinoma.
A:Reference number: I46226; MUID:95150524; PMID:7847847
A:Accession: I46226
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-77 <DEV>
A:Cross-references: GB:I27630; NID:g508454; PID:AA037327.1; PID:g508455
A:Gene: p53
C:Genetics:
A:Introns: 24/1; 61/3
C:Superfamily: cellular tumor antigen p53

Query Match 7.6%; Score 259.5; DB 2; Length 77;
Best Local Similarity 60.3%; Pred. No. 2.2e-11;
Matches 47; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

OY 194 KAEHTEVYKRCRPNHLSREFNEGOIAPPSHLIRVGNSHAQVDEPIYTGROSLVYEP 253
Db 1 KSEVTVYVRCRPNHLSREFNEGOIAPPSHLIRVGNSHAQVDEPIYTGROSLVYEP 253
OY 254 POGTEFTYVLYNFMCSN 271
Db 60 PEVGFDTYTHYNYMCSN 77

RESULT 14

T19361

hypothetical protein C17G1.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T19361
R:White, S.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19114
A:Accession: T19361
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-925 <WIL>
A:Cross-references: EMBL:Z78415; PID:CA01670.1; GSPDB:GN00028; CESP:C17G1.4
A:Experimental source: clone C17G1
C:Genetics:
A:Gene: CESP:C17G1.4
A:Map position: X
A:Introns: 40/3; 98/2; 295/1; 443/3; 590/3; 619/3; 691/1; 810/1; 868/3

C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo

Query Match 4.4%; Score 149.5; DB 2; Length 925;
Best Local Similarity 23.3%; Pred. No. 0.028;
Matches 127; Conservative 54; Mismatches 199; Indels 167; Gaps 28;

OY 65 SDPMPOYTNI--GLINSMDQIQNGSSST-----SPYNTDHNQSVYADSP 109
Db 430 SSPGSSLMPLNGQVPSMTQNMQSPASTSMPEFKEPAVPIRHSPOQMTILOSVPVHSP 489
OY 110 YAGSSFTDASPSPALPSNDYFGPHSFVDSFQSSAKSATWTSTELKLYCQIAKT 169
Db 490 NGAPPA-VNAPSSSKT-PDPYQOQRPHS--PTFAVPTLPAAATLAQASAMQISTK-PKT 544
OY 170 CPQIK-----VMPFP-----PGAVYR-----AMPYKKAHY-----TEVVKRCPNHLSRE 213
Db 545 SPQKKHEDGVPEPPTADTPTTYTHYELPAAAFRLRQTLVAGNDKYNHPEYKHYFSRK 604
OY 214 FNEGOIAPPSHLIRVEG-NSHAQVDEPIYTGROSLVYEPPOVGETTYLVLYNFMCSN 272
Db 605 RQGLRVYR-----EGINSHPTPTTEBTEFGFMQGNFYDPK-----YNRM----- 645
OY 273 CVGGMNRPLIIVTETRDQVYLGRCFEARICACPRGRKKADEDSIRKQVSDSTKNG 332
Db 646 -----VPSQTSNPGPPLISR-----SOSWHTPMISPNFNAS 675
OY 333 DGTKRPFRONTHTGIQMTSIRKRSDDDEL-----LYLPRGRETEMLKIKESDELMOY 387
Db 676 -----QPSISGNO--PAKARASASDEPPFVNPVPPSSRGSGMDROLOOQOIQMOY 726
OY 388 LPQHTIETTYROOQOQHLLQKQTSI--OSPSSYGN-----SSPLINKNSMKNL 436
Db 727 -HGH-----MQMKQOQOQMAAQOQMSRKGSGSSAGGSQLPSLSPSLQADSMFOL 781
OY 437 PVSQQLINPQQRNALTPPTIPDGKGANIPMGTHMPMAGMDGSLPQALP----- 487
Db 782 PSQOO-----PPKGG--PPANMHGGMQPMNIGTTEGTYVNI 816
OY 488 -----PPLSM---PSTSHCTPPPPYPTDCISVFLARIGSSCLDYFTTQGLTT 533
Db 817 GLNSNNAAGLPPLSLRSQGPDSQNDPFGIPSTSS--SNQAHALCAGC--HHFLMPGSSST 873
OY 534 IYQIEH 539
Db 874 LSCLYH 879

RESULT 15

T15264

hypothetical protein F59E12.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15264
R:Johnson, D.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid F59E12.
A:Reference number: Z18318
A:Accession: T15264
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1621 <JOH>
A:Cross-references: EMBL:AF003386; NID:g2088833; PID:g2088843; PID:AA054259.1; GSPDB
A:Experimental source: strain Bristol N2; clone F59E12
C:Genetics:
A:Gene: F59E12.9
A:Map position: 2
A:Introns: 30/3; 55/1; 200/2; 299/2; 327/2; 369/3; 589/3; 860/1; 986/1; 1278/1; 1547/

Query Match 4.2%; Score 144.5; DB 2; Length 1621;
Best Local Similarity 19.6%; Pred. No. 0.14;
Matches 111; Conservative 69; Mismatches 239; Indels 147; Gaps 24;

OY 3 OSTQTFN-----FLSPVEVQHIIMDFLEQFICSVQPIDL-----NFVDEPSEDG 45

```
Db 920 QQTQENBEKETWKKDSRASISPK-----ICSKNADATSEAVNHSTPSTSEDL 967
QY 46 ATKKEISMDCIr-----MODSLD-----PMMPQYTNIGLN 79
Db 968 ASKKEVFILOIVSSAKOIEIVASAKDFMADPDVSDSKDKIKOIOEKIDEKALKAE 1027
QY 80 SMDQOJONGSSSTSPYNTDHAQNSVTAPS---PYAQPSSTFDALSPSP-AIRPSNTDYPG 134
Db 1028 KMKOKTQTSDDLEEPSISEOTLGAEVPSKSNLDFSRPPPIFSQOSAAPHVVTASMDVPS 1087
QY 135 PHSFDVSPQOOSSTAKSATWYSTELKLYCOIAKTCPIQIKVMTPPQGAIVIRAMPVYKK 194
Db 1088 -SSAAVQSQHPMTAQSVT-PMASHIVVAPVVPVPTIIPPPVPPPT--ATSTQSQ 1142
QY 195 AEHVTEVVKRCRNHELSRENEGQIAP-PSHLIRBGNSHAQYVEDPITGRQSVLVYEP 253
Db 1143 QPOFLEGLMTDNEIVADAIRGMVAPIQOELIMGSGPGHIRDSQPAL-TASVL----- 1196
QY 254 PQVGETFTVLYNFMGNSCQVGMNRPIIIVTLETRDQVLRGRCFEARIACPGDR 313
Db 1197 --TGSSLEADMRLM-----EMNR-----IQEKRFQ----- 1223
QY 314 KADEDSIRKQVSDSTKNGDGTKRPPRONTGIGMTSIKK-----RSPDDELLYL----- 364
Db 1224 --DMDEVERR--NIRRGYRPPPFHNGTDMERDMERDHSMMRPRPHPLQMDTAP 1279
QY 365 PVNGRETYEMLKIKESLELMQYLPOHTIE--TYRQOQOQOHOHLQKOTSIQSPSSYG 421
Db 1280 PQMGSDP-----PQPSSECPAPRNSSKRNRRNRGRNTNEHIOANHEDSDSFSTSR 1332
QY 422 NSSPPLNKMSNMKLPSQILNPQQRNALPTTIPDGMCANIPMGTHMPMAGDMNGIS 481
Db 1333 SSSPS-----PPPPPPPPPSDDLTPVPPPPPPPTMSKAPGVLP-----VP 1377
QY 482 PTOALPPPLSMPTSHCTPPPPYPTD 507
Db 1378 P---PPPLFSPSMILPPPPPLPSE 1399
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Search completed: August 7, 2003, 09:53:19
Job time : 23.2089 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:32:13 ; Search time 11.3675 Seconds

(without alignments)
2651.784 Million cell updates/sec

Title: US-09-538-106-13

Perfect score: 3405

Sequence: 1 MSOSTQTEHPSPEVQHIV.....FNFDMDARRNKQRIKEGE 641

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1790	52.6	636	1	P73_HUMAN
2	1769.5	52.0	637	1	P73_CERAE
3	847.5	24.9	396	1	P53_ONCMY
4	819.5	24.1	369	1	P53_BARBU
5	805.5	23.7	373	1	P53_BRARE
6	795	23.3	376	1	P53_ICTPU
7	777.5	22.8	363	1	P53_XENLA
8	776	22.8	367	1	P53_TETMU
9	771	22.6	386	1	P53_PIG
10	770	22.6	386	1	P53_FELCA
11	764.5	22.5	367	1	P53_CHICK
12	758.5	22.3	381	1	P53_CANFA
13	746.5	21.9	352	1	P53_ONYLA
14	740	21.7	386	1	P53_BOVIN
15	738	21.7	391	1	P53_MARMO
16	735	21.6	391	1	P53_RAT
17	732.5	21.5	391	1	P53_CAVPO
18	730	21.4	393	1	P53_TUPGP
19	729	21.4	382	1	P53_SHEEP
20	719	21.1	396	1	P53_MESAU
21	718	21.1	366	1	P53_PLAFA
22	718	21.1	393	1	P53_HUMAN
23	717	21.1	390	1	P53_MOUSE
24	715.5	21.0	393	1	P53_MACFA
25	714.5	21.0	393	1	P53_CERAE
26	713.5	21.0	393	1	P53_MACMU
27	710.5	20.9	342	1	P53_XIPHE
28	709.5	20.8	342	1	P53_XIPMA
29	707.5	20.8	393	1	P53_CRIGR
30	699.5	20.5	391	1	P53_RABIT
31	696	20.4	314	1	P53_SPEBE
32	689.5	20.2	280	1	P53_HORSE
33	591.5	17.4	207	1	P53_EQUAS

34	143.5	4.2	5147	1	PCTO_HUMAN
35	141.5	4.2	1081	1	GALY_YEAST
36	138	4.1	1520	1	ABL_DROME
37	134.5	4.0	1386	1	ZAP3_MOUSE
38	131	3.8	1544	1	TUSP_HUMAN
39	130.5	3.8	628	1	V70K_TYMC
40	129.5	3.8	766	1	TLE4_MOUSE
41	129	3.8	589	1	SPY_DROME
42	129	3.8	964	1	YOKA_SCHPO
43	128.5	3.8	766	1	TLE4_HUMAN
44	128	3.8	921	1	T2D3_DROME
45	127.5	3.7	628	1	V70K_TYMC

ALIGNMENTS

RESULT 1	ID	SEQUENCE	STANDARD	PRT	636 AA.
P73_HUMAN	AC	015350; 015351; Q9NTR8;			
DT	DT	16-OCT-2001 (Rel. 40, Created)			
DT	DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	DE	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	DE	Tumor protein p73 (p53-like transcription factor) (p53-related protein).			
GN	GN	TP73 OR P73.			
OS	OS	Homo sapiens (Human).			
OC	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	OX	NCBI_TaxID=9606;			
OX	OX	[1]			
RP	RP	SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).			
RC	RC	TISSUE=Colon;			
RC	RC	MEDLINE=97433090; PubMed=9288759;			
RA	RA	Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A.,			
RA	RA	Minty A., Chalon P., Lelias J.-M., Dumont X., Ferrara P., McKeon F.,			
RA	RA	Caput D.;			
RT	RT	"Monoclonally expressed gene related to p53 at 1p36, a region			
RT	RT	frequently deleted in neuroblastoma and other human cancers.;"			
RL	RL	Cell 90:809-819(1997).			
RL	RL	[2]			
RP	RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RC	RC	MEDLINE=99289209; PubMed=10362363;			
RA	RA	Yoshitake H., Nagashima M., Khan M.A., McMenamin M.G., Hagihara K.,			
RA	RA	Harris C.C.;			
RT	RT	"Mutational analysis of p73 and p53 in human cancer cell lines.;"			
RT	RT	Oncogene 18:3415-3421(1999).			
RL	RL	[3]			
RP	RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RC	RC	MEDLINE=98389621; PubMed=9721206;			
RA	RA	Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B.,			
RA	RA	Jenkins R., Smith D.L., Liu W.;			
RT	RT	"Genomic organization and mutation analysis of p73 in			
RT	RT	oligodendrogliomas with chromosome 1 p-arm deletions.;"			
RL	RL	Genomics 51:359-363(1998).			
RL	RL	[4]			
RP	RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).			
RC	RC	TISSUE=Neuroblastoma;			
RC	RC	MEDLINE=99021697; PubMed=9802988;			
RA	RA	De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,			
RA	RA	Annicchiarico-Petruzzelli M., Leverero M., Melino G.;			
RT	RT	"Two new p73 splice variants, gamma and delta, with different			
RT	RT	transcriptional activity.;"			
RT	RT	J. Exp. Med. 188:1763-1768(1998).			
RL	RL	[5]			
RP	RP	SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).			
RC	RC	TISSUE=Breast cancer, Hepatoma, Lymphocytes, and skin;			
RC	RC	MEDLINE=99310938; PubMed=10381648;			
RA	RA	De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G.,			
RA	RA	Costanzo A., Leverero M., Knight R.A.;			
RT	RT	"Additional complexity in p73: induction by mitogens in lymphoid cells			
RT	RT	and identification of two new splicing variants epsilon and zeta.;"			

RL Cell Death Differ. 6:389-390(1999).
 RP SEQUENCE FROM N.A. (ISOFORM KAPPA).
 RA Thomas D.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
 RX MEDLINE=99318135; PubMed=10391251;
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Kharbanda S., Welchelbaum R., Kufe D.;
 RT "p73 is regulated by tyrosine kinase c-abl in the apoptotic response
 RT to DNA damage.";
 RL Nature 399:814-817(1999).
 RN [8]
 RP ERRATUM.
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Kharbanda S., Welchelbaum R., Kufe D.;
 RL Nature 400:792-792(1999).
 RN [9]
 RP FUNCTION.
 RX MEDLINE=99217940; PubMed=10203277;
 RA Kaelin W.G., Jr.;
 RT "The emerging p53 gene family";
 RL J. Natl. Cancer Inst. 91:594-598(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 439-506.
 RX MEDLINE=99380160; PubMed=10449409;
 RA Chi S.W., Ayed A., Arrowsmith C.H.;
 RT "Solution structure of a conserved C-terminal domain of p73 with
 RT structural homology to the SAM domain.";
 RL EMBO J. 18:4438-4445(1999).
 CC -1 FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
 CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
 CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
 CC PROTEIN.
 CC
 CC -1 SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
 CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
 CC AND WITH P53. WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
 CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
 CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
 CC
 CC -1 SUBCELLULAR LOCATION: Nuclear.
 CC
 CC -1 ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=7;
 CC Name=Alpha;
 CC IsoId=015350-1; Sequence=Displayed;
 CC Name=beta;
 CC IsoId=015350-2; Sequence=VSP_006539;
 CC Name=gamma;
 CC IsoId=015350-3; Sequence=VSP_006540, VSP_006541;
 CC Note=The splicing of exon 11 results in a frameshift from the
 CC original reading frame;
 CC Name=delta;
 CC IsoId=015350-4; Sequence=VSP_006542, VSP_006543;
 CC Name=epsilon;
 CC IsoId=015350-5; Sequence=VSP_006544, VSP_006545;
 CC Note=The splicing of exon 11 results in a frameshift from the
 CC original reading frame. The splicing of exon 13 reverts the
 CC reading frame to the sequence of isoform Alpha;
 CC Name=zeta;
 CC IsoId=015350-6; Sequence=VSP_006546;
 CC Name=kappa;
 CC IsoId=015350-7; Sequence=VSP_006548;
 CC -1 TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER
 CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
 CC
 CC -1 INDUCTION: NOT INDUCED BY DNA DAMAGE.
 CC
 CC -1 DOMAIN: POSSESSES AN ACIDIC TRANSCRIPTION DOMAIN, A CENTRAL DNA
 CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BIND
 CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
 CC
 CC -1 DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVER
 CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
 CC IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
 CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.
 CC
 CC -1 SIMILARITY: BELONGS TO THE P53 FAMILY.

[illegible]

Query Match	52.6%;	Score 1790;	DB 1;	Length 636;
Best Local Similarity	55.1%;	Pred. No. 2.6e-113;		
Matches 366;	Conservative 94;	Mismatches 144;	Indels 60;	Gaps 18

OY			MASSTQTNFLELPE---VFQHMTDLELPICISVQPIDLNFDEESSEDGATNKKI-----EIS	53
Dd			1 MAOSTAT-----SPDGTFTEHLMSSLEP-----DSTYIDLPOSSRGNNVEVGDTSS	48
OY			54 MDCIRMOSDLSDPMPOVTNLIGLNMSMDQOIQNGSSSTSPYNTDHAONSVTAPSPAOP	113
Dd			49 MDVFHELGWTLS-----VMAGFNILISTMDQSSRAAGASPYTPEDIAA-SVPTHSPPYAOP	102
OY			114 SSTFDPLASPAIPENTIDYPGHSHDVFSFOOSSATAKSTWYTSTELKKLYCQIAKTPIQ	173
Dd			103 SSTFDPMASPAPIPSTNDPCGFHNHFVFQOOSTAKSTWYTSPLKLKYCQIAKTPIQ	162
OY			174 IKMTPRPGGAVIRAMPYKKKAHEHTYEVRCKPNHELSEREFNEFOIAPPSHLIRVEGNSH	233
Dd			163 IKVSTPRPPGTALIRAMPYKKKAHEHTDYVKCPNHHELGRDNEDQSAPASHLRIVEBNNL	222
OY			234 AQVEDPITKGOSVLVPPEPVQGETFTTVLYNEMCNSSCVGMNRRLIIYTLERDQ	293
Dd			223 SQYVDPPRYQRQSVVVYPPEPVQGETFTTVLYNEMCNSSCVGMNRRLIIYTLERDQ	282
OY			294 QVYGRCEFPARICACGRDRKADEDSIKKOQV--SDSFKNGDGTKRPFROTHGIOM--T	349
Dd			283 QVYGRCEFGRIACGRDRKADEDHYTEQDALNESSAKNKAAASKRAFQOSPVAIVPLGA	342
OY			350 STKKRRSPDELLEYLVPRGRETYEMALKIKESLEIMLOYLPQHTLETYRQQOQOOHQHLLQ	409
Dd			343 GYVKRRHGDEDITYLVQVRRENFETIMLKLESLEIMELVLPQVLDSYRQOQO----LTQ	397
OY			410 KQTSSIPSSYCNSSNPCLKKM-SNNKTPSYSQLIN--PQQRMLTPTTIPDGCANIPM	466
Dd			398 RPHQLD-PRSYGPVLSPMKNKVGGNNKLPSTYNOLGORPPSHSATNPGLGVGG----M	452
OY			467 MGTN---MPMADMGNSLPTQALPPLSPMSTSHCTPPRPYPDCSIYSFLARGSCSL	523
Dd			453 LNNHGAVPANEMESSHSQA-----SMVGSCHCTPPPHADPSLVSFELTGCPNCI	506
OY			524 DVFDTGGLTTIOIEHYSMDOLASIKTEPORRHAIWKIILDRLHFEFSSPHLTRPSS	583
Dd			507 EYFTSGLOSLIHLDLIETEDGALKITEQYRMTHWRGLDKOGHYSTAQQLRS-SN,	565
OY			584 ASTVSY-GGSETRGERVDAVRFLLQRTISEPPR-----DENNDENFMDDARRNQOR	635
Dd			566 AATISIGSGGELLQGRVMEAVHFRHRHITIPNRGPGCGGDENADGFPDLPCKAKQP	625
OY			636 IKEE 639	
Dd			626 IKEE 629	
<hr/>				
RESULT 2				
P73_CERAE				
ID	P73_CERAE	STANDARD:	PRT:	637 AA.
AC	G9XSR8; O9TSQ9;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Tumor protein p73 (p53-like transcription factor) (p53-related protein)			
CN	Tp73 OR P73.			
OS	Cercopithecus aethiops (Green monkey) (Grivet).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;			
OC	Cercopitheinae; Cercopithecus.			
OX	NCBI_TaxID=9534;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).			
CC	tissue=kidney;			
NA	Caput D.;			

Query Match	Best Local Similarity	Matches	Score	Length	DB 1	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382	DB 383	DB 384	DB 385	DB 386	DB 387	DB 388	DB 389	DB 390	DB 391	DB 392	DB 393	DB 394	DB 395	DB 396	DB 397	DB 398	DB 399	DB 400	DB 401	DB 402	DB 403	DB 404	DB 405	DB 406	DB 407	DB 408	DB 409	DB 410	DB 411	DB 412	DB 413	DB 414	DB 415	DB 416</
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OY 294 OYLGRCEARICACPGDRKADENSIRKOOV--SDSTKNGDGTFRPPRONTHTGIOM--T 349
DB 293 OYLGRSEEGRICACPGDRKADENHYREOQALNESSAKNGASRAKROSPAPVALGP 342
OY 350 SIKRRSPDELLIYVGRGRETMYELTKIKESLEMOVLPOHTIETVROOQOOHQHLLQ 409
DB 343 GYKRRHDEDELYIQVGRGREFELTKIKESLELMELVPOVLVSTIRKOOO----LIQ 397
OY 410 KOTSIQSPSSSYGNSSPPLKNKN-SMKLPSVSQLIN--POORNALPTTIPDGMANIP 466
DB 398 RPSHLQ-PPSYGPVLPSPNNKYGVNKLPSVNLQVGPPHSSAATPNLGPVGS----M 452
OY 467 MGTI---MPMAGDMNGLSPTQALPPPLMPSTSHCTPPPPPTDSTYSFLARLCCSSCL 523
DB 453 LNNHSHAVPANSEMSHGTQ-----SMVSGSHCTPPPPYADPSLVSFLGLCCPNCI 506
OY 524 DFTYQGLTITTYQIHYMSMDLASLKIPEQFRHAIWKGLDHRQLHEFSSPHLRTPS 583
DB 507 EFTYQGLTITTYQIHYMSMDLASLKIPEQFRHAIWKGLDHRQLHEFSSPHLRTPS 583
OY 564 ASTYVSV-GSSETRGERVIDAVRFTLRQITSEPPR-----DEWDFNFDMDARRNKOOR 635
DB 567 AAALISIGSGELORRVMHVAHFVRHTITTPNRGPGAGPDEMADFGFDLPCKARKOP 626
OY 636 IKKE 639
DB 627 IKKE 630

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RESULT 3

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P53_ONCMV
AC P25035. STANDARD; PRT; 396 AA.
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Procaracanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP MEDLINE-92210006; PubMed-1339362;
RA de Fromental C.C., Padkel F., Chapus A., Baney C., May P., Soussi T.;
RT "Rainbow trout p53: cDNA cloning and biochemical characterization.";
RL Gene 112:241-245(1992).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC Bax and Fas antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- CELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC -----
CC DR EMBL; M75145; AAA49605.1; -
CC DR PIR; JH0631; JH0631.
CC DR HSSP; P04637; ITUP.

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DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 90 281 BY SIMILARITY.
FT DOMAIN 325 356 OLIGOMERIZATION.
FT DOMAIN 369 392 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 303 318 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 396 AA; 43966 MW; 842225076545A1C CRC64;

```

Query Match 24.9%; Score 847.5; DB 1; Length 396;
Best Local Similarity 45.4%; Pred. No. 4.8e-50;

Matches 181; Conservative 61; Mismatches 102; Indels 55; Gaps 10;

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OY 11 LSPVEYQHIMDFLEOPICSVQPIDLNFVDESDGATNKIEISMDCIRMQDLSDPMP 70
DB 12 LSOESFEDLM-----KMNINLVAVQPPETE---SW 39
OY 71 QYTNGLNSMDQIQNGSSSTPYNTDHAQNSVAPSPYOPS-STFDALS-PSPAIS 128
DB 40 GIDNF-----KMEAPLQ-----VEPDSLEVSATPEAPQPSITLDTGSPPTSTVPT 87
OY 129 NTDPYGPSPFVSFOOSSTAKSATWTYSTELKIKYQIAKTCPIQIKYTPPGAVIRA 188
DB 88 TSDYRGALGPGQLRFQSSSTAKSVCTYSPDLNKLFCQIAKCPQIVIVDHPHPPGAVIRA 147
OY 189 MPYVKAHEVTEVYKRCFNHLSRENEGQIAPSPSHLIRVGNSHAQYVEDPITRGOSVL 248
DB 148 LAIYKKLSDVADVVARCPHOSHSTSENNEGP-APRHHILVRVGNORSEYEMEGNTLRHSVL 206
OY 249 VPPEPQVGTETTYLVNFMKNSGVGMNRPILITLTETRGQVGRGRCFEARICAC 308
DB 207 VPPEPQVGSCTTYLVNFMKNSGVGMNRPILITLTETRGQVGRGRCFEARICAC 266
OY 309 PGDRKADENSIKROO---VSDSTKNGDGTFRPFRQ-NTHTGIOMTSIKRRS---PDDE 360
DB 267 PGDRKTEINLKKQOETLTETKTPAGIKRAMKESALPAPQPGASAKTKTSSPAVSDE 326
OY 361 LLYLPVGRGRETMYELTKIKESLELMOVLPOHTIETVROO 399
DB 327 IYTLQIRGKERKYEMLKKNFDSLELSELPVADADKYRQK 365

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RESULT 4

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P53_BARBU
ID P53_BARBU STANDARD; PRT; 369 AA.
AC O9W678;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN tp53 OR P53.
OS Barbus barbus (Barbel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Barbus.
OX NCBI_TaxID=40830;
RN [1]
RP MEDLINE-92210006; PubMed-1339362;
RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
RT "Evolutionary conservancy of p53 gene sequences in fish.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.

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CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF071570; AAD34212.1; -.
DR HSSP: P04637; 1TUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA BIND 66 256 BY SIMILARITY.
FT DOMAIN 298 329 OLIGOMERIZATION.
FT DOMAIN 342 365 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 276 292 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 368 368 PHOSPHORYLATION (By similarity).
SQ SEQUENCE 369 AA; 41233 MW; 0BE2CFCEA74C304 CRC64;

Query Match 24.1%; Score 819.5; DB 1; Length 369;
Best local Similarity 51.2%; Pred. No. 3.3e-48;
Matches 167; Conservative 49; Mismatches 87; Indels 23; Gaps 8;

OY 84 QIONGSSSTSPYNTDHAQNSVT-APSRYAQPSTFDALSPSPAPSPNTDYPGHSFVSF 142
DB ELINDEYLPSPFPDNIFFDNVLTQGPQSP-----PTAVPAITDVGSHKGLCF 77
OY 143 QOOSTKASATWYITELKLYCOIATCPQIKVMTPPPGAVIRAMPYKKAHEVTV 202
DB 78 POSGTAKSVCTYSSDLNKLFCOLAKTCVQVNVNAPPGSVIRATATIKKSEHAEEV 137
OY 203 KRCPNHELRENEGOIAPPSHLIRVGNSHQVYEDPITGRSULVYPPVGVGEFTT 262
DB 138 KRCPNHEKTPD-GDG-LAPPAHLIRVGNRSLYREDVDNRSVYVEVPQSGSEFTT 195
OY 263 VLYNFGNSSCVGNMRRPILITVLETRDQGYLGRCEFEARICACPGDRKADDEDSIRK 322
DB 196 VLYNFGNSSCMGNMRRPILITVLETHDGLGRSPFVRKACPGDRKTEESNFKR 255
OY 323 QQVSDSTKMGD-----GTRPF--QONTGIGMTSIKRR---SPDELLYLPVGRRETV 373
DB 256 DQ---ETKTLDKIPSNKRSILTKDSTSVPRPESGSKAKLSSGSDDEIYTLQYGRKERVE 312
OY 374 MLTKIKESLEIMQVLPQHTIENYRQ 399
DB 313 MLTKINDSLSDVVPSEMDRYRQK 338

RESULT 5
P53_BRARE
ID P53_BRARE STANDARD; PRT; 373 AA.
AC P79734; Q90440.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR DRP53.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Osteichthyes; Cypriniformes;
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OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97344388; PubMed=9200835;
RA Cheng R., Ford B.L., O'Neal P.E., Bradford C.S.,
RA "Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
RT expression during embryogenesis."
RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
RN [2]
RP SEQUENCE OF 140-212 FROM N.A.
RA Winge P.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U60804; AAB40617.1; -.
DR EMBL: U46693; AAA97408.1; -.
DR HSSP: P04637; 1TUP.
DR ZFIN: ZDB-GENE-990415-270; tp53.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA BIND 70 260 BY SIMILARITY.
FT DOMAIN 301 332 OLIGOMERIZATION.
FT DOMAIN 345 365 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 280 296 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 372 372 PHOSPHORYLATION (By similarity).
SQ SEQUENCE 373 AA; 41899 MW; AC7AB724FA6B1EF CRC64;

Query Match 23.7%; Score 805.5; DB 1; Length 373;
Best local Similarity 53.9%; Pred. No. 3e-47;
Matches 158; Conservative 42; Mismatches 82; Indels 11; Gaps 4;

OY 112 QPSTFDALSPSPAIPSNNDYDPGHSFVDFQOSTAKSATWYITELKLYCOIATCP 171
DB 55 QPSTVETSDYDPDGHGRLRFPQSGTAKSVCTYVSPDLNKLFCQGLAKTTP 110
OY 172 IQIKVMTPPPGAVIRAMPYKKAHEVTVKCCPNHELRENEGOIAPPSHLIRVEGN 231
DB 111 VQMVVDVAPPGQGVNATATLYKRSHEVAEVRRCPHNE--RTPDGQNLPAAGHLIRVEGN 168
OY 232 SHAQYVEDPTGSGSVLVYEPPOVGEFTTVYNFGNSSCVGNMRRPILITVLETR 291
DB 169 QRANTREDNITLHRSFVPEAFQIGAEKTTVLLNFGNSSCMGNMRRPILITVLETR 228
OY 292 DQGVLRRCFEARICACPGDRKADDEDSIRK-QQVSDSTKMGDTRKRRPQONTGIGM-- 348
DB 229 EGQLLRSPFEVAVACACPGDRKTEESNFKKQDETMAKTTGTGTRSLYKSSSATLRR 288
```

QY 349 -TSIKRRSPDDELLYPVGRREYEMLIKRESLEMOYLPOHTIETFRQ 399
 Db 289 EGSKRKSSSDEEFTLVQVRGEREYELIKKLINDSLSDVVPADAEKRYOK 341

RESULT 6
 P53_XENIA
 ID P53_XENIA STANDARD: PRT; 376 AA.
 AC 093379;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Ictalurus punctatus (Channel catfish).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OX NCBI_TaxID=7998;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99071979; PubMed=9854815;
 RA Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
 RT "Identification and characterization of the tumor suppressor p53 in
 channel catfish (Ictalurus punctatus).";
 RL Comp. Biochem. Physiol. 120B:675-682(1998).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 growth arrest or apoptosis depending on the physiological
 circumstances and cell type. Involved in cell cycle regulation as
 a trans-activator that acts to negatively regulate cell division
 by controlling a set of genes required for this process. One of
 the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 BAX and FAS antigen expression, or by repression of Bcl-2
 expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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DR EMBL: AF074967; AAC26824.1; -
 DR HSSP: P04637; ITUP.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 36 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 77 268 BY SIMILARITY.
 FT DOMAIN 303 334 OLIGOMERIZATION.
 FT DOMAIN 347 372 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 286 298 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 375 375 PHOSPHORYLATION (By SIMILARITY).
 SQ SEQUENCE 376 AA: 41989 MW: 1889CD9BDB3289F2 CRC64:

Query Match 23.3%; Score 795; DB 1; Length 376;
 Best Local Similarity 53.4%; Pred. No. 1.5e-46;
 Matches 156; Conservative 44; Mismatches 88; Indels 4; Gaps 3;

QY 108 SPVAPSTFDALSPFAPISNTDYPGFHSFDVQSGSTAKSATWTSTELKLYCOIA 167
 Db 56 SDMLQPOSS--SSPTSTVPTSDYDGLNFTLHQSSGKRSVCTYSPDLNKFQOLA 113

QY 168 KTCPIQIVMPPPOGAVIRAMPYKKAHVTEYVKRCPNHLSREFNEGQIAPPSHLR 227
 Db 114 KTCPIVMAVSSPPGSLVATAYKRESEHVAEVRCPHHERSNDSDGP-APPGHLR 172

QY 228 VEGNSHAQYVEDPITGRGOSVLYPPEPVGEFTLVLYNFKNSCSCGMMRRPLTIYT 287
 Db 173 VEGNSRAYQEDGNTQAHSSVVPPEPVGQSOSTVLVLYNFKNSCSCGMMRRPLTIYT 232

QY 288 LETRDGOYLGRRCFARICACPGDRKADSDSIRKQVSDSTKNDGTRPPFRONTGHIQ 347
 Db 233 LETDGHILGRTEFVRACACGDRKKEESNEKQO-EPRTSGKTLTKRSMKDPSPHE 291

QY 348 MTSIKRRSPDDELLYPVGRREYEMLIKRESLEMOYLPOHTIETFRQ 399
 Db 292 ASKSKSSSDEEFTLVQVRGEREYELIKKLINDSLSDVVPADAEKRYOK 343

RESULT 7
 P53_XENIA
 ID P53_XENIA STANDARD: PRT; 363 AA.
 AC P07193;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88143684; PubMed=2830576;
 RA Soussi T., de Fromental C.C., Mechali M., May P., Kress M.;
 RT "Cloning and characterization of a cDNA from Xenopus laevis coding
 for a protein homologous to human and murine p53.";
 RL Oncogene 1:71-78(1987).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94134403; PubMed=8302570;
 RA Hoefer M., Clement J.H., Medlich D., Montenarh M., Knoechel W.;
 RT "Overexpression of wild-type p53 interferes with normal development
 in Xenopus laevis embryos.";
 RL Oncogene 9:109-120(1994).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 growth arrest or apoptosis depending on the physiological
 circumstances and cell type. Involved in cell cycle regulation as
 a trans-activator that acts to negatively regulate cell division
 by controlling a set of genes required for this process. One of
 the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 BAX and FAS antigen expression, or by repression of Bcl-2
 expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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 or send an email to license@sib-sib.ch).

DR EMBL: M36962; AAA49923.1; -
 DR EMBL: X05191; CAA28821.1; -
 DR EMBL: X77546; CAA54672.1; -
 DR EMBL: S68353; AAC60746.1; -
 DR PIR: A29376; A29376.
 DR HSSP: P04637; ITUP.

DR InterPro; IP002117; P53.
 DR Pfam; PF00870; P53.1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 29 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA BIND 76 267 BY SIMILARITY.
 FT DOMAIN 300 331 OLIGOMERIZATION.
 FT DOMAIN 344 356 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 281 293 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD.RES 362 362 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 52 52 T -> S (IN REF. 2).
 FT CONFLICT 71 71 MISSING (IN REF. 2).
 FT CONFLICT 296 296 MISSING (IN REF. 2).
 SQ SEQUENCE 363 AA; 40692 MW; CELF3E58F020D74D CRC64;

Query Match
 Best Local Similarity 42.8%; Score 777.5; DB 1; Length 363;
 Matches 171; Conservative 55; Mismatches 95; Indels 81; Gaps 11;

QY 2 SOSTNTEFLSEVYQHWDLEQPI---CSVQPIDLNFVDEPSEDCATNKIEISMDCI 57
 DB 4 SSETGMDEPLLSQETPEDEMLSLPDLQVTCRLDMLS-EFPDYP-----LAADWT 52
 QY 58 RMQDSDLSQPMWPQYTNGLNLSMDQIQNGSSSPYTHAQNVSATPSPYADPSSSF 117
 DB 53 VIOE-----GLMGN-----AVPTV- 67
 QY 118 DALSPALPSNTDYPGPHSPDVSFOQSSTAKSATWYSTELKLYCOIAKTCPIQIKW 177
 DB 68 -----SCAVSTDDYAGKGLQDLFOQNGTAKSVCTYSPELNKLFQCAKCPILVRYE 122
 QY 178 TPPEGATYRAMPYVKKAEHYEVYKRCPNHLSREFNGLAPSHLRVGNSHAQYV 237
 DB 123 SPPEGSLIRATAYVKKSEHAENVYKRCPNHERSVEPGE-DAAPSHLMRVGNLQAYYM 181
 QY 238 EDPINGROSVALPYPPQVGTFTVLYNFMCNSSCVGGMNRPILIIYLETETRGQVYG 297
 DB 182 EDVNGSRHSVCYPIYGPOVGTCTTYLYNMGNSSCGMGMMRPIILITLETPOGLLG 241
 QY 298 RRCFEARICACPGDRKADSDS-IRKQVSDSTKNGDGTKRPFQNTHT--GIQMTSIKKR 354
 DB 242 RRCFEVYACACGDRRTEEDNYTKRGLKPSGK-----RELAPHPSEPPLPKKR 292
 QY 355 R---SPDDELILPYRGRETYEMLIKIKESLELMQYLPQHTI 393
 DB 293 LVVVDDDEIFTLRIKGRSRREMIKRLNDALEIQLQESLDQKV 334

RESULT 8

P53_TETMU STANDARD; PRT; 367 AA.
 AC Q9W679;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Tetradon minus (Congo puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OC NCBI_TaxId=94908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RA Bhakaran A., May D., Rand-Weaver M., Tyler C.R.;
 RT "Evolutionary conservancy of p53 gene sequences in fish."
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces

CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC -----

DR EMBL; AF071571; MAD34213.1; -.
 DR HSSP; P04637; ITUP.
 DR InterPro; IP002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA BIND 86 273 BY SIMILARITY.
 FT DOMAIN 308 337 OLIGOMERIZATION.
 FT DOMAIN 342 363 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 288 301 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD.RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 367 AA; 41266 MW; ACC10EE2E5F9CED CRC64;

Query Match
 Best Local Similarity 42.8%; Score 776; DB 1; Length 367;
 Matches 165; Conservative 53; Mismatches 105; Indels 64; Gaps 7;

QY 11 LSEVYQHWDLEQPICSVQPIDLNFVDEPSEDCATNKIEISMDCIRMQDSDLSQPMW 70
 DB 10 LQDFQFDLMDVNSAP-----PLS-----TIQTALAEHNP 41
 QY 71 QYTNGLL-NSMDQIQNGSSSTPYTHAQNVSATPSPYADPSSFPALSPALP 129
 DB 42 AEROMNMCMNFMDSTFENALFNILP-----EPPSRDGNSSSPVPT 84
 QY 130 TDYPGPHSPDVSFOQSSTAKSATWYSTELKLYCOIAKTCPIQIKWPPQGAIRAM 189
 DB 85 TDYPGYGRKLRFOKSGTAKSVTSTYSELNKLCOIATSLVEYLIGADPPMGAVLRAT 144
 QY 190 PYKKAHEHYEVYKRCPNHLSREFNEGOIAPSHLRVGNSHAQYVEDPTTGRQSVLY 249
 DB 145 AIYKKEHYAEVYVRCRPHQ-----NEDSAEHRSHLRMEGSEBAQYFEPHTKRSQVYV 199
 QY 250 PTEPPQVGTFTVLYNFMCNSSCVGGMNRPILIIYLETEDQVYLGRCFEARICAC 309
 DB 200 PYEPQLGSEFTTILSFMCNSSCGMGMMRPIILITLETDEGYLGRCFEVYACAP 259
 QY 310 GDRKADSDSIRKQVSDSTKNGDGTKRPFQNTHTGIIQMTSIKKRS-----PPDELLY 363
 DB 260 GDRKTEETENSTKMQ-----NDAKDAKKRSVPPDSTTIKSKTASAEEDNNEVYT 312
 QY 364 LPVGRRETYEMLIKIKESLELMQYLPQ 390
 DB 313 LQIRGRKRYEMLKIKINDGLDLENNPKK 339

RESULT 9

P53_PIG STANDARD; PRT; 386 AA.
 ID P53_PIG

AC Q9UBZ2; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR p53.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99422034; PubMed=10490836;
 RA Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;
 RT "Nucleotide sequence of the porcine p53 cDNA, and the detection of
 RT recombinant porcine p53 expressed in vitro with a variety of anti-p53
 RT antibodies.";
 RL Oncogene 18:5005-5009(1999).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression.
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DISEASE: p53 is found in increased amounts in a wide variety
 CC of transformed cells. p53 is frequently mutated or inactivated
 CC in many types of cancer.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF098067; AAF04620.1; -
 CC HSSP: P04637; 1c26.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 2.
 DR PROSITE: PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 45
 FT DNAS_BIND 94 285
 FT DOMAIN 318 349
 FT DNAS_BIND 361 380
 FT DOMAIN 304 316
 FT MOD_RES 15 15
 FT MOD_RES 385 385
 FT SEQUENCE 386 AA; 42862 MW; AAC3D88EBDF55162 CRC64;
 SQ
 Query Match 22.68; Score 771; DB 1; Length 386;
 Best Local Similarity 40.38; Pred. No. 6,6e-45;
 Matches 166; Conservative 68; Mismatches 124; Indels 54; Gaps 9;
 QY 11 LSPFVQHIMDFOPICVOPIDLVNVEDESGATNKRIISMDCIKRMOSDSDPMWP 70
 Db 14 LSGTFEDLKLKLE-----NNLSSESLAAVNDLLISP----- 48
 QY 71 QYTNLGLNSMDQOIQNGSSSTPYNTDHQNSVTAPSPVQPSSTFDALSPSPAIRSNT 130
 Db 49 -----VTNWLDEKPDASRVAP-----PATATADAPAPATATSPPL--SSEFVSQK 93

QY 131 DYPGHSFVSVFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPGAVIRAMP 190
 Db 94 TTPGSYDRIRGLFHSHTGKATYCTYSPNLNLFQOLAKTCYQVLWSSPPPGFVRMA 153
 QY 191 VYKKAHYTEVYKRCRNHELSEFNEGOIAPPSHILIRVGNSSHAQYVEDPTTGROSLVP 250
 Db 154 IYKSEYMTVEVYRRCPHERSSDYSDG--IAPPOHILIRVEGNLRVEYLDRTFFRSVVP 212
 QY 251 YEPPGVEFTVLYFMGNSSCYGMMRRPLILIVLETBDGVLGRGFEARCAACPG 310
 Db 213 YEPPEVSDCTTIHNFMCNSSCYGMMRRPLILITTEDASGNLGNSEFVYACAPG 272
 QY 311 RDRKAEDESIKQGYSDSTKNGDGTGRPFONTGICQMTSIKRRSPDDELLYLVGRG 370
 Db 273 RDRTEENRFLKGGSCPEPPGSTKRALPTST--SSSPVQKKPLDGEFTLQIRGRE 329
 QY 371 TYEMLKIKESLELMQYLPQHTIETYRO--Q000QHLLQKQISIGSPSSY 420
 Db 330 REEMRELDALTELKD-----AQTARESGENRAHSHLSKRGK--GSPSRH 373
 RESULT 10
 ID P53_FELCA STANDARD; PRT; 386 AA.
 AC P41685;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR p53.
 OS Fells silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
 OX NCBI_Taxid=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph node;
 RX MEDLINE=94333960; PubMed=8056458;
 RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y.,
 RA Watarai T., Goitsuka R., Tsujimoto H., Hasegawa A.;
 RT "Cloning of feline p53 tumor-suppressor gene and its aberration in
 RT hematopoietic tumors.";
 RL Int. J. Cancer 56:602-607(1994).
 RN [2]
 RP SEQUENCE OF 34-354 FROM N.A.
 RX MEDLINE=94114699; PubMed=8286534;
 RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watarai T., Goitsuka R.,
 RA O'Brien S.J., Tsujimoto H., Hasegawa A.;
 RT "Molecular cloning and chromosomal mapping of feline p53 tumor
 RT suppressor gene.";
 RL J. Vet. Med. Sci. 55:801-805(1993).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression.
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DISEASE: p53 is found in increased amounts in a wide variety
 CC of transformed cells. p53 is frequently mutated or inactivated
 CC in many types of cancer.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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CC EMBL: D26608; BAA05653.1; -
CC EMBL: D16460; BAA03927.1; -
CC HSSP: P04637; 10LG.
CC InterPro: IPR002117; P53.
CC Pfam: PF00870; P53; 1.
CC PRINTS: PR00386; P53SUPPRESSR.
CC Prodom: PD002681; P53; 1.
CC PROSITE: PS00348; P53; 1.
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
CC Nuclear protein; Phosphorylation; Apoptosis.
CC DNA BIND 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
CC DOMAIN 318 285 BY SIMILARITY.
CC DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
CC DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
CC MOD_RES 385 385 SIMILARITY).
CC MOD_RES 285 285 PHOSPHORYLATION (BY SIMILARITY).
CC CONFLICT 285 285 K -> R (IN REF. 2).
CC SEQUENCE 386 AA; 42692 MW; D08B43BA1BC8E78 CRC64;

Query Match 22.6%; Score 770; DB 1; Length 386;
Best Local Similarity 42.1%; Pred. No. 7.7e-45;
Matches 161; Conservative 58; Mismatches 103; Indels 60; Gaps 7;

QY 11 LSPFYQHIMDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMODSLSPMP 70
DB 14 LSOETFSLEMLNLP- - - - -NNVLSSELSSAMNLPJSED- - - - - 48
QY 71 QYTNGLINSMDOQIONGSSSTSPYNTDHAQNSVTPAPGASSTFDALSPSPAI- - - - 126
DB 49 - - - - -VAMWDEA- - - - -PDASGMSAVPAAPAPAP- - - - -PAPALSWPL 85
QY 127 - - - - -PSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 182
DB 86 SSEFVSQKTYPGAYGPHLGLQSGTAKSVTCFYSPLNKLFCQLATCPQVLWVRSPPP 145
QY 183 GAVIRAMPYKKAENHTEVYKRCRNHELRENEGQIAPSHLIRVGNSHAOYVEDPIT 242
DB 146 GTCVRRAMALYKKESEFTEVYRRCRPHERCPSDSG- - -LAPQHLIRVGNLHAAYLDDRYT 204
QY 243 GRSVLYPEPPOVGEFTTVLYNFMNCSSCVGAMRRPILITVLETRDGOVLGRCE 302
DB 205 FHSVYVPEPEVSGDCTTIHNFMCNSSCMGAMRRPILITITLEDNGLLGNSTFE 264
QY 303 ARIACPGRRKRADEDSIRKQVSDSTKNGDGTFRPFONTGICQMTSIRKRRSPDELL 362
DB 265 VAVCACPGRDRTEENFRKGPCEPPPGSTKRALPPST- - -SSTPQKKKPLDGEYF 321
QY 363 YLPVGRTEYEMLIKIKESLEL 384
DB 322 TLQIRGERFEREMFRELNALEL 343

RESULT 11
P53_CHICK STANDARD; PRT; 367 AA.
AC P10360;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX 11
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=SPAFAS;
```

DB 317 GRRREMLKEINELQIAE 335

RESULT 12

AC 0295377; Q9P78; STANDARD; PRT; 381 AA.

DT 01-NOV-1997 (Rel. 35, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor p53).

GN TP53 OR p53

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Leukocyte;

RX MEDLINE=98178696; PubMed=9519881;

RA Veldhoen N., Milner J.;

RT "Isolation of canine p53 cDNA and detailed characterization of the full length canine p53 protein."

RL Oncogene 16:1077-1084(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T., Watarai T., Hasegawa A., Tsujimoto H.;

RT "Alterations of p53 tumor suppressor gene in various spontaneous tumors in the dog."

RL Submitted (Dec-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE OF 25-300 FROM N.A.

RC STRAIN=Beagle;

RX MEDLINE=95323915; PubMed=7600529;

RA Kraegel S.A., Pazzi K.A., Madewell B.R.;

RT "Sequence analysis of canine p53 in the region of exons 3-8."

RL Cancer Lett. 92:181-186(1995).

CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of Bax and Fas antigen expression, or by repression of Bcl-2 expression.

CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC -----

CC EMBL; AF060514; AAC16909.1; -

CC EMBL; AB020761; BAA78379.1; -

CC EMBL; S77819; AAB42022.1; -

CC HSSP; P04637; 10IG; -

CC InterPro; IPR002117; P53.

CC Pfam; PF00870; P53; 1.

CC PRINTS; PR00386; P53SUPPRESSR.

CC ProDom; PD002681; P53; 1.

CC PROSITE; PS00348; P53; 1.

KW Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.

FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).

FT DNA_BIND 89 280 BY SIMILARITY.

FT DOMAIN 313 344 OLIGOMERIZATION.

FT DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).

FT DOMAIN 299 311 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY SIMILARITY).

FT MOD_RES 380 380 PHOSPHORYLATION (BY SIMILARITY).

FT CONFLICT 1 4 MEES -> MORE (1N REF. 2).

FT CONFLICT 378 378 L->P (1N REF. 2).

SQ SEQUENCE 381 AA; 42486 MW; 761A718FDC93DA59 CRC64;

Query Match 22.3%; Score 758.5; DB 1; Length 381;

Best Local Similarity 39.3%; Pred. NO. 4.5e-44;

Matches 164; Conservative 63; Mismatches 129; Indels 61; Gaps 9;

QY 11 LSEVFOHIMDFLEOPICSVOPIDINFEVDESDGATNKIEISMDCIKMOQSDLS-D-PMW 69

DB 14 LSQETFSRLMWLP-----NNVLSRLCPAVDELPLPESVNMWLDSDSDADRM 63

QY 70 PQYTMGLGNSMDQIQNGSSSTSPYNDHQNSTAPYAPQPSFTDALSPATPSN 129

DB 64 P-----ATSAFATGP--APSWPL-----SSVSP 87

QY 130 TDYPGHSDVFSFOOSTAKSATWTYSTELKKIKQIAKCPICPIQIKVTPPGGAVIRAM 189

DB 88 KTYPTGYFRIGLHSGTAKSVWTYSLKLKFCQGLAKTCYQIWMVSSPPPNVCVAM 147

QY 190 PYKKAHVTEYVKRCPHELSREFNEQIAPPSHLIVEGNSHNOYVEDPIYGOSLV 249

DB 148 AIYKRSFEVTEVRCRPHERCSDSDS-LAPQHLIVEGNLRKAYLDDNTFPHSVV 206

QY 250 PYEPQVGEFTTYVYNFMCNSCGVGNRRPILITVLEFRDGOVLGRFEARICAP 309

DB 207 PYEPPEVSDTTTHYNYMCSSCGGNRRPILITVLEDSGNGVLRNSFEVAVCAP 266

QY 310 GRRRADSDSIRKQOVSDSTKNGDTKRPFRONTHGIOMTSIKRRSPDDELIVPVRG 369

DB 267 GDRRTRENFHKKGEPCPEPPGSTRKALPST---SSSPQKKRPDGEVFTLQIRGR 323

QY 370 EYEVMLIKESLEMLQIP-----QHT--IEFYQQQQQOHHLQKQTSIQS 416

DB 324 EYEMFNMLELELKDAQSGKEPGSRAHSSHLAKKQGSTSRKKIMFRKIGDS 380

RESULT 13

AC P53_ORYLA STANDARD; PRT; 352 AA.

DT 01-NOV-1997 (Rel. 35, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor p53).

GN TP53 OR p53

OS Oryzias latipes (Medaka fish) (Japanese ricefish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Belontiiformes; Adiantichthyidae; Oryziinae; Oryzias.

OX NCBI_TaxID=8090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=97305153; PubMed=9161419;

RA Krause M.K., Rhodes L.D., van Beneden R.J.;

RT "Cloning of the p53 tumor suppressor gene from the Japanese medaka (Oryzias latipes) and evaluation of mutational hotspots in MNNG-exposed fish."

RL Gene 189:101-106(1997).

RN [2]

RP SEQUENCE FROM N.A., AND VARIANT THR-91.

DR PRODOM: PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 94 285 BY SIMILARITY.
 FT DOMAIN 318 349 OLIGOMERIZATION.
 FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
 FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 380 380 R -> T (IN REF. 2).
 FT SEQUENCE 386 AA; 43255 MM; 222473FE28C548F31 CRC64;
 Query Match 21.7%; Score 740; DB 1; Length 386;
 Best Local Similarity 45.8%; Pred. No. 8.1e-43;
 Matches 152; Conservative 57; Mismatches 94; Indels 29; Gaps 8;
 QY 108 SPYAPSPSTFDALSPSPA-----IPSNTPYGPSPFVSFOOSSTAKSATWTSTEL 159
 DB APAAPSPAT-----PATATSWPLSSFPVSQKTYPGNGFRLGLQSGTAKSVCTYPSPL 122
 QY 160 KLLYCOLAKTCPIQIKMTTPPOCAVIRAMVYKKAENVYVYKRCNHELSPENSGOI 219
 DB 123 NKLFQCLAKTCPPVLWDSPPPPTRVRAAIYKLEHMEVVRCPHERSDYSDG-L 181
 QY 220 APPSHLIRVEGNSHAQVDEPITGROGVLYPEEPQVTEFTVLYNFMNCSSCGVMNR 279
 DB 182 APQHLIRVEGNSHAQVDEPITGROGVLYPEEPQVTEFTVLYNFMNCSSCGVMNR 241
 QY 280 RPLIIVYLETROGVYGRRCFEARICACPGDRKADSDIRKQVSDSTNGDKTRPF 339
 DB 242 RPLIIVYLETROGVYGRRCFEARICACPGDRKADSDIRKQVSDSTNGDKTRPF 301
 QY 340 RQNHGIGMTSIRKRSR-PDELLLYPVGRREYEMLLIKESLELMQYLQHTIETRYQ 398
 DB 302 PNTN-----SSPQKKRPDLGEYFTLQIRGFRKREMPRELDALEL-----KDALDGERP 352
 QY 399 QQQQOH-QHLLQKOTSIQSPSSYGNSSPPLNK 429
 DB 353 GESRAHSHLSK-----KRPSCHKKRMLKR 380
 RESULT 15
 P53_MARMO STANDARD; PRT; 391 AA.
 ID P53_MARMO 036006;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN P53.
 OS Marmota monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Marmota.
 OX NCBI_TaxID=9995;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97376996; PubMed=9233767;
 RA Frittelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
 RT Partial characterization of the woodchuck tumor suppressor, p53, and
 RT its interaction with woodchuck hepatitis virus X antigen in
 RT hepatocarcinogenesis.";
 RL Oncogene 15:327-336(1997).
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of

CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression.
 CC -!- SUBUNIT: Binds DNA as a homotetramer (by similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DISEASE: p53 is found in increased amounts in a wide variety
 CC of transformed cells. p53 is frequently mutated or inactivated
 CC in many types of cancer.
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC -----
 CC EMBL; AJ001022; CAA04478.1; -.
 DR HSSP; P04637; 1IUP.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 100 290 BY SIMILARITY.
 FT DOMAIN 323 354 OLIGOMERIZATION.
 FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
 FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
 FT SEQUENCE 391 AA; 43468 MM; EIDSD8B4BA0182 CRC64;
 Query Match 21.7%; Score 738; DB 1; Length 391;
 Best Local Similarity 37.7%; Pred. No. 1.1e-42;
 Matches 163; Conservative 70; Mismatches 121; Indels 78; Gaps 10;
 QY 11 LSPFVPHINDPFLQPCSVQPIDLVNFDSESGATNKIEISMDICRMDDSLSDPMP 70
 DB 14 LSOETFSDDLWMLP-----ENNVLSPVLS 38
 QY 71 QYTNGLINSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAPSTFDALSPSPA----- 125
 DB 39 PMNDL-LISSED--VENMFDK-----GPDALQMSAARAPKAPPAATLAAPSPATSMPL 91
 QY 126 ---IPSNTPYGPSPFVSFOOSSTAKSATWTSTELKLYCQIATKTCPIQIKYTPPO 182
 DB 92 SSVSPSONTPYGVYGFRLGLHSGTAKSVCTYSPSLNKLFQCLAKTCPPVLWDSPPP 151
 QY 183 GAVIRAMPVYKKAENVYVYKRCNHELSPENSGOIAAPSHLIRVEGNSHAQVDEPIT 242
 DB 152 GTRVRAAIYKKSQHMEEVVRCPNHE--KCSDDGAPLQHLIRVEGNSHAQVDEPIT 209
 QY 243 GROSLVLYPEEPQVTEFTVLYNFMNCSSCGVMNRPLIIVYLETROGVYGRRCFE 302
 DB 210 FRHSVVYLYPEEPQVTEFTVLYNFMNCSSCGVMNRPLIIVYLETROGVYGRRCFE 269
 QY 303 ARICACPGDRKADSDIRKQVSDSTNGDKTRPRONT-----HGIMTSIKKRRSP 357
 DB 270 VRVACACGRRRRREEMFRKR-----GEPCPEPPRSTKRALPMTSSSPQKKKPL 321
 QY 358 DDELLLYPVGRREYEMLLIKESLELMQYLQHTIETRYQ 407
 DB 322 DGEFTYTKIRGRARFEFQELNEALELKDQAQKEPESRPHPSYLSKKGQSTSRKKI 381
 QY 408 LQKOTSIQSPSS 419
 DB 382 IFKR---EGPDS 390

Thu Aug 7 14:42:49 2003

us-09-538-106-13.rsp

Page 13

Search completed: August 7, 2003, 09:47:22
Job time : 13.3675 secs

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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:41:09 ; Search time 51.5747 Seconds
(without alignments) 3207.225 Million cell updates/sec

Title: US-09-538-106-13

Perfect score: 3405
Sequence: 1 MSQSTQTFNEFLSPVEVQHIV.....FNPDMDARRNKKQRIKEGE 641

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3405	100.0	680	4	Q9H3D4
2	3401	99.9	641	4	075195
3	3397	99.8	680	4	Q9UE10
4	3353	98.5	663	11	Q99J63
5	3353	98.5	680	11	Q99J66
6	3353	98.5	680	11	Q98898
7	3033	88.1	586	4	Q9UBV9
8	3029	88.0	586	4	Q9P1B4
9	3016	88.6	586	4	075080
10	2995	88.0	586	11	Q89097
11	2991	87.8	586	11	Q99J62
12	2898	85.1	582	13	Q9DDE7
13	2722	79.9	516	4	Q9P1B7
14	2722	79.9	555	4	Q9H3D3
15	2685	78.9	538	11	Q99J67
16	2685	78.9	555	11	Q99J68

17	2685	78.9	555	11	Q9QWZ0
18	2583	75.9	501	4	Q9H3P8
19	2449	71.9	471	4	Q9NPH7
20	2350	69.0	461	4	Q9P1B5
21	2350	69.0	461	4	Q9UP26
22	2327	68.3	461	11	Q9QWY9
23	2323	68.2	461	11	Q99J66
24	2297	67.5	576	13	Q8JFE3
25	2283	67.0	588	13	Q8JFE6
26	2185	64.2	487	4	Q9H3D2
27	2164	63.6	487	11	Q99J61
28	2164	63.6	487	11	Q99J60
29	2124	62.4	483	11	Q88897
30	2077	61.0	416	4	Q9P1B6
31	1835.5	53.9	641	13	Q9W664
32	1813	53.2	393	4	075922
33	1802	52.9	393	11	Q99J69
34	1801	52.9	356	4	Q9UP74
35	1780.5	52.3	631	11	Q9JJP2
36	1779	52.2	457	13	Q8JH25
37	1766	51.9	389	11	Q88899
38	1748	51.3	590	11	Q9JJP1
39	1741	51.1	587	4	Q8TDY6
40	1667.5	49.0	365	13	Q98SW0
41	1562	45.9	514	11	Q9CU77
42	1459.5	42.9	497	11	Q9WU70
43	1418	41.6	284	11	Q8C826
44	1415.5	41.6	450	4	Q8TDY5
45	1251	36.7	426	4	Q8NHW9

ALIGNMENTS

RESULT 1	
Q9H3D4	PRELIMINARY; PRT; 680 AA.
AC	Q9H3D4; Q9UP28;
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	TA p63 alpha (Tumor protein p63).
GN	p63.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE-98448095; PubMed-9774969;
RA	Yang A., Kaghad M., Wang Y., Gallet E., Fleming M.D., Dotsch V.,
RA	Andrews N.C., Caput D., McKenon F.;
RT	"p63, a p53 homolog at 3q27-29, encodes multiple products with
RT	transactivating, death-inducing, and dominant-negative activities.";
RL	Mol. Cell 2:305-316(1998).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Haglwara K., McMenamin M.G., Harris C.C.;
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Lymph;
RA	Strausberg R.;
RL	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR	EMBL; AF124539; AAG45607.1; -
DR	EMBL; AF124529; AAG45607.1; JOINED.
DR	EMBL; AF124529; AAG45607.1; JOINED.
DR	EMBL; AF124531; AAG45607.1; JOINED.
DR	EMBL; AF124532; AAG45607.1; JOINED.
DR	EMBL; AF124533; AAG45607.1; JOINED.
DR	EMBL; AF124534; AAG45607.1; JOINED.

DR EMBL: AF124535; AAG45607.1; JOINED.
 DR EMBL: AF124536; AAG45607.1; JOINED.
 DR EMBL: AF124537; AAG45607.1; JOINED.
 DR EMBL: AF124538; AAG45607.1; JOINED.
 DR EMBL: AF075430; AAC62635.1; -.
 DR EMBL: BC039815; AAH39815.1; -.
 DR HSSP: P04637; IYCS.
 DR Genew: HGNC:15979; TP63.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 DR Nucleic protein.
 KW Nucleic protein.
 SQ SEQUENCE 680 AA; 76785 MW; F66ECD45E87D9799 CRC64;

Query Match 100.0%; Score 3405; DB 4; Length 680;
 Best Local Similarity 100.0%; Pred. No. 5.2e-282;
 Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTONEFLSPVFOHIMDFLEOPICSVQPIDLNFVDESEEGATNKIEISMDCTRMQ 60
 DB 40 MSQSTQNEFLSPVFOHIMDFLEOPICSVQPIDLNFVDESEEGATNKIEISMDCTRMQ 99
 QY 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSYTAAPSAQPSSTFDAL 120
 DB 100 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSYTAAPSAQPSSTFDAL 159
 QY 121 SPSPAIRSNDYPPGPHSFDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
 DB 160 SPSPAIRSNDYPPGPHSFDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 219
 QY 181 PGAVIRAMPYKKAHEVTEVKKCPNHELSEFNEGOIAPPSHLIVEGSHAOYEDP 240
 DB 220 PGAVIRAMPYKKAHEVTEVKKCPNHELSEFNEGOIAPPSHLIVEGSHAOYEDP 279
 QY 241 ITGRQSVLVPEPPOVGTETFTVLYNFMNCSSCVGGMNRRPILITVLETRDGOVLGRRC 300
 DB 280 ITGRQSVLVPEPPOVGTETFTVLYNFMNCSSCVGGMNRRPILITVLETRDGOVLGRRC 339
 QY 301 FEARICACPGDRKADSDSTKQOVSSTKKGDTKRPFRONTGIGMTSIKKRRSPDE 360
 DB 340 FEARICACPGDRKADSDSTKQOVSSTKKGDTKRPFRONTGIGMTSIKKRRSPDE 399
 QY 361 LLYLPVGRRETYEMLIKESLELMQYLPQHTIETVROQOQOHOHLQKOTSIOSSPY 420
 DB 400 LLYLPVGRRETYEMLIKESLELMQYLPQHTIETVROQOQOHOHLQKOTSIOSSPY 459
 QY 421 GNSSPPLKNKSNMKNLPSVQOLINPOQRNALPTTIPDGMGANIPMGMTHMPMAGDMNGL 480
 DB 460 GNSSPPLKNKSNMKNLPSVQOLINPOQRNALPTTIPDGMGANIPMGMTHMPMAGDMNGL 519
 QY 481 SPQALPPLSPMSTSHCTPPRPYPTDCSTYSFLARAGCSSCLDYFTTQGLTTIYQIEHY 540
 DB 520 SPQALPPLSPMSTSHCTPPRPYPTDCSTYSFLARAGCSSCLDYFTTQGLTTIYQIEHY 579
 QY 541 SMDLASLIKTEQFRAHIMKGLDHRQLHEFSSPSHLIRTPSSASTVSGSSETRGERVI 600
 DB 580 SMDLASLIKTEQFRAHIMKGLDHRQLHEFSSPSHLIRTPSSASTVSGSSETRGERVI 639
 QY 601 DAVAFITLQRTISPPRDEMDNFMDARRNKQORIKEEGE 641
 DB 640 DAVAFITLQRTISPPRDEMDNFMDARRNKQORIKEEGE 680

RESULT 2
 075195 PRELIMINARY; PRT; 641 AA.
 AC 075195;
 DT 01-NOV-1998 (TRENBLREL. 08, Created)
 DT 01-NOV-1998 (TRENBLREL. 08, last sequence update)

DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
 DE p51 isoform TAP63ALPHA (P51B protein).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE-98324755; PubMed-9662378;
 RA Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I.,
 RA Ikawa Y., Mimura Y., Nakagawara A., Oblinata M.;
 RT "Cloning and functional analysis of human p51, which structurally and
 RT functionally resembles p53.";
 RL Nat. Med. 4:839-844(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20388515; PubMed-10935472;
 RA Tanl M., Shintzu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
 RA Yokota J.;
 RT "Mutation and expression of the p51 gene in human lung cancer.";
 RL Neoplasia 1:71-79(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL: AB016073; BAA32593.1; -.
 DR EMBL: AF116769; AAF43487.1; -.
 DR EMBL: AF116756; AAF43487.1; JOINED.
 DR EMBL: AF116757; AAF43487.1; JOINED.
 DR EMBL: AF116759; AAF43487.1; JOINED.
 DR EMBL: AF116760; AAF43487.1; JOINED.
 DR EMBL: AF116761; AAF43487.1; JOINED.
 DR EMBL: AF116762; AAF43487.1; JOINED.
 DR EMBL: AF116763; AAF43487.1; JOINED.
 DR EMBL: AF116764; AAF43487.1; JOINED.
 DR EMBL: AF116765; AAF43487.1; JOINED.
 DR EMBL: AF116766; AAF43487.1; JOINED.
 DR EMBL: AF116767; AAF43487.1; JOINED.
 DR EMBL: AF116768; AAF43487.1; JOINED.
 DR HSSP: P04637; IYCS.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Nucleic protein.
 SQ SEQUENCE 641 AA; 72019 MW; 97AE61F66E63F618 CRC64;

Query Match 99.9%; Score 3401; DB 4; Length 641;
 Best Local Similarity 99.8%; Pred. No. 1.1e-281;
 Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTONEFLSPVFOHIMDFLEOPICSVQPIDLNFVDESEEGATNKIEISMDCTRMQ 60
 DB 1 MSQSTQNEFLSPVFOHIMDFLEOPICSVQPIDLNFVDESEEGATNKIEISMDCTRMQ 60
 QY 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSYTAAPSAQPSSTFDAL 120
 DB 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSYTAAPSAQPSSTFDAL 120
 QY 121 SPSPAIRSNDYPPGPHSFDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
 DB 121 SPSPAIRSNDYPPGPHSFDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
 QY 181 PGAVIRAMPYKKAHEVTEVKKCPNHELSEFNEGOIAPPSHLIVEGSHAOYEDP 240
 DB 181 PGAVIRAMPYKKAHEVTEVKKCPNHELSEFNEGOIAPPSHLIVEGSHAOYEDP 240
 QY 241 ITGRQSVLVPEPPOVGTETFTVLYNFMNCSSCVGGMNRRPILITVLETRDGOVLGRRC 300
 DB 241 ITGRQSVLVPEPPOVGTETFTVLYNFMNCSSCVGGMNRRPILITVLETRDGOVLGRRC 300

QY	301	PEARLCA	PGDRKAD	DEDSIRKQO	SDSKNGD	GTRKPR	ONTHTG	IOMTSIRK	RRBPDE	360													
Db	301	PEARLCA <td>PGDRKAD<td>DEDSIRKQO<td>SDSKNGD<td>GTRKPR<td>ONTHTG<td>IOMTSIRK<td>RRBPDE<td>360</td></td></td></td></td></td></td></td>	PGDRKAD <td>DEDSIRKQO<td>SDSKNGD<td>GTRKPR<td>ONTHTG<td>IOMTSIRK<td>RRBPDE<td>360</td></td></td></td></td></td></td>	DEDSIRKQO <td>SDSKNGD<td>GTRKPR<td>ONTHTG<td>IOMTSIRK<td>RRBPDE<td>360</td></td></td></td></td></td>	SDSKNGD <td>GTRKPR<td>ONTHTG<td>IOMTSIRK<td>RRBPDE<td>360</td></td></td></td></td>	GTRKPR <td>ONTHTG<td>IOMTSIRK<td>RRBPDE<td>360</td></td></td></td>	ONTHTG <td>IOMTSIRK<td>RRBPDE<td>360</td></td></td>	IOMTSIRK <td>RRBPDE<td>360</td></td>	RRBPDE <td>360</td>	360													
QY	361	LLYLPVGR	RETYEM	MLKIKES	ELMQLY	POHTIET	YRQOQO	OHHLQK	OTSIO	SPSSY 420													
Db	361	LLYLPVGR	RETYEM	MLKIKES	ELMQLY	POHTIET	YRQOQO	OHHLQK	OTSIO	SPSSY 420													
QY	421	GNSSPPL	KNKSANK	LPVSQ	LINPO	QRNAL	PTTIPD	GMGAN	IPMGM	PMAGDMGL 480													
Db	421	GNSSPPL	KNKSANK	LPVSQ	LINPO	QRNAL	PTTIPD	GMGAN	IPMGM	PMAGDMGL 480													
QY	481	SPQALP	PLPCL	MPSTSH	CTPPPP	YTD	DSIS	FLARL	GSSOLD	FTYTOGLTIOIEHY 540													
Db	481	SPQALP	PLPCL	MPSTSH	CTPPPP	YTD	DSIS	FLARL	GSSOLD	FTYTOGLTIOIEHY 540													
QY	541	SMDDL	SLAKI	PEOF	RHAI	WKIL	ILDRQ	LHE	SSPH	LRTPSAS	TVSGSSE	TRERY 600											
Db	541	SMDDL	SLAKI	PEOF	RHAI	WKIL	ILDRQ	LHE	SSPH	LRTPSAS	TVSGSSE	TRERY 600											
QY	601	DAVR	FTLR	QTSI	SPPR	DE	WNP	DM	DA	RNRK	QQR	IKEEGE 641											
Db	601	DAVR	FTLR	QTSI	SPPR	DE	WNP	DM	DA	RNRK	QQR	IKEEGE 641											
RESULT 3																							
Q9UE10																							
ID	Q9UE10																						
AC	Q9UE10																						
DT	01-MAY-2000																						
DT	01-MAY-2000																						
DT	01-OCT-2002																						
DE	KEP																						
GN	KEP																						
OS	Homo sapiens (Human)																						
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;																						
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.																						
OX	NCBI_TaxID=9606;																						
RN	[1]																						
RP	SEQUENCE FROM N.A.																						
RC	TISSUE=Skeletal muscle, and Keratinocytes;																						
RX	MEDLINE=99018225; PubMed=9799841;																						
RA	Augustin M., Bamberger C., Paul D., Schmale H.;																						
RT	"Cloning and chromosomal mapping of the human p53-related KET gene to																						
RL	chromosome 3q27 and its murine homolog Ket to mouse chromosome 16.";																						
CC	Mamm. Genome 9: 899-902(1998).																						
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).																						
CC	-1- SIMILARITY: BELONGS TO THE P53 FAMILY.																						
DR	EMBL: Y16961; CAI76562.1; -.																						
DR	HSSP: P04637; IYCS.																						
DR	InterPro: IPR002117; P53.																						
DR	InterPro: IPR001660; SAM.																						
DR	Pfam: PF008070; P53; 1.																						
DR	PRINTS: PR00386; P53SUPPRESSOR.																						
DR	PRODOM: PD002681; P53; 1.																						
DR	SMART: SM00454; SAM; 1.																						
DR	PROSITE: PS00348; P53; 1.																						
KW	Nuclear protein.																						
SO	SEQUENCE 680 AA; 76776 MW; 6548A6F2187D852E CRC64;																						
Query Match	99.8%;	Score 3397;	DB 4;	Length 680;																			
Best Local Similarity	99.8%;	Pred. No. 2.5e-281;																					
Matches 640;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0																			
QY	1	MSOST	QNE	F	S	P	E	V	F	O	H	I	M	P	L	E	P	I	C	S	V	O	P

Db	Accession	Length	Score	DB	Length
Db	160 SPSPAIPTNTDIPGHSPFDVSFQOSTAKSATWTYTELKLKLYCAKCPLOIKMTTP	219	98.5%	DB	11
Qy	181 POGAVIRAMPYKKAHEHTEVVKRCPNHLESEFNEGOIAPPSHLIRVGNSHAQYVEDP	240	98.1%	Qy	277
Db	220 POGAVIRAMPYKKAHEHTEVVKRCPNHLESEFNEGOIAPPSHLIRVGNSHAQYVEDP	279		Db	279
Qy	241 ITGROSUVAPEPPOVGTETFTTVLYNFMCSNCVCGMNRPLIIVTLETROGVLGRC	300		Qy	300
Db	280 ITGROSUVAPEPPOVGTETFTTVLYNFMCSNCVCGMNRPLIIVTLETROGVLGRC	339		Db	339
Qy	301 FEARCACPGDRKAKDEDSIRKQOVSDFKNDGTRKRPONTHGIOMTSIKRRSPDDE	360		Qy	360
Db	340 FEARCACPGDRKAKDEDSIRKQOVSDFKNDGTRKRPONTHGIOMTSIKRRSPDDE	399		Db	399
Qy	361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHIETERYRQOQOQHLLQKQTSIGSPSSY	420		Qy	420
Db	400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHIETERYRQOQOQHLLQKQTSIGSPSSY	459		Db	459
Qy	421 GNSSEPLLNKMSMNKLPVSQOLINPOQRNALPTPTIPDGGMANIPMGTHMPAGMGL	480		Qy	480
Db	460 GNSSEPLLNKMSMNKLPVSQOLINPOQRNALPTPTIPDGGMANIPMGTHMPAGMGL	519		Db	519
Qy	481 SPTQALPRLPLSMPSHSCPTPPPYPTDQSIYSEFLARLGGSSCLDFTTQGLTIVQIEHY	540		Qy	540
Db	520 SPTQALPRLPLSMPSHSCPTPPPYPTDQSIYSEFLARLGGSSCLDFTTQGLTIVQIEHY	579		Db	579
Qy	541 SMDDLAKIKIEQGFHAIWKGLIDRLQRLHEFSSPSHLITPSSASTVSAGSSETRGERYI	600		Qy	600
Db	580 SMDDLAKIKIEQGFHAIWKGLIDRLQRLHEFSSPSHLITPSSASTVSAGSSETRGERYI	639		Db	639
Qy	601 DAVRETLNQTISFPPEDEWDFNEDMDARRNKQRIKEGE	641		Qy	641
Db	640 DAVRETLNQTISFPPEDEWDFNEDMDARRNKQRIKEGE	680		Db	680
RESULT 4					
Q99JUE3	PRELIMINARY:	PRT:	663 AA.		
Q99JUE3	AC	Q99JUE3:			
DT	01-JUN-2001 (Tremblrel. 17, Created)				
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)				
DT	01-OCT-2002 (Tremblrel. 22, Last annotation update)				
DE	TAI KET alpha protein.				
GN	P63.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RT	STRAIN=Mistar; TISSUE= tongue;				
RX	MEDLINE=21363378; PubMed=11470269;				
RA	Bamberger C., Schmale H.;				
RT	"Identification and tissue distribution of novel KET/p63 splice				
RT	variants";				
RL	FEBS Lett. 501:121-126(2001).				
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE P53 FAMILY.				
DR	EMBL; AJ277446; CAC37098.1; -.				
DR	HSSP; P04637; 1YCS.				
DR	InterPro; IPR002117; P53.				
DR	InterPro; IPR001660; SAM.				
DR	Pfam; PF00870; P53; 1.				
DR	PRINTS; PR00386; P53SUPPRESSR.				
DR	PRODOM; PD002681; P53; 1.				
DR	SMART; SM00454; SAM; 1.				
DR	PROSITE; PS00348; P53; 1.				
KW	Nuclear protein.				
SO	SEQUENCE 663 AA; 74660 MW; C953BBAC389D5B70 CRC64;				
Query Match					
98.5%; Score 3353; DB 11; Length 663;					
98.1%; Pred.No. 1.4e-277;					
Best Local Similarity					

Matches		629; Conservative	7; Mismatches	5; Indels	0; Gaps	0;
QY	1	MSOSTQNEFLSPEVFOHIMDFLEOPICSVOPIDLNFDSESDGATKKIEISMDICIMQ	60			
Db	23	MSOSTQNEFLSPEVFOHIMDFLEOPICSVOPIDLNFDSESDGATKKIEISMDICIMQ	82			
QY	61	DSDSLDPMPQYNTNGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSSTFDAL	120			
Db	83	DSDSLDPMPQYNTNGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSSTFDAL	142			
QY	121	SPSPAIPSTNDYPCGHSFDVSEFOOSSTAKSATWTYSTECLKLYCOIATCPQIKVMP	180			
Db	143	SPSPAIPSTNDYPCGHSFDVSEFOOSSTAKSATWTYSTECLKLYCOIATCPQIKVMP	202			
QY	181	PGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVGNSHAQYVDP	240			
Db	203	PGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVGNSHAQYVDP	262			
QY	241	ITGRQSVLYPEPEPVGTETFTVLYNFMCSNCSVCGMNRRLIIVTLETBDGVLGRRC	300			
Db	263	ITGRQSVLYPEPEPVGTETFTVLYNFMCSNCSVCGMNRRLIIVTLETBDGVLGRRC	322			
QY	301	FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSIKKRRSPDE	360			
Db	323	FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSIKKRRSPDE	382			
QY	361	LLYLPVGRGRETVEMLIKESLELMQYLPQHTIETTYRQOQOHOHLQKOTSIOSSPY	420			
Db	383	LLYLPVGRGRETVEMLIKESLELMQYLPQHTIETTYRQOQOHOHLQKOTSIOSSPY	442			
QY	421	GNSSPPLKNNKSNKLPVSOLINPOQRNALTPTTIPGMCANIPMGTHMPMAGDNGL	480			
Db	443	GNSSPPLKNNKSNKLPVSOLINPOQRNALTPTTIPGMCANIPMGTHMPMAGDNGL	502			
QY	481	SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCCSCLDYFTTQGLTTIYQIEHY	540			
Db	503	SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCCSCLDYFTTQGLTTIYQIEHY	562			
QY	541	SMDLASIKTPEQFRHAIWKILDRHQLHESSSHLRTSSASTSVSGSSETRGEREVI	600			
Db	563	SMDLASIKTPEQFRHAIWKILDRHQLHESSSHLRTSSASTSVSGSSETRGEREVI	622			
QY	601	DAVRFTLRQITISPPRDEMDFNFDMDARRKKQORIKEGE	641			
Db	623	DAVRFTLRQITISPPRDEMDFNFDMDARRKKQORIKEGE	663			
RESULT 5						
QY	09JUP6	PRELIMINARY:	PRT:	680 AA.		
AC	09JUP6					
DT	01-OCT-2000	(TREMBLrel. 15, Created)				
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)				
DT	01-OCT-2002	(TREMBLrel. 22, Last annotation update)				
DE	TA2	key alpha.				
GN	P63.					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
OX	NCBI_TaxID=10116;					
RN	11					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Lingual epithelium;					
RC	MEDLINE=97460723; PubMed=9315105;					
RA	Schmale H.; Bamberger C.;					
RT	"A novel protein with strong homology to the tumor suppressor p53."					
RL	Oncogene 15:1363-1367(1997).					
RN	12					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Lingual epithelium;					
RA	Schmale H.;					
RL	submitted (APR-2000) to the EMBL/GenBank/DBJ databases.					
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).					

CC	-1- SIMILARITY: BELONGS TO THE P53 FAMILY.					
DR	EMBL; Y10258; CAB88216.1; -					
DR	HSSP; P04637; 1YCS.					
DR	InterPro: IPR002117; P53.					
DR	InterPro: IPR001660; SAM.					
DR	Pfam; PF00870; P53; 1.					
DR	PRINTS; PR00386; P53SUPERSSR.					
DR	PRODOM; PD002681; P53; 1.					
DR	SMART; SM00454; SAM; 1.					
DR	PROSITE; PS00348; P53; 1.					
KV	Nuclear protein					
SQ	SEQUENCE 680 AA; 76760 MW; AC45DAB8B6F61400 CRC64;					
Query Match						
Best Local Similarity		98.5%;	Score 3353;	DB 11;	Length 680;	
Matches		629; Conservative	7; Mismatches	5; Indels	0; Gaps	0;
QY	1	MSOSTQNEFLSPEVFOHIMDFLEOPICSVOPIDLNFDSESDGATKKIEISMDICIMQ	60			
Db	40	MSOSTQNEFLSPEVFOHIMDFLEOPICSVOPIDLNFDSESDGATKKIEISMDICIMQ	99			
QY	61	DSDSLDPMPQYNTNGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSSTFDAL	120			
Db	100	DSDSLDPMPQYNTNGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSSTFDAL	159			
QY	121	SPSPAIPSTNDYPCGHSFDVSEFOOSSTAKSATWTYSTECLKLYCOIATCPQIKVMP	180			
Db	160	SPSPAIPSTNDYPCGHSFDVSEFOOSSTAKSATWTYSTECLKLYCOIATCPQIKVMP	219			
QY	181	PGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVGNSHAQYVDP	240			
Db	220	PGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVGNSHAQYVDP	279			
QY	241	ITGRQSVLYPEPEPVGTETFTVLYNFMCSNCSVCGMNRRLIIVTLETBDGVLGRRC	300			
Db	280	ITGRQSVLYPEPEPVGTETFTVLYNFMCSNCSVCGMNRRLIIVTLETBDGVLGRRC	339			
QY	301	FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSIKKRRSPDE	360			
Db	340	FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSIKKRRSPDE	399			
QY	361	LLYLPVGRGRETVEMLIKESLELMQYLPQHTIETTYRQOQOHOHLQKOTSIOSSPY	420			
Db	400	LLYLPVGRGRETVEMLIKESLELMQYLPQHTIETTYRQOQOHOHLQKOTSIOSSPY	459			
QY	421	GNSSPPLKNNKSNKLPVSOLINPOQRNALTPTTIPGMCANIPMGTHMPMAGDNGL	480			
Db	460	GNSSPPLKNNKSNKLPVSOLINPOQRNALTPTTIPGMCANIPMGTHMPMAGDNGL	519			
QY	481	SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCCSCLDYFTTQGLTTIYQIEHY	540			
Db	520	SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCCSCLDYFTTQGLTTIYQIEHY	579			
QY	541	SMDLASIKTPEQFRHAIWKILDRHQLHESSSHLRTSSASTSVSGSSETRGEREVI	600			
Db	580	SMDLASIKTPEQFRHAIWKILDRHQLHESSSHLRTSSASTSVSGSSETRGEREVI	639			
QY	601	DAVRFTLRQITISPPRDEMDFNFDMDARRKKQORIKEGE	641			
Db	640	DAVRFTLRQITISPPRDEMDFNFDMDARRKKQORIKEGE	660			
RESULT 6						
QY	088898	PRELIMINARY:	PRT:	680 AA.		
AC	088898					
DT	01-NOV-1998	(TREMBLrel. 08, Created)				
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)				
DT	01-OCT-2002	(TREMBLrel. 22, Last annotation update)				
DE	TAP63	alpha.				
GN	TRP63.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					

OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
 RA Caput D., McKeon F.;
 RT "p53, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";
 RT Mol. Cell 2:305-316(1998).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC EMBL: AF075436; AAC62641.1; -.
 DR HSSP: P04637; IYCS.
 DR MGD: MG1:1330810; Trp63.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR ProDom: PD002681; P53; 1.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 680 AA; 76788 MW; 8DFE0284F247C68A CRC64;

Query Match 98.5%; Score 3353; DB 11; Length 680;
 Best Local Similarity 98.1%; Pred. No. 1.5e-277;
 Matches 659; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

1 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVOPIDLFNVEPSHGATNKIETISMDICRMQ 60
 40 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVOPIDLFNVEPSHGATNKIETISMDICRMQ 99
 61 DSDSDPMPPQNTNGLNSMDQOIONGSSSTPYNTDHAQNSVAPSPYADPSSTFDAL 120
 100 DSDSDPMPPQNTNGLNSMDQOIONGSSSTPYNTDHAQNSVAPSPYADPSSTFDAL 159
 121 SPSPAIPSTNDYPGHSPFVSFOOSSTAKATWTYTELKKLYCOIAKCPQIKVMTBP 180
 160 SPSPAIPSTNDYPGHSPFVSFOOSSTAKATWTYTELKKLYCOIAKCPQIKVMTBP 219
 181 PGCAVIRAMPVYKKAHEVTEVVKRCPNHEL.SREFNEGQIAPSHLIRVGNSHAQYVEDP 240
 220 PGCAVIRAMPVYKKAHEVTEVVKRCPNHEL.SREFNEGQIAPSHLIRVGNSHAQYVEDP 279
 241 ITGROSVALYVPEPPQVGETFTVLYNFMKNSSCVCGMNRPII.IYTLLETRDQVYGRRC 300
 280 ITGROSVALYVPEPPQVGETFTVLYNFMKNSSCVCGMNRPII.IYTLLETRDQVYGRRC 339
 301 FEARICACGRRKKADEDSIRKQVSDSTKNGDGRPRFRONTNGIOMTSIKKRSPDDE 360
 340 FEARICACGRRKKADEDSIRKQVSDSTKNGDGRPRFRONTNGIOMTSIKKRSPDDE 399
 361 LLYLVPRGRETEYEMLIKIKESLELMQYLPQHTLETYRQOQOQHLLQKQTSIGSSSY 420
 400 LLYLVPRGRETEYEMLIKIKESLELMQYLPQHTLETYRQOQOQHLLQKQTSIGSSSY 459
 421 GNSSPPLKNSMNLKPSVQLINQQRNALPTTTPDGMGANIPMGTHMPAGMNGI 480
 460 GNSSPPLKNSMNLKPSVQLINQQRNALPTTTPDGMGANIPMGTHMPAGMNGI 519
 481 SFTQALPPLSPSTSHCPPTPPYDCSIVSFIARLGSSCLDYTTGGLTITYIEHY 540
 520 SFTQALPPLSPSTSHCPPTPPYDCSIVSFIARLGSSCLDYTTGGLTITYIEHY 579
 541 SMDIASLKIPQFRHAIWKGLDHRQLHEFSSPSHLILTPSSASTVSVGSSSTRGERVY 600
 580 SMDIASLKIPQFRHAIWKGLDHRQLHEFSSPSHLILTPSSASTVSVGSSSTRGERVY 639
 601 DAVRFTLRQTIISFPPEDEWNPFDMDARRNKQQRKEGE 641
 640 DAVRFTLRQTIISFPPEDEWNPFDMDARRNKQQRKEGE 680

RESULT 7
 ID 09UBV9 PRELIMINARY; PRT; 586 AA.
 AC 09UBV9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DE 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE DN P53 alpha.
 GN P53.
 OS Homo sapiens (Human).
 OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
 OC Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKeon F.;
 RT "p53, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";
 RT Mol. Cell 2:305-316(1998).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Lee L.A., Walsh P., Prater C.A., Su L., Marchbank A., Egbert T.B.,
 RA dellavalle R.P., Targoff I.N., Kaufman K.M., Chorzeelski T.P.,
 RA Jablonska S.;
 RT "Characterization of an autoantigen associated with chronic ulcerative
 RT stomatitis: The CUSP autoantigen is a member of the p53 family.";
 RJ J. Invest. Dermatol. 0:0-0(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Hagivara K., McMenamin M.G., Harris C.C.;
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL: AF075431; AAC62636.1; -.
 DR EMBL: AF091627; AAC43038.1; -.
 DR EMBL: AF124539; AAG45610.1; JOINED.
 DR EMBL: AF124530; AAG45610.1; JOINED.
 DR EMBL: AF124531; AAG45610.1; JOINED.
 DR EMBL: AF124532; AAG45610.1; JOINED.
 DR EMBL: AF124533; AAG45610.1; JOINED.
 DR EMBL: AF124534; AAG45610.1; JOINED.
 DR EMBL: AF124535; AAG45610.1; JOINED.
 DR EMBL: AF124536; AAG45610.1; JOINED.
 DR EMBL: AF124537; AAG45610.1; JOINED.
 DR EMBL: AF124538; AAG45610.1; JOINED.
 DR HSSP: P04637; IYCS.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR ProDom: PD002681; P53; 1.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 586 AA; 65756 MW; 2E2F92ABF1A8629 CRC64;

Query Match 89.1%; Score 3033; DB 4; Length 586;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

70 PONTNGLNSMDQOIONGSSSTPYNTDHAQNSVAPSPYADPSSTFDALSPSPAIPSN 129
 15 PONTNGLNSMDQOIONGSSSTPYNTDHAQNSVAPSPYADPSSTFDALSPSPAIPSN 74
 130 TDVPGHSDVVSFOOSSTAKATWTYTELKKLYCOIATCPQIKVMTBPPOGAVIRAM 189
 75 TDVPGHSDVVSFOOSSTAKATWTYTELKKLYCOIATCPQIKVMTBPPOGAVIRAM 134
 190 PYYKKAHEVTEVVKRCPNHEL.SREFNEGQIAPSHLIRVGNSHAQYVEDPITGROSVALY 249

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Db 135 PVYKAEHTEVYKRCPNHELSEREFNEQIAPSPSHLRVEGNSHAQYVEDITGRQSYLV 194
QY 250 PYEPPQVGTETFTVLVYNFMCNSCGVGNRRPILITVLETRDQVILGRRCFEARICACP 309
    |||||
Db 195 PYEPPQVGTETFTVLVYNFMCNSCGVGNRRPILITVLETRDQVILGRRCFEARICACP 254
QY 310 GRDRKADEDSIRKQOVSDSTKNGDGTGRPFQNTNGHGIOMTSIKRRSPDDELLYLPVGR 369
    |||||
Db 255 GRDRKADEDSIRKQOVSDSTKNGDGTGRPFQNTNGHGIOMTSIKRRSPDDELLYLPVGR 314
QY 370 EYEMLKIKESLEIMQVLPQHTIETRYQOQOQOQHLLQKOTSIQSPSSYGNSSPPLNK 429
    |||||
Db 315 EYEMLKIKESLEIMQVLPQHTIETRYQOQOQOQHLLQKOTSIQSPSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOORNALPTTIPDGGANIPMAGTMAPAGDNGISPTQALPPP 489
    |||||
Db 375 MNSMNLKPSVSQILNPOORNALPTTIPDGGANIPMAGTMAPAGDNGISPTQALPPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLDSLK 549
    |||||
Db 435 LSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLDSLK 494
QY 550 IPEQFRHAIWKGIIDHROLHEFSSPSHLRTPPSSASTVSVGSSETRGRVDAVAFRTLQ 609
    |||||
Db 495 IPEQFRHAIWKGIIDHROLHEFSSPSHLRTPPSSASTVSVGSSETRGRVDAVAFRTLQ 554
QY 610 TISEPPRDEWDFNFDMDARRNKKOORIKEGE 641
    |||||
Db 555 TISEPPRDEWDFNFDMDARRNKKOORIKEGE 586
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RESULT 8

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ID 09P1B4 PRELIMINARY; PRT; 586 AA.
AC 09P1B4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE P51 isoform delNalplna.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF116769; AAF43491.1; JOINED.
DR EMBL: AF116758; AAF43491.1; JOINED.
DR EMBL: AF116759; AAF43491.1; JOINED.
DR EMBL: AF116760; AAF43491.1; JOINED.
DR EMBL: AF116761; AAF43491.1; JOINED.
DR EMBL: AF116762; AAF43491.1; JOINED.
DR EMBL: AF116763; AAF43491.1; JOINED.
DR EMBL: AF116764; AAF43491.1; JOINED.
DR EMBL: AF116765; AAF43491.1; JOINED.
DR EMBL: AF116766; AAF43491.1; JOINED.
DR EMBL: AF116767; AAF43491.1; JOINED.
DR EMBL: AF116768; AAF43491.1; JOINED.
DR HSSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.

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SO SEQUENCE 586 AA; 65726 MW; 9A2316B631AE8634 CRC64;

Query Match 89.0%; Score 3029; DB 4; Length 586;
 Best Local Similarity 99.8%; Pred. No. 5,66-250;
 Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 70 PQTNLGLINSDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFDALSPSPALPSN 129
    |||||
Db 15 PQTNLGLINSDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFDALSPSPALPSN 74
QY 130 TDYGRPHSFDVSFOQSSSTAKSATMTYSTELKKLYCQIAKTQIDQIKWTTPPGCAVIRAM 189
    |||||
Db 75 TDYGRPHSFDVSFOQSSSTAKSATMTYSTELKKLYCQIAKTQIDQIKWTTPPGCAVIRAM 134
QY 190 PVYKAEHTEVYKRCPNHELSEREFNEQIAPSPSHLRVEGNSHAQYVEDITGRQSYLV 249
    |||||
Db 135 PVYKAEHTEVYKRCPNHELSEREFNEQIAPSPSHLRVEGNSHAQYVEDITGRQSYLV 194
QY 250 PYEPPQVGTETFTVLVYNFMCNSCGVGNRRPILITVLETRDQVILGRRCFEARICACP 309
    |||||
Db 195 PYEPPQVGTETFTVLVYNFMCNSCGVGNRRPILITVLETRDQVILGRRCFEARICACP 254
QY 310 GRDRKADEDSIRKQOVSDSTKNGDGTGRPFQNTNGHGIOMTSIKRRSPDDELLYLPVGR 369
    |||||
Db 255 GRDRKADEDSIRKQOVSDSTKNGDGTGRPFQNTNGHGIOMTSIKRRSPDDELLYLPVGR 314
QY 370 EYEMLKIKESLEIMQVLPQHTIETRYQOQOQOQHLLQKOTSIQSPSSYGNSSPPLNK 429
    |||||
Db 315 EYEMLKIKESLEIMQVLPQHTIETRYQOQOQOQHLLQKOTSIQSPSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOORNALPTTIPDGGANIPMAGTMAPAGDNGISPTQALPPP 489
    |||||
Db 375 MNSMNLKPSVSQILNPOORNALPTTIPDGGANIPMAGTMAPAGDNGISPTQALPPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLDSLK 549
    |||||
Db 435 LSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLDSLK 494
QY 550 IPEQFRHAIWKGIIDHROLHEFSSPSHLRTPPSSASTVSVGSSETRGRVDAVAFRTLQ 609
    |||||
Db 495 IPEQFRHAIWKGIIDHROLHEFSSPSHLRTPPSSASTVSVGSSETRGRVDAVAFRTLQ 554
QY 610 TISEPPRDEWDFNFDMDARRNKKOORIKEGE 641
    |||||
Db 555 TISEPPRDEWDFNFDMDARRNKKOORIKEGE 586
    |||||

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RESULT 9

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ID 075080 PRELIMINARY; PRT; 586 AA.
AC 075080;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE P73H.
GN P73H.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98369596; PubMed=9703973;
RA Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,
RA Tanaka T., Shinkai Y., Kato H.;
RT "A second p53-related protein, p73L, with high homology to p73.";
RL Biochem. Biophys. Res. Commun. 248:603-607(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AB010153; BAA32433.1; -.
DR HSSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.

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DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 DR Nucleic protein.
 SQ SEQUENCE 586 AA; 65734 MW; 9DC102AB57120C0F CRC64;

Query Match 88.6%; Score 3016; DB 4; Length 586;
 Best Local Similarity 99.5%; Pred. No. 7, 2e-249;
 Matches 569; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSPSTFALSPSPALPSN 129
 |||||
 DB 15 PQTNLGLNSMDQOIRNSSSTSPYNTDHAQNSVTAAPSPYAPSPSTFALSPSPALPSN 74
 |||||
 QY 130 TDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKYCOIAKTCPIQIKVMTPPQGAIVRAM 189
 |||||
 DB 75 TDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKYCOIAKTCPIQIKVMTPPQGAIVRAM 134
 |||||
 QY 190 PYKKAHEHYEVVKKCPNHELSEFNEGOIAPPSHILIRVGNSHAQYVEDPITGRQSVLY 249
 |||||
 DB 135 PYKKAHEHYEVVKKCPNHELSEFNEGOIAPPSHILIRVGNSHAQYVEDPITGRQSVLY 194
 |||||
 QY 250 PYEPPOVGTETFTVLYNFCNNSCVGMNRRPILITVLETRDGOYLGRCFEARIACAP 309
 |||||
 DB 195 PYEPPOVGTETFTVLYNFCNNSCVGMNRRPILITVLETRDGOYLGRCFEARIACAP 254
 |||||
 QY 310 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHGIIOMTSIKRRSPDELLYLTPVRGR 369
 |||||
 DB 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHGIIOMTSIKRRSPDELLYLTPVRGR 314
 |||||
 QY 370 EYEMLLKIKESLELMQYLPQHTIETYYRQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 429
 |||||
 DB 315 EYEMLLKIKESLELMQYLPQHTIETYYRQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
 |||||
 QY 430 MNSMKNLPVSQILNQQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
 |||||
 DB 375 MNSMKNLPVSQILNQQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
 |||||
 QY 490 LSMPTSHCTPPPPYPTDCSYISFLARLCCSCLDYFTTQGLTTYIQIHYISMDLALSK 549
 |||||
 DB 435 LSMPTSHCTPPPPYPTDCSYISFLARLCCSCLDYFTTQGLTTYIQIHYISMDLALSK 494
 |||||
 QY 550 IPEQFRHAIWKGIILHROLHEFSSPSHLRTPSSASTVSGSSETRGGERVIAVAPRTLLQ 609
 |||||
 DB 495 IPEQFRHAIWKGIILHROLHEFSSPSHLRTPSSASTVSGSSETRGGERVIAVAPRTLLQ 554
 |||||
 QY 610 TISFPRDEMDNFMDARNRKQORIKEGE 641
 |||||
 DB 555 TISFPRDEMDNFMDARNRKQORIKEGE 586
 |||||

RESULT 10

089097 PRELIMINARY; PRT; 586 AA.
 AC 089097;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE DN P63 alpha.
 GN TRP63 OR P73H.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
 RA Caput D., McKean F.,
 RT "p53, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";

RL MOL. Cell 2:305-316(1998).

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Thymus;
 RX MEDLINE=98369596; PubMed=9703973;
 RA Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,
 RA Tanaka T., Shinkai Y., Kato H.;
 RT "A second p53-related protein, p73, with high homology to p73.";
 RT Biochem. Biophys. Res. Commun. 248:603-607(1998).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL: AF075439; AAC62644.1;
 DR EMBL: AB010152; BAA32432.1;
 DR HSSP: P04637; 1YCS.
 DR MGD: MGI:1330810; Trp63.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 DR Nucleic protein.
 SQ SEQUENCE 586 AA; 65789 MW; 622E24085B8BCB7 CRC64;

Query Match 88.0%; Score 2995; DB 11; Length 586;
 Best Local Similarity 98.4%; Pred. No. 4, 5e-247;
 Matches 563; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSPSTFALSPSPALPSN 129
 |||||
 DB 15 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSPSTFALSPSPALPSN 74
 |||||
 QY 130 TDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKYCOIAKTCPIQIKVMTPPQGAIVRAM 189
 |||||
 DB 75 TDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKYCOIAKTCPIQIKVMTPPQGAIVRAM 134
 |||||
 QY 190 PYKKAHEHYEVVKKCPNHELSEFNEGOIAPPSHILIRVGNSHAQYVEDPITGRQSVLY 249
 |||||
 DB 135 PYKKAHEHYEVVKKCPNHELSEFNEGOIAPPSHILIRVGNSHAQYVEDPITGRQSVLY 194
 |||||
 QY 250 PYEPPOVGTETFTVLYNFCNNSCVGMNRRPILITVLETRDGOYLGRCFEARIACAP 309
 |||||
 DB 195 PYEPPOVGTETFTVLYNFCNNSCVGMNRRPILITVLETRDGOYLGRCFEARIACAP 254
 |||||
 QY 310 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHGIIOMTSIKRRSPDELLYLTPVRGR 369
 |||||
 DB 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHGIIOMTSIKRRSPDELLYLTPVRGR 314
 |||||
 QY 370 EYEMLLKIKESLELMQYLPQHTIETYYRQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 429
 |||||
 DB 315 EYEMLLKIKESLELMQYLPQHTIETYYRQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
 |||||
 QY 430 MNSMKNLPVSQILNQQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
 |||||
 DB 375 MNSMKNLPVSQILNQQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
 |||||
 QY 490 LSMPTSHCTPPPPYPTDCSYISFLARLCCSCLDYFTTQGLTTYIQIHYISMDLALSK 549
 |||||
 DB 435 LSMPTSHCTPPPPYPTDCSYISFLARLCCSCLDYFTTQGLTTYIQIHYISMDLALSK 494
 |||||
 QY 550 IPEQFRHAIWKGIILHROLHEFSSPSHLRTPSSASTVSGSSETRGGERVIAVAPRTLLQ 609
 |||||
 DB 495 IPEQFRHAIWKGIILHROLHEFSSPSHLRTPSSASTVSGSSETRGGERVIAVAPRTLLQ 554
 |||||
 QY 610 TISFPRDEMDNFMDARNRKQORIKEGE 641
 |||||
 DB 555 TISFPRDEMDNFMDARNRKQORIKEGE 586
 |||||

RESULT 11

099JE2 PRELIMINARY; PRT; 586 AA.
 ID 099JE2

AC Q9JUE2: 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE DN KET alpha protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Banberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
variants";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AJ277447; CAC37099.1; -.
DR HSSP; P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00368; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SO SEQUENCE 586 AA; 65732 MW; 78AB8CC4F52BA743 CRC64;

Query Match 87.8%; Score 2991; DB 11; Length 586;
Best Local Similarity 98.3%; Pred. No. 9.9e-247;
Matches 562; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAPQSSSTFDALSPSPALPSN 129
DB 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAPQSSSTFDALSPSPALPSN 74
QY 130 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKKLCQIAKTCPIQIKWTPPPQCAVIRAM 189
DB 75 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKKLCQIAKTCPIQIKWTPPPQCAVIRAM 134
QY 190 PVYKAEHVEVYKRCPNHELREBNEQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKAEHVEVYKRCPNHELREBNEQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGTETTYLYNFMNCSSCVGGNNRRPILITVLETRDQVIGRRCFEARIACAP 309
DB 195 PYEPPOVGTETTYLYNFMNCSSCVGGNNRRPILITVLETRDQVIGRRCFEARIACAP 254
QY 310 GRDKRAEDSIRKQOVSDSTKNGDGTKRPFRONTHGLOMTSIRKRRSPDDELILPYRGR 369
DB 255 GRDKRAEDSIRKQOVSDSTKNGDGTKRPFRONTHGLOMTSIRKRRSPDDELILPYRGR 314
QY 370 ETYMLLKIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQSPSSYGNSSPPLNK 429
DB 315 ETYMLLKIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQSPSSYGNSSPPLNK 374
QY 430 MNSMNLKIPSVQSLNPOORNALPTTIPDGAGANIPMGITMPAGDMNGISPTQALPPP 489
DB 375 MNSMNLKIPSVQSLNPOORNALPTTIPDGAGANIPMGITMPAGDMNGISPTQALPPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGSSCDYFTTQGLTTIYQIEHSMDDLASLK 549
DB 435 LSMSTSHCTPPPPYPTDCSIVSFLARLGSSCDYFTTQGLTTIYQIEHSMDDLASLK 494
QY 550 IPEQFRRAIWKGIIDHROLHEFSSPHLLRTPPSASIVSVGSSSETRGERVIDAVFTLRQ 609
DB 495 IPEQFRRAIWKGIIDHROLHEFSSPHLLRTPPSASIVSVGSSSETRGERVIDAVFTLRQ 554
QY 610 TISPPRDEMNDFNFDMDARRNKQARIKEGE 641

DB 555 TISPPRDEMNDFNFDMDARRNKQARIKEGE 586
|||||
RESULT 12
ID Q9DEC7 PRELIMINARY; PRT; 582 AA.
AC Q9DEC7:
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE DN P63 alpha.
GN DNP63A.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20568966; PubMed=11118893;
RX Yasue A., Tao H., Nohno T., Moriyama K., Noji S., Ohuchi H.;
RA "Cloning and expression of a chick p63 gene";
RT Mech. Dev. 100:105-108(2001).
RL -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AB045224; BAB20631.1; -.
DR HSSP; P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00368; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SO SEQUENCE 582 AA; 65213 MW; 9D1C356B9CCABCE3 CRC64;

Query Match 85.1%; Score 2898; DB 13; Length 582;
Best Local Similarity 95.8%; Pred. No. 8.6e-239;
Matches 548; Conservative 7; Mismatches 13; Indels 4; Gaps 1;

QY 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAPQSSSTFDALSPSPALPSN 129
DB 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAPQSSSTFDALSPSPALPSN 74
QY 130 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKKLCQIAKTCPIQIKWTPPPQCAVIRAM 189
DB 75 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKKLCQIAKTCPIQIKWTPPPQCAVIRAM 134
QY 190 PVYKAEHVEVYKRCPNHELREBNEQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKAEHVEVYKRCPNHELREBNEQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGTETTYLYNFMNCSSCVGGNNRRPILITVLETRDQVIGRRCFEARIACAP 309
DB 195 PYEPPOVGTETTYLYNFMNCSSCVGGNNRRPILITVLETRDQVIGRRCFEARIACAP 254
QY 310 GRDKRAEDSIRKQOVSDSTKNGDGTKRPFRONTHGLOMTSIRKRRSPDDELILPYRGR 369
DB 255 GRDKRAEDSIRKQOVSDSTKNGDGTKRPFRONTHGLOMTSIRKRRSPDDELILPYRGR 310
QY 370 ETYMLLKIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQSPSSYGNSSPPLNK 429
DB 315 ETYMLLKIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQSPSSYGNSSPPLNK 370
QY 430 MNSMNLKIPSVQSLNPOORNALPTTIPDGAGANIPMGITMPAGDMNGISPTQALPPP 489
DB 371 MNSMNLKIPSVQSLNPOORNALPTTIPDGAGANIPMGITMPAGDMNGISPTQALPPP 430
QY 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGSSCDYFTTQGLTTIYQIEHSMDDLASLK 549
DB 431 LSMSTSHCTPPPPYPTDCSIVSFLARLGSSCDYFTTQGLTTIYQIEHSMDDLASLK 490

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QY 550 IPEORRAIWKGIILHROLHEFSSPSHLRPPSSATSVSSSETRGERVIDAVETLRO 609
DB 491 IPEORRAIWKGIILHROLHEFSSPSHLRPPSSATSVSSSETRGERVIDAVETLRO 550
QY 610 TISPPRDEWMDNFMDARNRKQORKEGE 641
DB 551 TISPPRDEWMDNFMDARNRKQORKEGE 582

RESULT 13
Q9PIB7 PRELIMINARY; PRT; 516 AA.
AC Q9PIB7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE P51 isoform TAP63beta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE-20388515; PubMed-10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF116769; AAF43488.1; -.
DR EMBL; AF116756; AAF43488.1; JOINED.
DR EMBL; AF116757; AAF43488.1; JOINED.
DR EMBL; AF116759; AAF43488.1; JOINED.
DR EMBL; AF116760; AAF43488.1; JOINED.
DR EMBL; AF116761; AAF43488.1; JOINED.
DR EMBL; AF116762; AAF43488.1; JOINED.
DR EMBL; AF116763; AAF43488.1; JOINED.
DR EMBL; AF116764; AAF43488.1; JOINED.
DR EMBL; AF116765; AAF43488.1; JOINED.
DR EMBL; AF116766; AAF43488.1; JOINED.
DR EMBL; AF116767; AAF43488.1; JOINED.
DR HSSP; P04637; LYCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 516 AA; 57598 MW; 07553781103738B1 CRC64;

Query Match 79.9%; Score 2722; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 7.9e-224;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 ITGROSLVLPYEPPOVGTETFTVLNFMNCSSCVGMNRRPILITVLTETRDGOVLGRRC 300
QY 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTFRPFRONTHTGIQTSIKRRSPDE 360
DB 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTFRPFRONTHTGIQTSIKRRSPDE 360
QY 361 LLYLPVGRRETEMLKIKESLEIMQYLPOHTLETYRQOOOQHOHLQKOTSIOSSPY 420
DB 361 LLYLPVGRRETEMLKIKESLEIMQYLPOHTLETYRQOOOQHOHLQKOTSIOSSPY 420
QY 421 GNSSPPLKMNKMLPSVSQLINPOQRNALPTTIPDCMGANIPMAGTHMPAGDMNL 480
DB 421 GNSSPPLKMNKMLPSVSQLINPOQRNALPTTIPDCMGANIPMAGTHMPAGDMNL 480
QY 481 SPTQALPPLSPSTSHCTPPPPPTDCSIV 511
DB 481 SPTQALPPLSPSTSHCTPPPPPTDCSIV 511

RESULT 14
Q9H3D3 PRELIMINARY; PRT; 555 AA.
AC Q9H3D3; Q9UP27;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE TA p63 beta.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE-98448095; PubMed-9774969;
RA Yang A., Kaghad M., Wang Y., Gallet E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKen F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RP Haglwa K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBI databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF124539; AAG45608.1; -.
DR EMBL; AF124528; AAG45608.1; JOINED.
DR EMBL; AF124529; AAG45608.1; JOINED.
DR EMBL; AF124531; AAG45608.1; JOINED.
DR EMBL; AF124532; AAG45608.1; JOINED.
DR EMBL; AF124533; AAG45608.1; JOINED.
DR EMBL; AF124534; AAG45608.1; JOINED.
DR EMBL; AF124535; AAG45608.1; JOINED.
DR EMBL; AF124536; AAG45608.1; JOINED.
DR EMBL; AF124537; AAG45608.1; JOINED.
DR EMBL; AF075432; AAC62637.1; -.
DR HSSP; P04637; LYCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 555 AA; 62433 MW; E22874B7DBABCBE CRC64;

Query Match 79.9%; Score 2722; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.7e-224;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```

Db 40 MSQSTOTNEFLSPEVFGHIMDFLEOPICSVOPIDLNFEVDESENGATNKIEISMDCIIMQ 99
Oy 61 DSDLSDPMPQYNTNGLINSMDOQIQNGSSSTSPYNTDHAONSVTAAPSVAOPSTFDAL 120
Db 100 DSDLSDPMPQYNTNGLINSMDOQIQNGSSSTSPYNTDHAONSVTAAPSVAOPSTFDAL 159
Oy 121 SPSPAIPSTNDYPCGPHSFDSVFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
Db 160 SPSPAIPSTNDYPCGPHSFDSVFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 219
Oy 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSREFNEGOIAPPSHLIRVEGSHAQYVEDP 240
Db 220 POGAVIRAMPYKKAHEHTEVVKRCPNHELSREFNEGOIAPPSHLIRVEGSHAQYVEDP 279
Oy 241 ITGROSVALPYEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILITVLETRDGOVLGRRC 300
Db 280 ITGROSVALPYEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILITVLETRDGOVLGRRC 339
Oy 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHTGQIOMTSIKRRSPDDE 360
Db 340 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHTGQIOMTSIKRRSPDDE 399
Oy 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETRYROOQOQOHLQKQTSIOSPSSY 420
Db 400 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETRYROOQOQOHLQKQTSIOSPSSY 459
Oy 421 GNSSPPLKMKNSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
Db 460 GNSSPPLKMKNSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 519
Oy 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
Db 520 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 550

```

RESULT 15

```

099JUD7 PRELIMINARY: PRT: 538 AA.
AC 099JUD7: 01-JUN-2001 (TREMBlrel. 17, Created)
DR 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE TAI KER beta protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KER/p63 splice
variants".
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AJ277452; CAC37104.1; -.
DR HSSP; P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 538 AA; 60326 MW; 66D0CA19786BF21B CRC64;

```

Query Match 78.9%; Score 2685; DB 11; Length 538;
 Best Local Similarity 98.4%; Pred. No. 1.2e-220;
 Matches 503; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MSQSTOTNEFLSPEVFGHIMDFLEOPICSVOPIDLNFEVDESENGATNKIEISMDCIIMQ 60

```

Db 23 MSQSTOTNEFLSPEVFGHIMDFLEOPICSVOPIDLNFEVDESENGATNKIEISMDCIIMQ 82
Oy 61 DSDLSDPMPQYNTNGLINSMDOQIQNGSSSTSPYNTDHAONSVTAAPSVAOPSTFDAL 120
Db 83 DSDLSDPMPQYNTNGLINSMDOQIQNGSSSTSPYNTDHAONSVTAAPSVAOPSTFDAL 142
Oy 121 SPSPAIPSTNDYPCGPHSFDSVFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
Db 143 SPSPAIPSTNDYPCGPHSFDSVFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 202
Oy 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSREFNEGOIAPPSHLIRVEGSHAQYVEDP 240
Db 203 POGAVIRAMPYKKAHEHTEVVKRCPNHELSREFNEGOIAPPSHLIRVEGSHAQYVEDP 262
Oy 241 ITGROSVALPYEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILITVLETRDGOVLGRRC 300
Db 263 ITGROSVALPYEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILITVLETRDGOVLGRRC 322
Oy 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHTGQIOMTSIKRRSPDDE 360
Db 323 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHTGQIOMTSIKRRSPDDE 382
Oy 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETRYROOQOQOHLQKQTSIOSPSSY 420
Db 383 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETRYROOQOQOHLQKQTSIOSPSSY 442
Oy 421 GNSSPPLKMKNSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
Db 443 GNSSPPLKMKNSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 502
Oy 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
Db 503 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 533

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Search completed: August 7, 2003, 09:51:37
 Job time : 56.5747 secs

PT New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours

PS Claim 23; Fig 10; 161pp; English.

The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isoforms exist. Splice variants differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as delta1 and TA forms, where the delta1 form lacks the transactivation domain. The present sequence represents human p63 isoform Tap63 beta. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. Delta1 isoforms of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in hematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AA05953-64), polynucleotides (see AA058572-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.

SQ Sequence 516 AA;

Query Match	100.0%;	Score 2751;	DB 20;	Length 516;
Best Local Similarity	100.0%;	Pred. NO. 2.2e-26;		

QY	MSOSTQTNELSEFEVQHIMDFLEQPICSVQPIDLNFDESEEGATKKEISDCCRQ	60
Db	1 MSOSTQTNELSEFEVQHIMDFLEQPICSVQPIDLNFDESEEGATKKEISDCCRQ	60
QY	DSLSLSPMPQTYTNGLNLSMDQOIQIONSSSTSPYNTDHAQNSVTABSPAQSPSTFAL	120
Db	61 DSLSLSPMPQTYTNGLNLSMDQOIQIONSSSTSPYNTDHAQNSVTABSPAQSPSTFAL	120
QY	SPSPALPSTNDYGPSPDFSVFOQSSSTAKSATWTYSTELKLYCOIAKTCIQIAKWTPP	180
Db	121 SPSPALPSTNDYGPSPDFSVFOQSSSTAKSATWTYSTELKLYCOIAKTCIQIAKWTPP	180
QY	SPSPALPSTNDYGPSPDFSVFOQSSSTAKSATWTYSTELKLYCOIAKTCIQIAKWTPP	180
Db	121 SPSPALPSTNDYGPSPDFSVFOQSSSTAKSATWTYSTELKLYCOIAKTCIQIAKWTPP	180
QY	PGCAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDP	240
Db	181 PGCAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDP	240
QY	PGCAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDP	240
Db	181 PGCAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDP	240
QY	ITGRQSVLVPEPRPOVGETFTYVLKPNFQNSSCVCGNMRRLIILVLETRFDGVLGRRC	300
Db	241 ITGRQSVLVPEPRPOVGETFTYVLKPNFQNSSCVCGNMRRLIILVLETRFDGVLGRRC	300
QY	ITGRQSVLVPEPRPOVGETFTYVLKPNFQNSSCVCGNMRRLIILVLETRFDGVLGRRC	300
Db	241 ITGRQSVLVPEPRPOVGETFTYVLKPNFQNSSCVCGNMRRLIILVLETRFDGVLGRRC	300
QY	FEARICACGGRDKADEOSIRKQOVSdstKNDGGRKPFRONTGIIQWTSIARRSPDDE	360
Db	301 FEARICACGGRDKADEOSIRKQOVSdstKNDGGRKPFRONTGIIQWTSIARRSPDDE	360
QY	FEARICACGGRDKADEOSIRKQOVSdstKNDGGRKPFRONTGIIQWTSIARRSPDDE	360
Db	301 FEARICACGGRDKADEOSIRKQOVSdstKNDGGRKPFRONTGIIQWTSIARRSPDDE	360
QY	LFLYLPARGRETYEMLKIKESLELMQYLPQHTIEFYRQOOOQOHLLQKOTSIQSPSSY	420
Db	361 LFLYLPARGRETYEMLKIKESLELMQYLPQHTIEFYRQOOOQOHLLQKOTSIQSPSSY	420
QY	LFLYLPARGRETYEMLKIKESLELMQYLPQHTIEFYRQOOOQOHLLQKOTSIQSPSSY	420
Db	361 LFLYLPARGRETYEMLKIKESLELMQYLPQHTIEFYRQOOOQOHLLQKOTSIQSPSSY	420
QY	GNSSPPLNKMSNNKRLPSVSQLINQOORNALPTPIRGMKANIRPMGTHHPYAGDMNGL	480
Db	421 GNSSPPLNKMSNNKRLPSVSQLINQOORNALPTPIRGMKANIRPMGTHHPYAGDMNGL	480
QY	GNSSPPLNKMSNNKRLPSVSQLINQOORNALPTPIRGMKANIRPMGTHHPYAGDMNGL	480
Db	421 GNSSPPLNKMSNNKRLPSVSQLINQOORNALPTPIRGMKANIRPMGTHHPYAGDMNGL	480
QY	SPTQALPPLMSFSTSHCTPPPYPTDCSIVARIWOV	516

Db 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIWQV 516

RESULT 2

ID AAB11363 standard; Protein; 516 AA.

AC AAB1.1363,

DT 21-FEB-2001 (first entry)

Human p63 protein isoform #7.

KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;

How do you
XX

XX
PN W0300061613-A3

19-OCT-2000
XX
XX
PD03-APP-2000: 2000WO-TSC08885
XX
DE

XX 02-APP-1000. 9975-0285479
 PR

PR	17-DEC-1999;	99US-0466396.
PR	30-DEC-1999:	99US-0476496.

PR 10-JAN-2000; 2000US-04808884.
PR 22-FEB-2000; 2000US-05103376

XX
PA (CORT-) CORTXA CORP.

Wanda T. Egan L.

XX WP.T. 2000-628399/50
DB

DR N-PSDB; AAC66033.
XX

PT isolated polypeptide protein is used for

PI In a patient -
XX

Ps
XX
disclosure; page 23

comprising an immun

used in compositions

CC especially lung cancer
CC can be used to monitor

different time points

CC are created with P2
CC cells expressing P2

XX development of cancer

sequence 210 AA,

Best Local Similarity
Query match

MACLEOD, J. W., CONSULTANT

[illegible]

QY 181 POGAVIRAMPYKKAHEVTEYKRCPNHLSREFNEGQIAPPSHLIRVGENSHAQYVEDP 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 181 POGAVIRAMPYKKAHEVTEYKRCPNHLSREFNEGQIAPPSHLIRVGENSHAQYVEDP 240
 QY 241 ITGRQSVLVYPPPOVGTETFTVLVNFMCNSSCVGGMNRPILLIIVTLETTRDGOVLGRRC 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 241 ITGRQSVLVYPPPOVGTETFTVLVNFMCNSSCVGGMNRPILLIIVTLETTRDGOVLGRRC 300
 QY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTTRPPRONTHTGIOMTSIKRRSPDDE 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTTRPPRONTHTGIOMTSIKRRSPDDE 360
 QY 361 LLYLVPRGRETEYEMLKIKESLELMQYLPQHTIETRYROOQOOHOLQKOTSIOSSPY 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 361 LLYLVPRGRETEYEMLKIKESLELMQYLPQHTIETRYROOQOOHOLQKOTSIOSSPY 420
 QY 421 GNSSPPLNKMNSMNLKPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPAGDMNGL 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 421 GNSSPPLNKMNSMNLKPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPAGDMNGL 480
 QY 481 SPTQALPPLSMPSSTHCTPPPPYPTDCSIVRIMQY 516
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 481 SPTQALPPLSMPSSTHCTPPPPYPTDCSIVRIMQY 516

RESULT 3

ABG95141
 ID ABG95141 standard; protein; 516 AA.

XX ABG95141;

DT 04-DEC-2002 (first entry)

XX Human oncogene p63 isoform TA p63 beta.

XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.

XX Homo sapiens.

XX WO200269900-A2.

XX 12-SEP-2002.

XX 01-MAR-2002; 2002MO-US06518.

XX 01-MAR-2001; 2001US-272751P.

XX (CONF-) CONFORMA THERAPEUTICS CORP.

XX Fritz LC, Burrows FU;

XX WPI; 2002-698710/75.

XX N-PSDB; ABS73333.

PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90

PT -

XX Disclosure; Page 349-351; 389pp; English.

XX The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant

CC protein or cellular protein isoforms (II) dependent on heat shock
 CC protein (HSP)-90, or selectively treating cells expressing (II)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.
 XX

Sequence 516 AA:

Query Match 100.0%; Score 2751; DB 23; Length 516;

Best Local Similarity 100.0%; Pred. No. 2, 2e-226;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNEFLSPVEYQHIMDFLEQICVQPIDLNFVDEPSEDGATNKIEISMDCIHQ 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 MSOSTQTNEFLSPVEYQHIMDFLEQICVQPIDLNFVDEPSEDGATNKIEISMDCIHQ 60
 QY 61 DSDLDSPMWPQYTNIGLNSMDQIQONGSSSTSPYTDNAONSVPAPSSYFDAL 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 DSDLDSPMWPQYTNIGLNSMDQIQONGSSSTSPYTDNAONSVPAPSSYFDAL 120
 QY 121 SPSPAIPTNDYGPSPFVSFOQSSSTAKATWTYSTELKLYCQIAKCPQIQIKWTP 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 SPSPAIPTNDYGPSPFVSFOQSSSTAKATWTYSTELKLYCQIAKCPQIQIKWTP 180
 QY 181 POGAVIRAMPYKKAHEVTEYKRCPNHLSREFNEGQIAPPSHLIRVGENSHAQYVEDP 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 181 POGAVIRAMPYKKAHEVTEYKRCPNHLSREFNEGQIAPPSHLIRVGENSHAQYVEDP 240
 QY 241 ITGRQSVLVYPPPOVGTETFTVLVNFMCNSSCVGGMNRPILLIIVTLETTRDGOVLGRRC 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 241 ITGRQSVLVYPPPOVGTETFTVLVNFMCNSSCVGGMNRPILLIIVTLETTRDGOVLGRRC 300
 QY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTTRPPRONTHTGIOMTSIKRRSPDDE 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTTRPPRONTHTGIOMTSIKRRSPDDE 360
 QY 361 LLYLVPRGRETEYEMLKIKESLELMQYLPQHTIETRYROOQOOHOLQKOTSIOSSPY 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 361 LLYLVPRGRETEYEMLKIKESLELMQYLPQHTIETRYROOQOOHOLQKOTSIOSSPY 420
 QY 421 GNSSPPLNKMNSMNLKPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPAGDMNGL 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 421 GNSSPPLNKMNSMNLKPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPAGDMNGL 480
 QY 481 SPTQALPPLSMPSSTHCTPPPPYPTDCSIVRIMQY 516
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 481 SPTQALPPLSMPSSTHCTPPPPYPTDCSIVRIMQY 516

RESULT 4

ABP61915
 ID ABP61915 standard; protein; 516 AA.

XX ABP61915;

XX 07-OCT-2002 (first entry)

DE Human lung cancer associated protein sequence SEQ ID NO:344.

XX Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.

XX Homo sapiens.

```

XX  WO200247534-A2.
PN  |||
XX  20-JUN-2002.
PD  |||
XX  30-NOV-2001; 2001WO-US47576.
XX  |||
XX  12-DEC-2000; 2000US-0735705.
XX  |||
PR  07-MAY-2001; 2001US-0850716.
PR  28-JUN-2001; 2001US-0897778.
XX  |||
PA  (CORI-) CORIXA CORP.
PI  Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI  McNeill PD, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI  Carter D, Watanabe Y, Peckham DW, Cal F, Foy TM;
XX  |||
DR  WPI: 2002-583465/62.
XX  N-PSDB; ABQ92438.
XX  |||
PT  Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT  by the polynucleotides, useful in pharmaceutical compositions such as
PT  vaccines and as markers to indicate the presence of lung cancer -
XX  |||
XX  Example 2; Page 334-335; 381pp; English.
XX  |||
CC  The present invention describes isolated human lung carcinoma
CC  polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC  activity, and can be used in gene therapy and in vaccines. Compositions
CC  comprising (I) or (II) can be used for stimulating an immune response in
CC  a patient and for treating lung cancer in a patient. Oligonucleotides of
CC  (I) can be used for detecting the presence of a cancer in a patient, by
CC  obtaining a biological sample from the patient, contacting the
CC  biological sample with the oligonucleotide, detecting in the sample, an
CC  amount of polynucleotide that hybridises to the oligonucleotide and
CC  comparing the amount of polynucleotide that hybridises to the
CC  oligonucleotide to a predetermined cut-off value, and determining the
CC  presence of a cancer in the patient. (I) and (II) are useful in
CC  pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
CC  indicate the presence or absence of a cancer such as lung cancer.
CC  ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used
CC  in the exemplification of the present invention.
XX  |||
XX  Sequence 516 AA;
XX  |||
Query Match 100.0%; Score 2751; DB 23; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.2e-226; Indels 0; Gaps 0;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 MSOSTQTNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDCI RMQ 60
    |||
DB  1 MSOSTQTNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDCI RMQ 60
    |||
QY  61 DSDLSDPWMPQYTNMGLINSMDQOIQNGSSSTSPYNDHQAONSTAPSPYAPQSTPDAL 120
    |||
DB  61 DSDLSDPWMPQYTNMGLINSMDQOIQNGSSSTSPYNDHQAONSTAPSPYAPQSTPDAL 120
    |||
QY  121 SPSPAIRSNNDYDPGPHSFDVSFOOSTAKSATWTYSTELKLYCOIAKTCIOLKVMPP 180
    |||
DB  121 SPSPAIRSNNDYDPGPHSFDVSFOOSTAKSATWTYSTELKLYCOIAKTCIOLKVMPP 180
    |||
QY  121 SPSPAIRSNNDYDPGPHSFDVSFOOSTAKSATWTYSTELKLYCOIAKTCIOLKVMPP 180
    |||
DB  121 SPSPAIRSNNDYDPGPHSFDVSFOOSTAKSATWTYSTELKLYCOIAKTCIOLKVMPP 180
    |||
QY  181 POGAVIRAMPYKKAHEVTEYVKRCPNHELSTREFNEGOIAPPSHLIRVGNASHQAYEDP 240
    |||
DB  181 POGAVIRAMPYKKAHEVTEYVKRCPNHELSTREFNEGOIAPPSHLIRVGNASHQAYEDP 240
    |||
QY  181 POGAVIRAMPYKKAHEVTEYVKRCPNHELSTREFNEGOIAPPSHLIRVGNASHQAYEDP 240
    |||
DB  181 POGAVIRAMPYKKAHEVTEYVKRCPNHELSTREFNEGOIAPPSHLIRVGNASHQAYEDP 240
    |||
QY  241 ITGROSQVLYVEPPQVTEFTTYLYNFMCNSSCYGKNNRRPILITVLETRDGOVLRRC 300
    |||
DB  241 ITGROSQVLYVEPPQVTEFTTYLYNFMCNSSCYGKNNRRPILITVLETRDGOVLRRC 300
    |||
QY  241 ITGROSQVLYVEPPQVTEFTTYLYNFMCNSSCYGKNNRRPILITVLETRDGOVLRRC 300
    |||
DB  241 ITGROSQVLYVEPPQVTEFTTYLYNFMCNSSCYGKNNRRPILITVLETRDGOVLRRC 300
    |||
QY  301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPRNTHGIOMTSIKRRSPDDE 360
    |||
DB  301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPRNTHGIOMTSIKRRSPDDE 360
    |||

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QY  361 LLYLPVGRRETYEMLNLIKESLELMQYLPOHTIEFYRQOQOQHOLKOTSIQSPSSY 420
    |||
DB  361 LLYLPVGRRETYEMLNLIKESLELMQYLPOHTIEFYRQOQOQHOLKOTSIQSPSSY 420
    |||
QY  421 GNSSPPLKNKNSMKNLPSVSOLINPOORNALPTPTIDGKANTPMAGTHMPAGDMNGL 480
    |||
DB  421 GNSSPPLKNKNSMKNLPSVSOLINPOORNALPTPTIDGKANTPMAGTHMPAGDMNGL 480
    |||
QY  481 SPTQALPPPLSPSTSHCTPPPEPTCCSIYRIQOV 516
    |||
DB  481 SPTQALPPPLSPSTSHCTPPPEPTCCSIYRIQOV 516
    |||

RESULT 5
ABB74995
ID  ABB74995 standard; Protein: 516 AA.
XX  |||
XX  ABB74995;
XX  |||
DT  01-MAY-2002 (first entry)
XX  |||
DE  Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:344.
XX  |||
KW  Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW  immune response.
XX  |||
XX  Homo sapiens.
XX  |||
XX  WO200200174-A2.
XX  |||
XX  03-JAN-2002.
XX  |||
XX  28-JUN-2001; 2001WO-US21065.
XX  |||
XX  28-JUN-2000; 2000US-0606421.
XX  |||
PR  02-AUG-2000; 2000US-0630940.
XX  |||
PR  21-AUG-2000; 2000US-0643597.
XX  |||
PR  15-SEP-2000; 2000US-0662786.
XX  |||
PR  09-OCT-2000; 2000US-0685696.
XX  |||
PR  12-DEC-2000; 2000US-0735705.
XX  |||
PR  07-MAY-2001; 2001US-0850716.
XX  |||
XX  (CORI-) CORIXA CORP.
XX  |||
XX  Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
XX  McNeill PD, Retter MW, Marnerakis M, Fanger GR;
XX  Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX  |||
DR  WPI: 2002-090513/12.
XX  N-PSDB; ABL49252.
XX  |||
PT  Polynucleotides encoding lung tumor polypeptides, useful for treating
PT  lung cancer or stimulating an immune response -
XX  |||
XX  Example 2; Page 327-328; 374pp; English.
XX  |||
CC  The present invention describes human lung tumour proteins. Human lung
CC  tumour proteins and polynucleotides have cytostatic and immunostimulant
CC  activities, and can be used in vaccine production. Compositions
CC  comprising the lung tumour proteins, polynucleotides, antibodies,
CC  fusion proteins, T cell populations, or antigen presenting cells that
CC  express the lung tumour proteins are useful for treating lung cancer or
CC  stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
CC  ABB75070 represent sequences used in the exemplification of the present
CC  invention.
XX  |||
XX  Sequence 516 AA;
XX  |||
Query Match 100.0%; Score 2751; DB 23; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.2e-226; Indels 0; Gaps 0;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 MSOSTQTNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDCI RMQ 60
    |||

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Db      1 MSQSTQNEFLSPVEFOHIMDFLEQPICSVQPIDLNFDEPSEDAATKIEISMCICIMQ 60
Qy      61 DSDLSDPMMPOYTINGLINSMDOQIQNGSSSTSPYNTDHAQNSVAPSPYAPQSSSTFDAL 120
Db      61 DSDLSDPMMPOYTINGLINSMDOQIQNGSSSTSPYNTDHAQNSVAPSPYAPQSSSTFDAL 120
Qy      121 SPSPAIPSNTDYPGPHSFDVSFQOQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Db      121 SPSPAIPSNTDYPGPHSFDVSFQOQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Qy      181 POGAVIRAMPYKKAEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVDP 240
Db      181 POGAVIRAMPYKKAEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVDP 240
Qy      241 ITGRQSVLYPEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILIVTLETRDGOVLAGRRC 300
Db      241 ITGRQSVLYPEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILIVTLETRDGOVLAGRRC 300
Qy      301 FEARICACPGDRKADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIRKRRSPDE 360
Db      301 FEARICACPGDRKADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIRKRRSPDE 360
Qy      361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSISPS 420
Db      361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSISPS 420
Qy      421 GNSSPPLKNNMKNKLPSVSOLINPQORNALPTTIPGMCANIPMGTHMPMAGDMNGL 480
Db      421 GNSSPPLKNNMKNKLPSVSOLINPQORNALPTTIPGMCANIPMGTHMPMAGDMNGL 480
Qy      481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIYRIMOV 516
Db      481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIYRIMOV 516

RESULT 6
ABG95135
ID   ABG95135 standard; Protein: 516 AA.
XX
AC   ABG95135;
XX
DT   04-DEC-2002 (first entry)
XX
DE   Human oncogene p51 isoform Tap63beta.
XX
KW   Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW   proliferative disease; cellular protein isoform; heat shock protein 90;
KW   HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW   T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW   acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW   acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW   papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW   rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
OS   Homo sapiens.
XX
PN   WO200269900-A2.
XX
PD   12-SEP-2002.
XX
PF   01-MAR-2002; 2002WO-US06518.
XX
PR   01-MAR-2001; 2001US-272751P.
XX
PA   (CONF-) CONFORMA THERAPEUTICS CORP.
XX
PI   Filtz LC, Burrows FJ;
XX
DR   WPI: 2002-698710/75.
XX
PT   Treating genetically-defined disease associated with chromosomal
XX   aberrations yielding oncogenic fusion proteins, e.g. cell proliferative

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PT      diseases, involves administering an inhibitor of heat shock protein 90
PT
PS      Disclosure: Page 336-338; 389pp; English.
XX
XX      The invention describes a method of treating genetically-defined disease
XX      associated with chromosomal aberrations yielding oncogenic fusion
XX      proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX      cell population, treating proliferative diseases associated with mutant
XX      protein or cellular protein isoforms (II) dependent on heat shock
XX      protein (HSP)-90, or selectively treating cells expressing (II)
XX      involving administering HSP90-inhibitor. The method is useful for
XX      treating genetically-defined disease with chromosomal aberration yielding
XX      oncogenic fusion protein, treating cancerous cells containing fusion
XX      protein in heterogeneous cell population, treating proliferative disease
XX      (e.g. Rheumatoid arthritis or cancer) associated with mutant protein or
XX      cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX      p53), or selectively treating cells expressing mutant protein or cellular
XX      protein isoform in a patient heterozygous for (II). The method is useful
XX      for treating a disease e.g. haematopoietic disorder such as T or B cell
XX      lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
XX      or a disease characterised by a solid tumour such as papillary thyroid
XX      carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX      synovial sarcoma. The method is also useful for treating viral
XX      infections. This is the amino acid sequence of a human oncogenic protein.
XX
SQ      Sequence 516 AA:
XX
Query Match 99.7%; Score 2744; DB 23; Length 516;
Best Local Similarity 99.8%; Pred. No. 8.9e-226;
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1 MSQSTQNEFLSPVEFOHIMDFLEQPICSVQPIDLNFDEPSEDAATKIEISMCICIMQ 60
Db      1 MSQSTQNEFLSPVEFOHIMDFLEQPICSVQPIDLNFDEPSEDAATKIEISMCICIMQ 60
Qy      61 DSDLSDPMMPOYTINGLINSMDOQIQNGSSSTSPYNTDHAQNSVAPSPYAPQSSSTFDAL 120
Db      61 DSDLSDPMMPOYTINGLINSMDOQIQNGSSSTSPYNTDHAQNSVAPSPYAPQSSSTFDAL 120
Qy      121 SPSPAIPSNTDYPGPHSFDVSFQOQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Db      121 SPSPAIPSNTDYPGPHSFDVSFQOQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Qy      181 POGAVIRAMPYKKAEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVDP 240
Db      181 POGAVIRAMPYKKAEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVDP 240
Qy      241 ITGRQSVLYPEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILIVTLETRDGOVLAGRRC 300
Db      241 ITGRQSVLYPEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILIVTLETRDGOVLAGRRC 300
Qy      301 FEARICACPGDRKADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIRKRRSPDE 360
Db      301 FEARICACPGDRKADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIRKRRSPDE 360
Qy      361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSISPS 420
Db      361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSISPS 420
Qy      421 GNSSPPLKNNMKNKLPSVSOLINPQORNALPTTIPGMCANIPMGTHMPMAGDMNGL 480
Db      421 GNSSPPLKNNMKNKLPSVSOLINPQORNALPTTIPGMCANIPMGTHMPMAGDMNGL 480
Qy      481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIYRIMOV 516
Db      481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIYRIMOV 516

RESULT 7
AAV45247
ID   AAV45247 standard; Protein: 641 AA.
XX

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AC	AAV45247;
XX	
DT	07-JAN-2000 (first entry)
XX	
DE	Human p51 protein B.
KW	Human: p51; p53 related gene; cell proliferation; regulation; cancer; tumour suppression; diagnosis.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Domain .1..59.
FT	/label= transactivation_domain
FT	Domain 142..321
FT	/label= DNA_binding_domain
FT	Domain 353..397
FT	/label= oligomerisation_domain
XX	
PN	WO950412-A1.
PD	
PD	07-OCT-1999.
XX	
PE	24-MAR-1999; 99WO-JP01512.
XX	
PR	27-MAR-1998; 98JP-0100467.
XX	
PA	(SAKA) OTSUKA PHARM CO LTD.
PA	(IKAW/) IKAWA Y.
XX	
PI	Ikawa Y, Ikawa S, Obinata M;
XX	
DR	WPI; 1999-591318/50.
DR	N-PSDB; AAZ25771.
XX	
PT	New p53 related human gene p51, useful for diagnosis, investigation and treatment of cancers and screening for potential cell proliferation and agents -
PT	
XX	
Example 1:	Page 152-154; 163pp; Japanese.
XX	
CC	The present sequence represents a human p51 protein, which is related to
CC	p53 and has cell proliferation regulation and tumour suppression
CC	activity. The p51 gene can be used in the investigation, diagnosis and
CC	treatment of diseases such as cancer, with which the p53 family cell
CC	proliferation regulation is associated. The p51 protein may be used for
CC	screening potential agonists and antagonists of its regulatory function,
CC	for use as drugs,
XX	
SO	Sequence 641 AA;
Query Match	98.9%; Score 2722; DB 20; Length 641;
Best Local Similarity	100.0%; Pred. No. 9.2e-224;
Matches 511; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MSOSTQTNEFISPEVFQHIMDFLEQPITCSVPIDLNFVEDSESGATNKIEISMDCIRMQ 60
DB	1 MSOSTQTNEFISPEVFQHIMDFLEQPITCSVPIDLNFVEDSESGATNKIEISMDCIRMQ 60
QY	.61 DSDLSDPMPQPYTNGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPAOPSSFDAL 120
DB	.61 DSDLSDPMPQPYTNGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPAOPSSFDAL 120
QY	121 SPSPAISSNDYPGPHSEFVSFOQSSTAKSATWTYSTELKILYCOIAKTCPFIQIKWMTPP 180
DB	121 SPSPAISSNDYPGPHSEFVSFOQSSTAKSATWTYSTELKILYCOIAKTCPFIQIKWMTPP 180
QY	181 POGAVIRAMPYYKKAHEVTYVKRCPNHSELREFNEG IAPPSHLIRVEGNSHAQYEDP 240
DB	181 POGAVIRAMPYYKKAHEVTYVKRCPNHSELREFNEG IAPPSHLIRVEGNSHAQYEDP 240
QY	241 ITGGSVLVPERPPQVGTEFFTYLYNFCNCS CYGGMRRRIILLIVLETGDGYLGARC 300
DB	241 ITGGSVLVPERPPQVGTEFFTYLYNFCNCS CYGGMRRRIILLIVLETGDGYLGARC 300

Db	241	ITGRQSVLVPYPPPOVGIEFTTVLYLNFMGNSSCVGGMNRPLLITVLTETRGQVLYGRRC	300
Qy	301	FEARICACPGDRKRAKDEDSIRKQOVSdstSKNDGTRKRPpRONTHTGIOMTSIKRRSPDDE	360
Db	301	FEARICACPGDRKRAKDEDSIRKQOVSdstKNGDGTGRPRpRONTHTGIOMTSIKRRSPDDE	360
Qy	361	LLYLEVRGRETYEMLKIKESLELMQYLFQHTIETRYRQOOOQHLLQKTSIOSpSSy	420
Db	361	LLYLEVRGRETYEMLKIKESLELMQYLFQHTIETRYRQOOOQHLLQKTSIOSpSSy	420
Qy	421	GNSSPPLKMNMSMNKLPSVSOLINPOORNALPPTTIPDGMGANIPMGTHMPAGGMNGL	480
Db	421	GNSSPPLKMNMSMNKLPSVSQQLINPOORNALPPTTIPDGMGANIPMGTHMPAGGMNGL	480
Qy	481	SPTQALPPPLSMPTSTSHCTPPPPPTDGSIV	511
Db	481	SPTQALPPPLSMPTSTSHCTPPPPPTDGSIV	511
RESULT 8			
AAV05953			
ID	AAV05953	standard; Protein; 641 AA.	
AC	AAV05953;		
DT	16-AUG-1999	(first entry)	
DE	Human cell regulatory protein p63, isoform hUTAP63 alpha.		
KM	Cell regulatory protein; p63; hUTAP63 alpha; TAP63 alpha; human;		
KW	cancer; tumour suppressor; cell cycle control; apoptosis;		
KW	cell proliferation; cell differentiation; therapy.		
OS	Homo sapiens.		
PN	WO9919357-A2.		
PD	22-APR-1999.		
PF	02-OCT-1998;	98MO-US21992.	
PR	29-MAY-1998;	98US-0087216.	
PR	15-OCT-1997;	97US-0062076.	
PA	(HARD) HARVARD COLLEGE.		
PI	McKeon F, Yang A;		
DR	WPI: 1999-277595/23.		
DR	N-PSDB; AAX58572.		
PT	New isolated p63 cell regulatory protein for, e.g. treatment of		
PT	tumours		
PS	Claim 23; Fig 9; 161pp; English.		
XX	The present invention concerns the discovery of a new family of		
CC	cell regulatory proteins (CRPs) termed the p63 family of proteins,		
CC	which demonstrate certain sequence identity to known tumour		
CC	suppressor proteins p53 and p73. It has been observed that the		
CC	intron-exon organisation is conserved between p73 and p53, and from		
CC	known exon and intron sizes for these 2 genes, it was possible to		
CC	identify new members of this gene family using a PCR-based strategy		
CC	of amplifying 2 exons in a conserved domain and their intervening		
CC	intron. The human p53 gene was localised to chromosomal position		
CC	3q27-29. At least 6 different isootypes exist. Splice variants		
CC	differing at the C-terminus have been designated as alpha, beta and		
CC	gamma forms, while p63 members differing in the N-terminus are		
CC	designated as delta and TA forms, where the delta form lacks the		
CC	transactivation domain. The present sequence represents human		
CC	p63 isootype TAP63 alpha. p63 was detected in a variety of		
CC	human and mouse tissue. It demonstrates remarkably divergent		
CC	activities, such as the ability to transactivate p53 reporter genes		

CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. Delta isotopes of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AA05953-64), polynucleotides (see
 CC AA8572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.

CC Sequence 641 AA:

Query Match 98.9%; Score 2722; DB 20; Length 641;
 Best Local Similarity 100.0%; Pred. No. 9.2e-224;
 Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNFELSPEVFOHIMDFLEQPCISVQPIDLNFVDESEDAATNKIEISMDCIRMQ 60
 DB 1 MSOSTQTNFELSPEVFOHIMDFLEQPCISVQPIDLNFVDESEDAATNKIEISMDCIRMQ 60
 QY 61 DSDLSDPMPQYNTNLGLNSMDQIQNCSSTSPYNTDHAQNSVTAAPSPYAPSSFPDAL 120
 DB 61 DSDLSDPMPQYNTNLGLNSMDQIQNCSSTSPYNTDHAQNSVTAAPSPYAPSSFPDAL 120
 QY 121 SPSPAIPNTDYPGHSFSDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 DB 121 SPSPAIPNTDYPGHSFSDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
 DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
 QY 241 ITGRQSVLYPEPEPOVGTETFTVLYNFMCNSSCVGAMRRPILLITVLETRDGOVLGRRC 300
 DB 241 ITGRQSVLYPEPEPOVGTETFTVLYNFMCNSSCVGAMRRPILLITVLETRDGOVLGRRC 300
 QY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIOMTSIKKRRSPDE 360
 DB 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIOMTSIKKRRSPDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYYRQOQOQHLLQKOTSIOSSPSY 420
 DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYYRQOQOQHLLQKOTSIOSSPSY 420
 QY 421 GNSSPPLKMSMKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
 DB 421 GNSSPPLKMSMKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
 QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
 DB 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511

RESULT 9

AA01358
 ID AAB1358 standard; Protein: 641 AA.

AC AAB1358;

DT 21-FEB-2001 (first entry)

DE Human p63 protein isoform #2.

XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 KW vaccine; detection.

OS Homo sapiens.

PN WO200061612-A2.

XX 19-OCT-2000.

XX 03-APR-2000; 2000WO-US08896.

PR 02-APR-1999; 99US-0285479.

PR 17-DEC-1999; 99US-0466396.

PR 30-DEC-1999; 99US-0476496.

PR 10-JAN-2000; 2000US-0480884.

PR 22-FEB-2000; 2000US-0510376.

PA (CORI-) CORIXA CORP.

PI Wang T, Fan L;

DR WPI: 2000-628399/60.

DR N-PSDB: AAC66028.

PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
 protein is used for detecting and monitoring progression of lung cancer
 in a patient -

CC This invention describes a novel isolated polypeptide (I) which
 comprising an immunogenic portion of a lung tumor protein or variant (P2)
 which have cytostatic activity. The polypeptides and polynucleotides are
 used in compositions and vaccines to inhibit the development of cancer.

CC especially lung cancer, in a patient. Methods described in the invention
 can be used to monitor the progression of a cancer by carrying out the
 detection at subsequent time points and comparing the results from the

CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient
 are treated with P2, polynucleotides encoding P2 or antigen presenting
 cells expressing P2, and then administered to the patient to inhibit

CC development of cancer.

XX Sequence 641 AA:

Query Match 98.9%; Score 2722; DB 21; Length 641;
 Best Local Similarity 100.0%; Pred. No. 9.2e-224;
 Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNFELSPEVFOHIMDFLEQPCISVQPIDLNFVDESEDAATNKIEISMDCIRMQ 60
 DB 1 MSOSTQTNFELSPEVFOHIMDFLEQPCISVQPIDLNFVDESEDAATNKIEISMDCIRMQ 60
 QY 61 DSDLSDPMPQYNTNLGLNSMDQIQNCSSTSPYNTDHAQNSVTAAPSPYAPSSFPDAL 120
 DB 61 DSDLSDPMPQYNTNLGLNSMDQIQNCSSTSPYNTDHAQNSVTAAPSPYAPSSFPDAL 120
 QY 121 SPSPAIPNTDYPGHSFSDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 DB 121 SPSPAIPNTDYPGHSFSDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
 DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
 QY 241 ITGRQSVLYPEPEPOVGTETFTVLYNFMCNSSCVGAMRRPILLITVLETRDGOVLGRRC 300
 DB 241 ITGRQSVLYPEPEPOVGTETFTVLYNFMCNSSCVGAMRRPILLITVLETRDGOVLGRRC 300
 QY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIOMTSIKKRRSPDE 360
 DB 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIOMTSIKKRRSPDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYYRQOQOQHLLQKOTSIOSSPSY 420
 DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYYRQOQOQHLLQKOTSIOSSPSY 420
 QY 421 GNSSPPLKMSMKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
 DB 421 GNSSPPLKMSMKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
 QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
 DB 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511

[illegible]

Db	161	POGAVIRAMPYKKAHEHTVEVKKRCNMHLSNEFNQOLAPSHLIRVGNNAQYEDP	240
Oy	241	ITGRQSVLVPPEPPOVGETTEFTVLVYEMCNSSCVGGMNRPILIVTLETRDQVIGRR	300
Db	241	ITGRQSVLVPPEPPOVGETTEFTVLVYEMCNSSCVGGMNRPILIVTLETRDQVIGRR	300
Oy	301	FEARICACPGRRRKADDESIIRKQVSDSKNDGTRPRPROMHGIOMTSIKRRSPDDE	360
Db	301	FEARICACPGRRRKADDESIIRKQVSDSKNDGTRPRPROMHGIOMTSIKRRSPDDE	360
Oy	361	LLYLFVRGREYTEMILKIKESIELMOYLPOHITETFRQOOQOOHQHILQKQTSIQSPSSY	420
Db	361	LLYLFVRGREYTEMILKIKESIELMOYLPOHITETFRQOOQOOHQHILQKQTSIQSPSSY	420
Oy	421	GNSSPPLKMKNSMKNLPSVSQLINPOQRNALPTPTIPDGMGANIPMGTHMPMAGDMNGI	480
Db	421	GNSSPPLKMKNSMKNLPSVSQLINPOQRNALPTPTIPDGMGANIPMGTHMPMAGDMNGI	480
Oy	481	SPTQALPPPLSMPTSHCTHCPPTPTDGSIV	511
Db	481	SPTQALPPPLSMPTSHCTHCPPTPTDGSIV	511
RESULT 11			
ABG95128			
ID	ABG95128	standard; Protein; 641 AA.	
AC	ABG95128;		
XX			
DT	04-DEC-2002	(first entry)	
XX			
DE	Human oncogene p5B.		
XX			
KW	Chromosome aberration; oncogenic fusion protein; cancer; oncogene;		
KW	proliferative disease; cellular protein isoform; heat shock protein 90;		
KW	HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;		
KW	T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;		
KW	acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;		
KW	acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;		
KW	papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;		
KW	rhabdomyosarcoma; synovial sarcoma; viral infection.		
XX			
OS	Homo sapiens.		
XX			
XX	WO200269900-A2.		
XX			
PD	12-SEP-2002.		
XX			
PE	01-MAR-2002; 2002WO-US06518.		
XX			
PR	01-MAR-2001; 2001US-272751P.		
XX			
PA	(CONF-) CONFORMA THERAPEUTICS CORP.		
XX			
PI	Fritz LC; Burrows FU;		
XX			
DR	WPI: 2002-698710/75.		
DR	N-PSDB; ABS73328.		
XX			
PT	Treating genetically-defined disease associated with chromosomal		
PT	aberrations yielding oncogenic fusion proteins, e.g. cell proliferative		
PT	diseases, involves administering an inhibitor of heat shock protein 90		
XX			
PS	Disclosure; Paeg 322-324; 389pp; English.		
XX			
CC	The invention describes a method of treating genetically-defined disease		
CC	associated with chromosomal aberrations yielding oncogenic fusion		
CC	proteins (I), treating cancerous cells containing (I) in a heterogeneous		
CC	cell population, treating proliferative diseases associated with mutant		
CC	protein or cellular protein isoforms (II) dependent on heat shock		
CC	protein (HSP)-90, or selectively treating cells expressing (II)		
CC	involving administering HSP90-inhibitor. The method is useful for		

treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cancer cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. hematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.

Sequence 641 AA:

Query Match 98.9%; Score 2722; DB 23; Length 641;

Best Local Similarity 100.0%; Pred. No. 9.2e-224;

Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSOSTQTNELSPVEFQIHMDLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
 1 MSOSTQTNELSPVEFQIHMDLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
 61 DSDLSDPMPQYTNIGLINSMDQOIONGSSSTPYNTDHAONSVTAPSPYAPSSSTFPAAL 120
 61 DSDLSDPMPQYTNIGLINSMDQOIONGSSSTPYNTDHAONSVTAPSPYAPSSSTFPAAL 120
 121 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKLYCOIACTCPQIQIKVMP 180
 121 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKLYCOIACTCPQIQIKVMP 180
 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVEDP 240
 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVEDP 240
 241 ITGROSVLVPEPPQVGTETFTVLYNFMCNSSCVGGMNRRPILLIVTLETBDRGQVLYGRRC 300
 241 ITGROSVLVPEPPQVGTETFTVLYNFMCNSSCVGGMNRRPILLIVTLETBDRGQVLYGRRC 300
 301 FEAKICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGSIQMTSIRKRRSPDE 360
 301 FEAKICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGSIQMTSIRKRRSPDE 360
 361 LLYLVPRGRETENMLTKESLELMQYLPQHTIETRYROOQOQHLLQOKTOSIOSPSY 420
 361 LLYLVPRGRETENMLTKESLELMQYLPQHTIETRYROOQOQHLLQOKTOSIOSPSY 420
 421 GNSSPPLKNKNSMKLPSVQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
 421 GNSSPPLKNKNSMKLPSVQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
 481 SPTQALPPPLSMSTSHCTPPPPYPTDCSIV 511
 481 SPTQALPPPLSMSTSHCTPPPPYPTDCSIV 511

RESULT 12

ABG95136 standard; Protein; 641 AA.

ABG95136;

04-DEC-2002 (first entry)

Human oncogene p51 isoform Tap63alpha.

Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; hematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;

papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.

Homo sapiens.

WO200269900-A2.

12-SEP-2002.

01-MAR-2002; 2002MO-US06518.

01-MAR-2001; 2001US-272751P.

(CONF-) CONFORMA THERAPEUTICS CORP.

Fritz LC, Burrows PJ;

WPL; 2002-698710/75.

Treating genetically-defined disease associated with chromosomal
 aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 diseases, involves administering an inhibitor of heat shock protein 90

Disclosure: Page 338-340; 389pp; English.

The invention describes a method of treating genetically-defined disease
 associated with chromosomal aberrations yielding oncogenic fusion
 proteins (I), treating cancerous cells containing (I) in a heterogeneous
 cell population, treating proliferative diseases associated with mutant
 protein or cellular protein isoforms (II) dependent on heat shock
 protein (HSP)-90, or selectively treating cells expressing (II)
 involving administering HSP90-inhibitor. The method is useful for
 treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cancer cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. hematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.

Sequence 641 AA:

Query Match 98.9%; Score 2722; DB 23; Length 641;

Best Local Similarity 100.0%; Pred. No. 9.2e-224;

Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSOSTQTNELSPVEFQIHMDLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
 1 MSOSTQTNELSPVEFQIHMDLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
 61 DSDLSDPMPQYTNIGLINSMDQOIONGSSSTPYNTDHAONSVTAPSPYAPSSSTFPAAL 120
 61 DSDLSDPMPQYTNIGLINSMDQOIONGSSSTPYNTDHAONSVTAPSPYAPSSSTFPAAL 120
 121 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKLYCOIACTCPQIQIKVMP 180
 121 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKLYCOIACTCPQIQIKVMP 180
 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVEDP 240
 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVEDP 240
 241 ITGROSVLVPEPPQVGTETFTVLYNFMCNSSCVGGMNRRPILLIVTLETBDRGQVLYGRRC 300
 241 ITGROSVLVPEPPQVGTETFTVLYNFMCNSSCVGGMNRRPILLIVTLETBDRGQVLYGRRC 300

QY 301 FEARICACPRDRKADSDSIRKQOVSSTNGDGTCKRPFQNTHGIMTISIKRRSPDDE 360
DB 301 FEARICACPRDRKADSDSIRKQOVSSTNGDGTCKRPFQNTHGIMTISIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSY 420
DB 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSY 420
QY 421 GNSSPPLNKNMKNKLPVSQSLNPOQRNALTPPTIPDGAGANIPMAGTHMPAGDMNGL 480
DB 421 GNSSPPLNKNMKNKLPVSQSLNPOQRNALTPPTIPDGAGANIPMAGTHMPAGDMNGL 480
QY 481 SPTQALPPLPLSMSTSHCTPPPPYPTDCSIV 511
DB 481 SPTQALPPLPLSMSTSHCTPPPPYPTDCSIV 511

RESULT 13
ABG95142
ID ABG95142 standard; Protein: 641 AA.
XX
AC ABG95142;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human oncogene p63 isoform TA p63 alpha.
XX
XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW Proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; Rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
XX Homo sapiens.
OS
XX
PN WO200269900-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-US06518.
XX
PR 01-MAR-2001; 2001US-272751P.
XX
PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX
PI Fritz LC, Burrows FJ;
XX
PI WPI; 2002-698710/75.
XX
PI N-PADB; ABS73334.
XX
DR
XX
PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases; involves administering an inhibitor of heat shock protein 90
XX
XX
XX Disclosure; Page 352-354; 3899p; English.
XX
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock
XX protein (HSP)-90, or selectively treating cells expressing (II)
XX involving administering HSP90-inhibitor. The method is useful for
XX treating genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular

CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
XX
SQ Sequence 641 AA;
XX
Query Match 98.9%; Score 2722; DB 23; Length 641;
Best Local Similarity 100.0%; Pred. No. 9.2e-224;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQSTQNEFLSPEVFOHIMDFLEQPCISVQPIDLNFVDEPSEGGATNKIEISMDCTRMQ 60
DB 1 MSQSTQNEFLSPEVFOHIMDFLEQPCISVQPIDLNFVDEPSEGGATNKIEISMDCTRMQ 60
QY 61 DSDLSDBPMWQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDAL 120
DB 61 DSDLSDBPMWQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDAL 120
QY 121 SPSPAIPSNNDYCGPHSEFVSPFOSSSTAKATMTYSTELKKLCOIAKTCPIQIKWTPP 180
DB 121 SPSPAIPSNNDYCGPHSEFVSPFOSSSTAKATMTYSTELKKLCOIAKTCPIQIKWTPP 180
QY 181 PGQAVIRAMPVYKKAHEVTEVYKCPNHELSREFNEGOIAPPSHLRVEGNSHAQYEDP 240
DB 181 PGQAVIRAMPVYKKAHEVTEVYKCPNHELSREFNEGOIAPPSHLRVEGNSHAQYEDP 240
QY 241 ITRGQSLVLYEPPQVTEETTYLYNFMCSVCVGGNNRRPILLYTLERDQVLCGRRC 300
DB 241 ITRGQSLVLYEPPQVTEETTYLYNFMCSVCVGGNNRRPILLYTLERDQVLCGRRC 300
QY 301 FEARICACPRDRKADSDSIRKQOVSSTNGDGTCKRPFQNTHGIMTISIKRRSPDDE 360
DB 301 FEARICACPRDRKADSDSIRKQOVSSTNGDGTCKRPFQNTHGIMTISIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSY 420
DB 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSY 420
QY 421 GNSSPPLNKNMKNKLPVSQSLNPOQRNALTPPTIPDGAGANIPMAGTHMPAGDMNGL 480
DB 421 GNSSPPLNKNMKNKLPVSQSLNPOQRNALTPPTIPDGAGANIPMAGTHMPAGDMNGL 480
QY 481 SPTQALPPLPLSMSTSHCTPPPPYPTDCSIV 511
DB 481 SPTQALPPLPLSMSTSHCTPPPPYPTDCSIV 511

RESULT 14
ABP61910
ID ABP61910 standard; Protein: 641 AA.
XX
AC ABP61910;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human lung cancer associated protein sequence SEQ ID NO:339.
XX
XX Human lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
KW Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
XX
XX Homo sapiens.
OS
XX
PN WO200247534-A2.
XX
PD 20-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-US47576.
XX
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.

PR 28-JUN-2001; 2001US-0897778.
 XX
 XX (CORI-) CORIXA CORP.
 PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
 PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
 PI Carter D, Matanabe Y, Peckham DW, Cai F, Foy TM;
 XX
 DR WPI: 2002-583465/62.
 DR N-PSDB: ABQ92433.
 XX
 PT Novel lung carcinoma polynucleotide sequences and polypeptides encoded
 PT by the polynucleotides, useful in pharmaceutical compositions such as
 PT vaccines and as markers to indicate the presence of lung cancer
 XX
 PS Example 2; Page 328-329; 381pp; English.
 XX
 CC The present invention describes isolated human lung carcinoma
 CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
 CC activity, and can be used in gene therapy and in vaccines. Compositions
 CC comprising (I) or (II) can be used for stimulating an immune response in
 CC a patient and for treating lung cancer in a patient. Oligonucleotides of
 CC (I) can be used for detecting the presence of a cancer in a patient, by
 CC obtaining a biological sample from the patient, contacting the
 CC biological sample with the oligonucleotide, detecting in the sample, an
 CC amount of polynucleotide that hybridizes to the oligonucleotide and
 CC comparing the amount of polynucleotide that hybridizes to the
 CC oligonucleotide to a predetermined cut-off value, and determining the
 CC presence of a cancer in the patient. (I) and (II) are useful in
 CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
 CC indicate the presence or absence of a cancer such as lung cancer.
 CC ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 641 AA:

Query Match 98.9%; Score 2722; DB 23; Length 641;
 Best Local Similarity 100.0%; Pred. No. 9.2e-224;
 Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNEFLSPYFOHIMDFLEOPICSVOPIDLFNVDSESGATKIEISMDCIRMQ 60
 DB 1 MSOSTQTNEFLSPYFOHIMDFLEOPICSVOPIDLFNVDSESGATKIEISMDCIRMQ 60
 QY 61 DSDLSDBPMWPQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPQPSSTFAL 120
 DB 61 DSDLSDBPMWPQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPQPSSTFAL 120
 QY 121 SPSPAIPTNDYPGHPSFDVGFQOSTAKSATWTYSTFLKLYCOIAKTCPIQIKVMP 180
 DB 121 SPSPAIPTNDYPGHPSFDVGFQOSTAKSATWTYSTFLKLYCOIAKTCPIQIKVMP 180
 QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRFGNSHAQYVBDP 240
 DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRFGNSHAQYVBDP 240
 QY 241 ITGROSIVLPEPPOVGEFTVLYNFMCNSSCVGMMRRPILITVLETEDGOVLGRRC 300
 DB 241 ITGROSIVLPEPPOVGEFTVLYNFMCNSSCVGMMRRPILITVLETEDGOVLGRRC 300
 QY 301 FEARICACPGDRKADEDSIRKQOVSDTKNGDGTAKRFRONTGIGQTSIKRRSPDE 360
 DB 301 FEARICACPGDRKADEDSIRKQOVSDTKNGDGTAKRFRONTGIGQTSIKRRSPDE 360
 QY 361 LLYLPVNGRETYEMLLIKESLELMOYLPOHTIETRYOQOQOHOHLQOKOTSIOSSPY 420
 DB 361 LLYLPVNGRETYEMLLIKESLELMOYLPOHTIETRYOQOQOHOHLQOKOTSIOSSPY 420
 QY 421 GNSSPPLNKMSMKRLSVSOLINPOQRNALPTTIPGCMANIPMMGTNHPMAGDMGL 480
 DB 421 GNSSPPLNKMSMKRLSVSOLINPOQRNALPTTIPGCMANIPMMGTNHPMAGDMGL 480
 QY 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511

DB 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511

RESULT 15
 ABB74990
 ID ABB74990 standard; Protein; 641 AA.
 XX
 AC ABB74990;
 XX
 DF 01-MAY-2002 (first entry)
 XX
 DE Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:339.
 XX
 KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 KW immune response.
 XX
 OS Homo sapiens.
 XX
 PN WO200200174-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 28-JUN-2001; 2001WO-US21065.
 XX
 PR 28-JUN-2000; 2000US-0606421.
 PR 02-AUG-2000; 2000US-0630940.
 PR 21-AUG-2000; 2000US-0643597.
 PR 15-SEP-2000; 2000US-0662786.
 PR 09-OCT-2000; 2000US-0685696.
 PR 12-DEC-2000; 2000US-0735705.
 PR 07-MAY-2001; 2001US-0850716.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
 PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
 PI Vedvick TS, Carter D, Matanabe Y, Peckham DW;
 XX
 DR WPI: 2002-090513/12.
 DR N-PSDB: ABL49247.
 XX
 PT Polynucleotides encoding lung tumor polypeptides, useful for treating
 PT lung cancer or stimulating an immune response -
 XX
 PS Example 2; Page 321-322; 374pp; English.

The present invention describes human lung tumor proteins. Human lung
 CC tumor proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumor proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumor proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL49959 to ABL49300 and ABL74946 to
 CC ABL75070 represent sequences used in the exemplification of the present
 CC invention.
 CC
 XX
 SQ Sequence 641 AA:

Query Match 98.9%; Score 2722; DB 23; Length 641;
 Best Local Similarity 100.0%; Pred. No. 9.2e-224;
 Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNEFLSPYFOHIMDFLEOPICSVOPIDLFNVDSESGATKIEISMDCIRMQ 60
 DB 1 MSOSTQTNEFLSPYFOHIMDFLEOPICSVOPIDLFNVDSESGATKIEISMDCIRMQ 60
 QY 61 DSDLSDBPMWPQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPQPSSTFAL 120
 DB 61 DSDLSDBPMWPQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPQPSSTFAL 120
 QY 121 SPSPAIPTNDYPGHPSFDVGFQOSTAKSATWTYSTFLKLYCOIAKTCPIQIKVMP 180
 DB 121 SPSPAIPTNDYPGHPSFDVGFQOSTAKSATWTYSTFLKLYCOIAKTCPIQIKVMP 180

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Db 121 SPSPAIPTNDYDEPHSFVDSFOOSTAKSATWTYTELKKLYCQIAKTCPIQIKVMTTP 180
QY 181 POGAVIRAMPVYKKAHEVTEVVKRCPNHEL.SREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
Db 181 POGAVIRAMPVYKKAHEVTEVVKRCPNHEL.SREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITGRQSVLVPEPPQVTEFTTYLVXNFMCNSSCVGMMRRPILIIYVLETRDGOVLGRRC 300
Db 241 ITGRQSVLVPEPPQVTEFTTYLVXNFMCNSSCVGMMRRPILIIYVLETRDGOVLGRRC 300
QY 301 FEARICACPGDRRADEDSIRKQOVSDSTKNGDSTKRPFONTHTGIOMTSIKRRSPDDE 360
Db 301 FEARICACPGDRRADEDSIRKQOVSDSTKNGDSTKRPFONTHTGIOMTSIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOOQOQHHLQKOTSIOSSPSY 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOOQOQHHLQKOTSIOSSPSY 420
QY 421 GNSSPPLNKMSMNKLPSVSQILNPOORNALPTTIPDGMGANIPMAGTHPMAGDMNGL 480
Db 421 GNSSPPLNKMSMNKLPSVSQILNPOORNALPTTIPDGMGANIPMAGTHPMAGDMNGL 480
QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
Db 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511

```

Search completed: August 7, 2003, 09:46:23
 Job time : 37.5862 secs

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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:54 ; Search time 14.2345 Seconds

(without alignments)
1533.769 Million cell updates/sec

Title: US-09-538-106-14

Perfect score: 2751

Sequence: 1 MSOSTQTNEFLSPFVQHIM.....HCTPPPPYPTDCSTIRIMQV 516

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA.*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2751	100.0	516	US-09-643-597-344	Sequence 344, App
2	2751	100.0	516	US-09-542-615A-344	Sequence 344, App
3	2751	100.0	516	US-09-606-421B-344	Sequence 344, App
4	2722	98.9	641	US-09-643-597-339	Sequence 339, App
5	2722	98.9	641	US-09-542-615A-339	Sequence 339, App
6	2722	98.9	641	US-09-606-421B-339	Sequence 339, App
7	2714	98.7	680	US-09-643-597-342	Sequence 342, App
8	2714	98.7	680	US-09-542-615A-342	Sequence 342, App
9	2714	98.7	680	US-09-606-421B-342	Sequence 342, App
10	2379	86.5	461	US-09-643-597-343	Sequence 343, App
11	2379	86.5	461	US-09-542-615A-343	Sequence 343, App
12	2379	86.5	461	US-09-606-421B-343	Sequence 343, App
13	2333	84.8	586	US-09-643-597-338	Sequence 338, App
14	2333	84.8	586	US-09-542-615A-338	Sequence 338, App
15	2333	84.8	586	US-09-606-421B-338	Sequence 338, App
16	2326	84.6	586	US-09-643-597-152	Sequence 152, App
17	2326	84.6	586	US-09-480-884A-152	Sequence 152, App
18	2326	84.6	586	US-09-542-615A-152	Sequence 152, App
19	2326	84.6	586	US-09-606-421B-152	Sequence 152, App
20	2222	80.8	426	US-09-606-421B-19	Sequence 19, App1
21	2185	79.4	448	US-09-643-597-340	Sequence 340, App
22	2185	79.4	448	US-09-542-615A-340	Sequence 340, App
23	2185	79.4	448	US-09-606-421B-340	Sequence 340, App
24	1801	65.5	356	US-09-643-597-341	Sequence 341, App
25	1801	65.5	356	US-09-277-196-2	Sequence 2, App11
26	1801	65.5	356	US-09-542-615A-341	Sequence 341, App
27	1801	65.5	356	US-09-606-421B-341	Sequence 341, App

28	1464.5	53.2	635	4	US-09-081-975-3	Sequence 3, App1
29	1328.5	48.3	420	4	US-09-277-196-20	Sequence 20, App1
30	738.5	27.6	381	4	US-09-257-580-2	Sequence 2, App1
31	723	26.3	393	1	US-08-047-041A-27	Sequence 27, App1
32	723	26.3	393	1	US-08-390-516C-8	Sequence 8, App1
33	723	26.3	393	1	US-08-390-515A-8	Sequence 8, App1
34	723	26.3	393	2	US-08-801-718-8	Sequence 8, App1
35	718	26.1	393	1	US-08-047-041A-25	Sequence 25, App1
36	718	26.1	393	1	US-08-047-041A-26	Sequence 26, App1
37	718	26.1	393	1	US-08-347-792-2	Sequence 2, App1
38	718	26.1	393	1	US-08-390-516C-6	Sequence 6, App1
39	718	26.1	393	1	US-08-390-516C-7	Sequence 7, App1
40	718	26.1	393	1	US-08-431-357-2	Sequence 2, App1
41	718	26.1	393	1	US-08-390-515A-6	Sequence 6, App1
42	718	26.1	393	1	US-08-390-515A-7	Sequence 7, App1
43	718	26.1	393	2	US-08-795-006A-32	Sequence 32, App1
44	718	26.1	393	2	US-08-697-221-2	Sequence 2, App1
45	718	26.1	393	2	US-08-801-718-6	Sequence 6, App1

ALIGNMENTS

RESULT 1	US-09-643-597-344	Application US/09643597
Sequence 344, App	Sequence 344, App	
Patent No. 6426072	Patent No. 6426072	
GENERAL INFORMATION	GENERAL INFORMATION	
APPLICANT: Wang, Tonglong	APPLICANT: Wang, Tonglong	
APPLICANT: Fan, Liqun	APPLICANT: Fan, Liqun	
APPLICANT: Kalos, Michael D.	APPLICANT: Kalos, Michael D.	
APPLICANT: Bangur, Chaitanya S.	APPLICANT: Bangur, Chaitanya S.	
APPLICANT: Hosken, Nancy	APPLICANT: Hosken, Nancy	
APPLICANT: Fanger, Gary R.	APPLICANT: Fanger, Gary R.	
APPLICANT: Li, Samuel X.	APPLICANT: Li, Samuel X.	
APPLICANT: Wang, Aijun	APPLICANT: Wang, Aijun	
APPLICANT: Skelky, Yashir A.W.	APPLICANT: Skelky, Yashir A.W.	
APPLICANT: Henderson, Robert A.	APPLICANT: Henderson, Robert A.	
APPLICANT: McNeill, Patricia D.	APPLICANT: McNeill, Patricia D.	
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY	
FILE REFERENCE: 210121.455C11	FILE REFERENCE: 210121.455C11	
CURRENT APPLICATION NUMBER: US/09/643,597	CURRENT APPLICATION NUMBER: US/09/643,597	
CURRENT FILING DATE: 2000-08-21	CURRENT FILING DATE: 2000-08-21	
NUMBER OF SEQ ID NOS: 369	NUMBER OF SEQ ID NOS: 369	
SOFTWARE: FastSeq for Windows Version 3.0	SOFTWARE: FastSeq for Windows Version 3.0	
SEQ ID NO 344	SEQ ID NO 344	
LENGTH: 516	LENGTH: 516	
TYPE: PRT	TYPE: PRT	
ORGANISM: Homo sapiens	ORGANISM: Homo sapiens	
US-09-643-597-344	US-09-643-597-344	
Query Match	100.0%; Score 2751; DB 4; Length 516;	
Best Local Similarity	100.0%; Pred. No. 4e-241;	
Matches 516; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MSOSTQTNEFLSPFVQHIMPTDEPDEGATNKIEISMOCIRMQ 60	Sequence 3, App1
DB	1 MSOSTQTNEFLSPFVQHIMPTDEPDEGATNKIEISMOCIRMQ 60	Sequence 27, App1
QY	61 DSDLDPMWPOVTNIGLNSMDQOIONGSSSPYNTDHAQNSVAPSPYAPSSFTDL 120	Sequence 8, App1
DB	61 DSDLDPMWPOVTNIGLNSMDQOIONGSSSPYNTDHAQNSVAPSPYAPSSFTDL 120	Sequence 25, App1
QY	121 SPSPAIPTNTDYPGPHSEFDVSFOQSSSTAKSATWTYSTELEKLYCQIAKCPQIKVMPP 180	Sequence 26, App1
DB	121 SPSPAIPTNTDYPGPHSEFDVSFOQSSSTAKSATWTYSTELEKLYCQIAKCPQIKVMPP 180	Sequence 6, App1
QY	181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSSEFNEGQIAPPSHLIRVGNSHAQYVEDP 240	Sequence 7, App1
DB	181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSSEFNEGQIAPPSHLIRVGNSHAQYVEDP 240	Sequence 32, App1
QY	241 ITGRQSVLVPTPEPQVGTEFTTVLVNFMKNSSCVGMNRPILLITVLTETRGQVIGRRRC 300	Sequence 6, App1

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Db 241 ITGROSALVPEPQVGTETFTVLYNFMCMSSCGVGNRRPILITVLETRDQVLRRC 300
Qy 301 FEARICACGRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGLOMTSIKKRRSPDDE 360
Db 301 FEARICACGRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGLOMTSIKKRRSPDDE 360
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQHLLQKOTSIOSSSY 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQHLLQKOTSIOSSSY 420
Qy 421 GNSSPPLNKNSMKNKLPSVSQOLNPOORNALPTTIDGAGANIPMGTHMPAGDMNGL 480
Db 421 GNSSPPLNKNSMKNKLPSVSQOLNPOORNALPTTIDGAGANIPMGTHMPAGDMNGL 480
Qy 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVRIWQV 516
Db 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVRIWQV 516
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RESULT 2

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US-09-542-615A-344
; Sequence 344, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-344
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Query Match 100.0%; Score 2751; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 4e-241;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MSSTQTNELSPFVQHIMDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCTRMQ 60
Db 1 MSSTQTNELSPFVQHIMDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCTRMQ 60
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Db 61 DSDLSDPMPQYTNLGLNMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDAL 120
Qy 121 SPSPALPSNTDYPGPHSFQVDFVSSFOOSTAKATWTYSELKKLVCQIAKTPQIQKWTTP 180
Db 121 SPSPALPSNTDYPGPHSFQVDFVSSFOOSTAKATWTYSELKKLVCQIAKTPQIQKWTTP 180
Qy 181 POGAVIRAMPVYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLRVEGNSHAQYEDP 240
Db 181 POGAVIRAMPVYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLRVEGNSHAQYEDP 240
Qy 241 ITGROSALVPEPQVGTETFTVLYNFMCMSSCGVGNRRPILITVLETRDQVLRRC 300
Db 241 ITGROSALVPEPQVGTETFTVLYNFMCMSSCGVGNRRPILITVLETRDQVLRRC 300
Qy 301 FEARICACGRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGLOMTSIKKRRSPDDE 360
Db 301 FEARICACGRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGLOMTSIKKRRSPDDE 360
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQHLLQKOTSIOSSSY 420
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Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQHLLQKOTSIOSSSY 420
Qy 421 GNSSPPLNKNSMKNKLPSVSQOLNPOORNALPTTIDGAGANIPMGTHMPAGDMNGL 480
Db 421 GNSSPPLNKNSMKNKLPSVSQOLNPOORNALPTTIDGAGANIPMGTHMPAGDMNGL 480
Qy 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVRIWQV 516
Db 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVRIWQV 516
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RESULT 3

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US-09-606-421B-344
; Sequence 344, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-344
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Query Match 100.0%; Score 2751; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 4e-241;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MSSTQTNELSPFVQHIMDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCTRMQ 60
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Db 121 SPSPALPSNTDYPGPHSFQVDFVSSFOOSTAKATWTYSELKKLVCQIAKTPQIQKWTTP 180
Qy 181 POGAVIRAMPVYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLRVEGNSHAQYEDP 240
Db 181 POGAVIRAMPVYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLRVEGNSHAQYEDP 240
Qy 241 ITGROSALVPEPQVGTETFTVLYNFMCMSSCGVGNRRPILITVLETRDQVLRRC 300
Db 241 ITGROSALVPEPQVGTETFTVLYNFMCMSSCGVGNRRPILITVLETRDQVLRRC 300
Qy 301 FEARICACGRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGLOMTSIKKRRSPDDE 360
Db 301 FEARICACGRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGLOMTSIKKRRSPDDE 360
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQHLLQKOTSIOSSSY 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQHLLQKOTSIOSSSY 420
Qy 421 GNSSPPLNKNSMKNKLPSVSQOLNPOORNALPTTIDGAGANIPMGTHMPAGDMNGL 480
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Db 421 GNSSPPLKNNKMLPSVSLINPOORNALPTTIPDGKGANIPMGTHMPMAGDMNGL 480
Qy 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 516
Db 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 516

RESULT 4
US-09-643-597-339
; Sequence 339, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-643-597-339

Query Match 98.9%; Score 2722; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 2,4e-238;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSOSTQNEFLSPYFOHIMDFLEQIPICSVOPIDLNFDSEDEGATKIKIISMDCIRMO 60
Db 1 MSOSTQNEFLSPYFOHIMDFLEQIPICSVOPIDLNFDSEDEGATKIKIISMDCIRMO 60
Qy 61 DSDLSDDPMPOYTNLGLNSMDQIQONSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDAL 120
Db 61 DSDLSDDPMPOYTNLGLNSMDQIQONSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDAL 120
Qy 121 SPSPAIPSNTDYPGPHSFDSVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Db 121 SPSPAIPSNTDYPGPHSFDSVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Qy 181 POGAVIRAMPYKKAHEVTEYVKKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
Db 181 POGAVIRAMPYKKAHEVTEYVKKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
Qy 241 ITGROSIVLPEPPOVGTETFTVLYNFMCNSSCVGMMRRPILITVLETRDGOVLGRRC 300
Db 241 ITGROSIVLPEPPOVGTETFTVLYNFMCNSSCVGMMRRPILITVLETRDGOVLGRRC 300
Qy 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIQMTSIIKRRSPDE 360
Db 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIQMTSIIKRRSPDE 360
Qy 361 LLYIPVGRRETYEMILKIKESLELMQYLPQHTIETRYOQOQOHOHLQKOTSIOSSPY 420
Db 361 LLYIPVGRRETYEMILKIKESLELMQYLPQHTIETRYOQOQOHOHLQKOTSIOSSPY 420
Qy 421 GNSSPPLKNNKMLPSVSLINPOORNALPTTIPDGKGANIPMGTHMPMAGDMNGL 480
Db 421 GNSSPPLKNNKMLPSVSLINPOORNALPTTIPDGKGANIPMGTHMPMAGDMNGL 480
Qy 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511

Db 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511

RESULT 5
US-09-542-615A-339
; Sequence 339, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-542-615A-339

Query Match 98.9%; Score 2722; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 2,4e-238;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSOSTQNEFLSPYFOHIMDFLEQIPICSVOPIDLNFDSEDEGATKIKIISMDCIRMO 60
Db 1 MSOSTQNEFLSPYFOHIMDFLEQIPICSVOPIDLNFDSEDEGATKIKIISMDCIRMO 60
Qy 61 DSDLSDDPMPOYTNLGLNSMDQIQONSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDAL 120
Db 61 DSDLSDDPMPOYTNLGLNSMDQIQONSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDAL 120
Qy 121 SPSPAIPSNTDYPGPHSFDSVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Db 121 SPSPAIPSNTDYPGPHSFDSVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Qy 181 POGAVIRAMPYKKAHEVTEYVKKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
Db 181 POGAVIRAMPYKKAHEVTEYVKKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
Qy 241 ITGROSIVLPEPPOVGTETFTVLYNFMCNSSCVGMMRRPILITVLETRDGOVLGRRC 300
Db 241 ITGROSIVLPEPPOVGTETFTVLYNFMCNSSCVGMMRRPILITVLETRDGOVLGRRC 300
Qy 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIQMTSIIKRRSPDE 360
Db 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIQMTSIIKRRSPDE 360
Qy 361 LLYIPVGRRETYEMILKIKESLELMQYLPQHTIETRYOQOQOHOHLQKOTSIOSSPY 420
Db 361 LLYIPVGRRETYEMILKIKESLELMQYLPQHTIETRYOQOQOHOHLQKOTSIOSSPY 420
Qy 421 GNSSPPLKNNKMLPSVSLINPOORNALPTTIPDGKGANIPMGTHMPMAGDMNGL 480
Db 421 GNSSPPLKNNKMLPSVSLINPOORNALPTTIPDGKGANIPMGTHMPMAGDMNGL 480
Qy 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511
Db 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511

RESULT 6
US-09-606-421B-339
; Sequence 339, Application US/09606421B
; Patent No. 6531315

```

: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C9
: CURRENT FILING DATE: 2000-06-28
: NUMBER OF SEQ ID NOS: 358
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 339
: LENGTH: 641
: TYPE: PR
: ORGANISM: Homo sapiens
US-09-606-421B-339

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Query Match 98.9%; Score 2722; DB 4; Length 641;

Best Local Similarity 100.0%; Pred. No. 2.4e-238;

Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVQPIDLNFVDEPSSDGAATNKIEISMDCI RMQ 60
DB 1 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVQPIDLNFVDEPSSDGAATNKIEISMDCI RMQ 60
QY 61 DSDLSPMWPQYTNGLNLGSLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDAL 120
DB 61 DSDLSPMWPQYTNGLNLGSLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDAL 120
QY 121 SPSPALPSNTDYGPHSFSDVSFOOSSSTAKATWTYSELKLYCQIAKTCPIQIKWTPP 180
DB 121 SPSPALPSNTDYGPHSFSDVSFOOSSSTAKATWTYSELKLYCQIAKTCPIQIKWTPP 180
QY 121 SPSPALPSNTDYGPHSFSDVSFOOSSSTAKATWTYSELKLYCQIAKTCPIQIKWTPP 180
DB 121 SPSPALPSNTDYGPHSFSDVSFOOSSSTAKATWTYSELKLYCQIAKTCPIQIKWTPP 180
QY 181 PGCAVIRAMPVYKKAHEVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 181 PGCAVIRAMPVYKKAHEVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITROSALVYEPPOVGTETFTVLYNPMCNSSCVGGNNRRPILITVLETRDQOVLGRRC 300
DB 241 ITROSALVYEPPOVGTETFTVLYNPMCNSSCVGGNNRRPILITVLETRDQOVLGRRC 300
QY 241 ITROSALVYEPPOVGTETFTVLYNPMCNSSCVGGNNRRPILITVLETRDQOVLGRRC 300
DB 241 ITROSALVYEPPOVGTETFTVLYNPMCNSSCVGGNNRRPILITVLETRDQOVLGRRC 300
QY 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIIOMTSIKKRSPDDE 360
DB 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIIOMTSIKKRSPDDE 360
QY 361 LLYLPVARGRETYEMLKIKESLELMQYLPQHTIETRYROOQOQOHOHLQKQTSIOSPSSY 420
DB 361 LLYLPVARGRETYEMLKIKESLELMQYLPQHTIETRYROOQOQOHOHLQKQTSIOSPSSY 420
QY 421 GNSSPPLNKNSMKNKLPVSQOLINPOORNALPTPTIPDGAGANI PMMGTHMPAGDMNGL 480
DB 421 GNSSPPLNKNSMKNKLPVSQOLINPOORNALPTPTIPDGAGANI PMMGTHMPAGDMNGL 480
QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSTV 511
DB 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSTV 511

```

RESULT 7

US-09-643-597-342

; Sequence 342, Application US/09643597

; Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tonglong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

```

: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C11
: CURRENT FILING DATE: 2000-08-21
: NUMBER OF SEQ ID NOS: 369
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 342
: LENGTH: 680
: TYPE: PR
: ORGANISM: Homo sapiens
US-09-643-597-342

```

Query Match 98.7%; Score 2714; DB 4; Length 680;

Best Local Similarity 99.8%; Pred. No. 1.4e-237;

Matches 510; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVQPIDLNFVDEPSSDGAATNKIEISMDCI RMQ 60
DB 40 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVQPIDLNFVDEPSSDGAATNKIEISMDCI RMQ 99
QY 61 DSDLSPMWPQYTNGLNLGSLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDAL 120
DB 100 DSDLSPMWPQYTNGLNLGSLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDAL 159
QY 121 SPSPALPSNTDYGPHSFSDVSFOOSSSTAKATWTYSELKLYCQIAKTCPIQIKWTPP 180
DB 160 SPSPALPSNTDYGPHSFSDVSFOOSSSTAKATWTYSELKLYCQIAKTCPIQIKWTPP 219
QY 181 PGCAVIRAMPVYKKAHEVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 220 PGCAVIRAMPVYKKAHEVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYEDP 279
QY 241 ITROSALVYEPPOVGTETFTVLYNPMCNSSCVGGNNRRPILITVLETRDQOVLGRRC 300
DB 280 ITROSALVYEPPOVGTETFTVLYNPMCNSSCVGGNNRRPILITVLETRDQOVLGRRC 339
QY 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIIOMTSIKKRSPDDE 360
DB 340 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIIOMTSIKKRSPDDE 399
QY 361 LLYLPVARGRETYEMLKIKESLELMQYLPQHTIETRYROOQOQOHOHLQKQTSIOSPSSY 420
DB 400 LLYLPVARGRETYEMLKIKESLELMQYLPQHTIETRYROOQOQOHOHLQKQTSIOSPSSY 459
QY 421 GNSSPPLNKNSMKNKLPVSQOLINPOORNALPTPTIPDGAGANI PMMGTHMPAGDMNGL 480
DB 460 GNSSPPLNKNSMKNKLPVSQOLINPOORNALPTPTIPDGAGANI PMMGTHMPAGDMNGL 519
QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSTV 511
DB 520 SPTQALPPPLSMPTSHCTPPPPYPTDCSTV 550

```

RESULT 8

US-09-542-615A-342

; Sequence 342, Application US/09542615A

; Patent No. 6518256

; GENERAL INFORMATION:

; APPLICANT: Wang, Tonglong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY


```

1  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
2  FILE REFERENCE:    210121.455C8
3  CURRENT APPLICATION NUMBER: US/09/542,615A
4  CURRENT FILING DATE:  2000-04-14
5  NUMBER OF SEQ ID NOS: 350
6  SOFTWARE:  FastSeq for Windows Version 3.0
7  SEQ ID NO 342
8  LENGTH: 680
9  TYPE:  PRT
10 ORGANISM: Homo sapiens
11 US-09-542-615A-342

```

Query Match	98.7%	Score	2714	DB 4	Length	680			
Best Local Similarity	99.8%	Pred. No.	1.4e-23						
Matches	510	Conservative	0	Mismatches	1	Indels	0	Gaps	0

QY	1	MSQSTQTNELSEPVQNHIMDLBPICISQVPIDNLFPDESEEGATNKIEISMDICRMQ	60
Db	40	MSQSTQTNELSEPVQNHIMDLBPICISQVPIDNLFPDESEEGATNKIEISMDICRMQ	99
QY	61	DSDSLSPMPPOXTNGLNLSMDQOQIQNGSSSTSPYNTIDHAQNSVTAESPQAQSPSTDAL	120
Db	100	DSDSLSPMPPOXTNGLNLSMDQOQIQNGSSSTSPYNTIDHAQNSVTAESPQAQSPSTDAL	159
QY	121	SPSPALPSTMDYDGRHSIDVSVFOQSTAKSATWITSTELKLYQOLAKTCPIQIKWTPP	180
Db	160	SPSPALPSTMDYDGRHSIDVSVFOQSTAKSATWITSTELKLYQOLAKTCPIQIKWTPP	219
QY	181	PGQAVIRAPVPYKKKEHYTEVYKRCPNHELSEEFNEGOIAPPSHLIRVEGNSHAQYEDP	240
Db	220	PGQAVIRAPVPYKKKEHYTEVYKRCPNHELSEEFNEGOIAPPSHLIRVEGNSHAQYEDP	279
QY	241	ITGRQSVLYPERPQVGETFTTVLYLNFMCNSSCVGGMNRRIILITVLETRDGOYLGRRC	300
Db	280	ITGRQSVLYPERPQVGETFTTVLYLNFMCNSSCVGGMNRRIILITVLETRDGOYLGRRC	339
QY	301	FEARICACGPRRKADDEDSIRKQOVSDBTKNDGCKRPFRONTNGIOMTSIKRRSPDDE	360
Db	340	FEARICACGPRRKADDEDSIRKQOVSDBTKNDGCKRPFRONTNGIOMTSIKRRSPDDE	399
QY	361	LILYLPARGRETEMLLKIKESLELMQYLPORHTIEFYRQOOQOOHOLQKOTSIOSPSSY	420
Db	400	LILYLPARGRETEMLLKIKESLELMQYLPORHTIEFYRQOOQOOHOLQKOTSIOSPSSY	459
QY	421	GNSSPPLNKMSNMKLPESVQOLINQOENALPPTIPGGMGANIPMGSTHHPMAGDNGL	480
Db	460	GNSSPPLNKMSNMKLPESVQOLINQOENALPPTIPGGMGANIPMGSTHHPMAGDNGL	519
QY	481	SPQALPPLSPMSTSHCTPPPPYPTDCSIY	511
Db	520	SPQALPPLSPMSTSHCTPPPPYPTDCSIY	550

RESULT 9
US-09-606-421B-342
Sequence 342, Application US/095606421B
Patient No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yassir A W
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45569
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358

```

: SOFTWARE: Fastseq for Windows Version 3.0.
: SEQ ID NO 342
: LENGTH: 680
: TYPE: prt
: ORGANISM: Homo sapiens
: US-09-606-421B-342

```

Query Match	98.7%	Score 2714	DB 4	Length 680
Best Local Similarity	99.8%	Pred No. 1.4e-237		
Matches 510; Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY	1	MSOSQTNTEBFSPEFEOHIMWLEBOPICISVOPDINEFVDEPSDQATNKEIEMSDCIRMQ	60
Db	40	MSOSQTNTEBFSPEFEOHIMWLEBOPICISVOPDINEFVDEPSDQATNKEIEMSDCIRMQ	99
QY	61	DSDLSDPMPOYTNIINGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSSFDAL	120
Db	100	DSDLSDPMPOYTNIINGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSSFDAL	159
QY	121	SPSPAIPENSTDPGHSHPFVSFOOASTASATMTVSTELKILYCOIAKRCIOIKMTTP	180
Db	160	SPSPAIPENSTDPGHSHPFVSFOOASTASATMTVSTELKILYCOIAKRCIOIKMTTP	219
QY	181	POGAITRAMPYVKKAEHYTEVVKRCPNHKLREBNEGQIAPPSHLIRVEGNSHAQVYEDP	240
Db	220	POGAITRAMPYVKKAEHYTEVVKRCPNHKLREBNEGQIAPPSHLIRVEGNSHAQVYEDP	279
QY	241	ITGRSVALPYPPPOVGTFFTYLVLFNKMKNSSCVGGMNRRPILIIYTLERDQOVLGRRC	300
Db	280	ITGRSVALPYPPPOVGTFFTYLVLFNKMKNSSCVGGMNRRPILIIYTLERDQOVLGRRC	339
QY	301	FEARICACPGRBRKKADEDSIRKQOVSdstKNGDGTGRPFPRONTNGIOMTSIKKRRSPDDE	360
Db	340	FEARICACPGRBRKKADEDSIRKQOVSdstKNGDGTGRPFPRONTNGIOMTSIKKRRSPDDE	399
QY	361	LIYLPVRGRETEYEMLLIKIESLELMQYLPOHTIETVRRQOOQOOHOLLQOTSIOSPSSY	420
Db	400	LIYLPVRGRETEYEMLLIKIESLELMQYLPOHTIETVRRQOOQOOHOLLQOTSIOSPSSY	459
QY	421	GNSSPPLKNMNSMKNLPSVSQOLINPOQRNALPTPTIPDCMGANIPMKGTHMPAAGMNGL	480
Db	460	GNSSPPLKNMNSMKNLPSVSQOLINPOQRNALPTPTIPDCMGANIPMKGTHMPAAGMNGL	519
QY	481	SPTQALPPLPSMPTSHCTPPPPYPPDCSIV	511
Db	520	SPTQALPPLPSMPTSHCTPPPPYPPDCSIV	550

```

RESULT 10
US-09-643-597-343
Sequence 343, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 21012.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461

```

TYPE: PRT
ORGANISM: Homo sapiens
US-09-643-597-343

Query Match 86.5%; Score 2379; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.9e-207;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 129
DB 15 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 74
QY 130 TDYPGHSPDVSVFOQSSSTAKSATWTYSTEELKLYCOIAKTCPIQIKVMPPPGAVIRAM 189
DB 75 TDYPGHSPDVSVFOQSSSTAKSATWTYSTEELKLYCOIAKTCPIQIKVMPPPGAVIRAM 134
QY 190 PVYKKAHVEYVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKKAHVEYVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGETFTTVLYNFMCNSSCVGGMNRPILIIYLTETRDGOVYGRRCFARICACP 309
DB 195 PYEPPOVGETFTTVLYNFMCNSSCVGGMNRPILIIYLTETRDGOVYGRRCFARICACP 254
QY 310 GRDKRADEDSIRKQOYSDSTKNGDGTKRPRONTHTGIQMTSIRKRSDDDELLYLPVGR 369
DB 255 GRDKRADEDSIRKQOYSDSTKNGDGTKRPRONTHTGIQMTSIRKRSDDDELLYLPVGR 314
QY 370 EYEMLLKIKESLEMOYLPOHTIETRYROOQOOHOLLOKOTSISQSSSYGSSPPLNK 429
DB 315 EYEMLLKIKESLEMOYLPOHTIETRYROOQOOHOLLOKOTSISQSSSYGSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
DB 375 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSMPSHCTPPPPYPTDCSIVRIWOY 516
DB 435 LSMPSHCTPPPPYPTDCSIVRIWOY 461

RESULT 11

US-09-542-615A-343
Sequence 343, Application US/09542615A
Patent No. 6518256
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542.615A
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-09-542-615A-343

Query Match 86.5%; Score 2379; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.9e-207;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 129
DB 15 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 74

QY 130 TDYPGHSPDVSVFOQSSSTAKSATWTYSTEELKLYCOIAKTCPIQIKVMPPPGAVIRAM 189
DB 75 TDYPGHSPDVSVFOQSSSTAKSATWTYSTEELKLYCOIAKTCPIQIKVMPPPGAVIRAM 134
QY 190 PVYKKAHVEYVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKKAHVEYVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGETFTTVLYNFMCNSSCVGGMNRPILIIYLTETRDGOVYGRRCFARICACP 309
DB 195 PYEPPOVGETFTTVLYNFMCNSSCVGGMNRPILIIYLTETRDGOVYGRRCFARICACP 254
QY 310 GRDKRADEDSIRKQOYSDSTKNGDGTKRPRONTHTGIQMTSIRKRSDDDELLYLPVGR 369
DB 255 GRDKRADEDSIRKQOYSDSTKNGDGTKRPRONTHTGIQMTSIRKRSDDDELLYLPVGR 314
QY 370 EYEMLLKIKESLEMOYLPOHTIETRYROOQOOHOLLOKOTSISQSSSYGSSPPLNK 429
DB 315 EYEMLLKIKESLEMOYLPOHTIETRYROOQOOHOLLOKOTSISQSSSYGSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
DB 375 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSMPSHCTPPPPYPTDCSIVRIWOY 516
DB 435 LSMPSHCTPPPPYPTDCSIVRIWOY 461

RESULT 12

US-09-606-421B-343
Sequence 343, Application US/09606421B
Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606.421B
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-09-606-421B-343

Query Match 86.5%; Score 2379; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.9e-207;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 129
DB 15 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 74
QY 130 TDYPGHSPDVSVFOQSSSTAKSATWTYSTEELKLYCOIAKTCPIQIKVMPPPGAVIRAM 189
DB 75 TDYPGHSPDVSVFOQSSSTAKSATWTYSTEELKLYCOIAKTCPIQIKVMPPPGAVIRAM 134
QY 190 PVYKKAHVEYVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKKAHVEYVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGETFTTVLYNFMCNSSCVGGMNRPILIIYLTETRDGOVYGRRCFARICACP 309

```
Db 195 PYEPVOGTEFTTVLYNFMCMSSCVGNNRRPILITVLETRDGVLCGRCEARICACP 254
Qy 310 GRDKRAEDSIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDDELLIYVGR 369
Db 255 GRDKRAEDSIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDDELLIYVGR 314
Qy 370 EYEMLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 EYEMLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Qy 430 MNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
Db 375 MNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
Qy 490 LSMSTSHCTPPPPYPPTDCSTIV 516
Db 435 LSMSTSHCTPPPPYPPTDCSTIV 461
```

RESULT 13

```
US-09-643-597-338
: Sequence 338, Application US/09643597
: Patent No. 6426072
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skelvy, Yastir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C11
: CURRENT APPLICATION NUMBER: US/09/643,597
: NUMBER OF SEQ ID NOS: 369
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 338
: LENGTH: 586
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-643-597-338
```

```
Query Match 84.8%; Score 2333; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 4e-203;
Matches 439; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 70 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAISN 129
Db 15 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAISN 74
Qy 130 TDYGPSPHSDVSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPQGAIVRAM 189
Db 75 TDYGPSPHSDVSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPQGAIVRAM 134
Qy 190 PYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGQOSVLY 249
Db 135 PYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGQOSVLY 194
Qy 250 PYEPVOGTEFTTVLYNFMCMSSCVGNNRRPILITVLETRDGVLCGRCEARICACP 309
Db 195 PYEPVOGTEFTTVLYNFMCMSSCVGNNRRPILITVLETRDGVLCGRCEARICACP 254
Qy 310 GRDKRAEDSIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDDELLIYVGR 369
Db 255 GRDKRAEDSIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDDELLIYVGR 314
```

```
Qy 370 EYEMLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 EYEMLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Qy 430 MNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
Db 375 MNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
Qy 490 LSMSTSHCTPPPPYPPTDCSTIV 511
Db 435 LSMSTSHCTPPPPYPPTDCSTIV 456
```

RESULT 14

```
US-09-542-615A-338
: Sequence 338, Application US/09542615A
: Patent No. 6518256
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C8
: CURRENT APPLICATION NUMBER: US/09/542,615A
: NUMBER OF SEQ ID NOS: 350
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 338
: LENGTH: 586
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-542-615A-338
```

```
Query Match 84.8%; Score 2333; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 4e-203;
Matches 439; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 70 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAISN 129
Db 15 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAISN 74
Qy 130 TDYGPSPHSDVSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPQGAIVRAM 189
Db 75 TDYGPSPHSDVSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPQGAIVRAM 134
Qy 190 PYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGQOSVLY 249
Db 135 PYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGQOSVLY 194
Qy 250 PYEPVOGTEFTTVLYNFMCMSSCVGNNRRPILITVLETRDGVLCGRCEARICACP 309
Db 195 PYEPVOGTEFTTVLYNFMCMSSCVGNNRRPILITVLETRDGVLCGRCEARICACP 254
Qy 310 GRDKRAEDSIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDDELLIYVGR 369
Db 255 GRDKRAEDSIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDDELLIYVGR 314
Qy 370 EYEMLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 EYEMLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Qy 430 MNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
Db 375 MNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
Qy 490 LSMSTSHCTPPPPYPPTDCSTIV 511
Db 435 LSMSTSHCTPPPPYPPTDCSTIV 456
```

```
RESULT 15
US-09-606-421B-338
; Sequence 338, Application US/09606421B
; Patent No. 653315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-606-421B-338

Query Match      84.8%; Score 2333; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 4e-203;
Matches 439; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 15 PoytNGLnSMQOIRNGSSSTSPYNTDHAONSVTAPSPYAOPTFDALSPSPALPSN 74
QY 130 TDYPGHSDVVSFOQSSSTAFATWYSTELKLYCQIAKTCPIQIKYMTPPPOGAVIRAM 189
Db 75 TDYPGHSDVVSFOQSSSTAFATWYSTELKLYCQIAKTCPIQIKYMTPPPOGAVIRAM 134
QY 190 PYKKAHEVTEVYKRCNHNLSREFNCOIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
Db 135 PYKKAHEVTEVYKRCNHNLSREFNCOIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGEFTTVLYNFMCNSSCVGGMNRPILITVLETRDQVIGRRCFEARIACAP 309
Db 195 PYEPPOVGEFTTVLYNFMCNSSCVGGMNRPILITVLETRDQVIGRRCFEARIACAP 254
QY 310 GRDRKADEDSIRKQOVSDSTKNGDGTKRPRONTHGIQMTSIKKRSPDDELLYLPVGR 369
Db 255 GRDRKADEDSIRKQOVSDSTKNGDGTKRPRONTHGIQMTSIKKRSPDDELLYLPVGR 314
QY 370 ETEYMLLKIKESLEIMQYLPQHTIETYROOQOOHOLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 ETEYMLLKIKESLEIMQYLPQHTIETYROOQOOHOLLQKOTSIOSSSYGNSSPPLNK 374
QY 430 MNSMNLKLPVSQILNQORNALPTTIPDGMGANIPMAGTHMPAGDMNGLSPTQALPPP 489
Db 375 MNSMNLKLPVSQILNQORNALPTTIPDGMGANIPMAGTHMPAGDMNGLSPTQALPPP 434
QY 490 LSMPTSHCTPPPPYPTDCSIV 511
Db 435 LSMPTSHCTPPPPYPTDCSIV 456
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Search completed: August 7, 2003, 09:54:51
Job time: 16.2345 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:46:34 ; Search time 22.0296 Seconds

(without alignments)
2781.719 Million cell updates/sec

Title: US-09-538-106-14

Perfect score: 2751

Sequence: 1 MSQSTQNEFLSPVEFQHIW.....HCRPPPPYPTDCSIVRIHQV 516

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
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8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2751	100.0	516	9	US-09-735-705-344
2	2751	100.0	516	10	US-09-850-716A-344
3	2751	100.0	516	10	US-09-897-778-344
4	2722	98.9	641	9	US-09-735-705-339
5	2722	98.9	641	10	US-09-850-716A-339
6	2722	98.9	641	10	US-09-897-778-339
7	2714	98.7	680	9	US-09-735-705-342
8	2714	98.7	680	10	US-09-850-716A-342
9	2714	98.7	680	10	US-09-897-778-342
10	2379	86.5	461	9	US-09-735-705-343
11	2379	86.5	461	10	US-09-850-716A-343
12	2379	86.5	461	10	US-09-897-778-343
13	2333	84.8	586	9	US-09-735-705-338
14	2333	84.8	586	10	US-09-850-716A-338
15	2333	84.8	586	10	US-09-897-778-338

16	2326	84.6	586	9	US-09-735-705-152	Sequence 152, App
17	2326	84.6	586	10	US-09-850-716A-152	Sequence 152, App
18	2326	84.6	586	10	US-09-897-778-152	Sequence 152, App
19	2326	84.6	586	11	US-09-466-396A-152	Sequence 152, App
20	2222	80.8	426	15	US-10-274-874-19	Sequence 19, App1
21	2185	79.4	448	9	US-09-735-705-340	Sequence 340, App
22	2185	79.4	448	10	US-09-850-716A-340	Sequence 340, App
23	2185	79.4	448	10	US-09-897-778-340	Sequence 340, App
24	1801	65.5	356	9	US-09-735-705-341	Sequence 341, App
25	1801	65.5	356	10	US-09-850-716A-341	Sequence 341, App
26	1801	65.5	356	10	US-09-897-778-341	Sequence 341, App
27	1801	65.5	356	15	US-10-274-874-2	Sequence 2, App1
28	1464.5	53.2	635	14	US-10-155-059-3	Sequence 3, App1
29	1464.5	53.2	635	14	US-09-732-884-10	Sequence 10, App1
30	1328.5	48.3	420	15	US-10-274-874-20	Sequence 20, App1
31	718	26.1	393	9	US-09-776-693-32	Sequence 32, App1
32	718	26.1	393	10	US-09-732-884-3	Sequence 3, App1
33	718	26.1	393	10	US-09-860-211-9	Sequence 9, App1
34	718	26.1	393	11	US-09-029-327-4	Sequence 4, App1
35	718	26.1	393	11	US-09-860-286-9	Sequence 9, App1
36	718	26.1	393	15	US-10-274-874-4	Sequence 4, App1
37	718	26.1	393	15	US-10-160-280-2	Sequence 2, App1
38	718	26.1	428	15	US-10-076-691-2	Sequence 2, App1
39	716.5	26.0	353	15	US-10-146-473-78	Sequence 78, App1
40	716	26.0	390	15	US-10-038-010-6	Sequence 6, App1
41	714.5	26.0	401	10	US-09-968-851-34	Sequence 34, App1
42	713	25.9	390	15	US-10-160-290-3	Sequence 3, App1
43	704.5	25.6	394	14	US-10-155-059-4	Sequence 4, App1
44	704	25.6	381	10	US-09-968-851-36	Sequence 36, App1
45	690.5	25.1	374	10	US-09-968-851-28	Sequence 28, App1

ALIGNMENTS

RESULT 1
US-09-735-705-344
Sequence 344, Application US/09735705
Patient No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Banpur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-705-344
Query Match 100.0%; Score 2751; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.6e-220;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQNEFLSPVEFQHIWPTLEQICVDPIDINFDVDEPSEGDATKIKIISMDICIMQ 60
DB 1 MSQSTQNEFLSPVEFQHIWPTLEQICVDPIDINFDVDEPSEGDATKIKIISMDICIMQ 60

OY	61	DSLSDSDPMMPQVNTNLGLNSMDOQJONGSSSRSPYTDHAONSVTAPSPAQSSSFEDAL	120
Dd	61	DSDSLSDPMMPQJNTNLGLNSMDOQJONGSSSRSPYTDHAONSVTAPSPAQSSSFEDAL	120
OY	121	SPSPAIPANTDYPGPHSEFDSVFSQOQSTAKSAATWTSETLKKLYLCQJLAKTCTPIDIKWTPP	180
Dd	121	SPSPAIPANTDYPGPHSEFDSVFSQOQSTAKSAATWTSETLKKLYLCQJLAKTCTPIDIKWTPP	180
OY	181	POGATIRAMPYKKAHEHTVEYVKRCPNHLSREFNNGQJAPSPHLLRVBESNSHAQYVEDP	240
Dd	181	POGATIRAMPYKKAHEHTVEYVKRCPNHLSREFNNGQJAPSPHLLRVBESNSHAQYVEDP	240
OY	241	ITGRQSVLVYPERPOVGTETFTVLVLFNMGNSSCVGGMNRRPILIIYTLERDQOVLGRRC	300
Dd	241	ITGRQSVLVYPERPOVGTETFTVLVLFNMGNSSCVGGMNRRPILIIYTLERDQOVLGRRC	300
OY	301	FEARICACPGDRKKADEDSIRKQOYSDSTKNGDGIKRPFRONTHTGIOMTISIKRRSPDDE	360
Dd	301	FEARICACPGDRKKADEDSIRKQOYSDSTKNGDGIKRPFRONTHTGIOMTISIKRRSPDDE	360
OY	361	LLYLFVPRGETEYEMLLIKIESLELMQOYLPOHTLETYRQOOQOOQHHLKQTSIQSPSSY	420
Dd	361	LLYLFVPRGETEYEMLLIKIESLELMQOYLPOHTLETYRQOOQOOQHHLKQTSIQSPSSY	420
OY	421	GNSSPPLKNKMSMNLKPSVSQJLINPOQRNALPTPTIPDGMGANIPMGGTHMPYAGDMNGL	480
Dd	421	GNSSPPLKNKMSMNLKPSVSQJLINPOQRNALPTPTIPDGMGANIPMGGTHMPYAGDMNGL	480
OY	481	SPTQALPPLISMBSHCTPPPPYPPDCSIVRTIMQV	516
Dd	481	SPTQALPPLISMBSHCTPPPPYPPDCSIVRTIMQV	516

	RESULT 2	
US-09-850-716A-344		
: Sequence 344, Application US/09850716A		
: Patent No. US20020115139A1		
: GENERAL INFORMATION:		
: APPLICANT: Kalos, Michael D.		
: APPLICANT: McNeill, Patricia D.		
: APPLICANT: Retter, Marc W.		
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY		
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER		
: FILE REFERENCE: 210121.455C15		
: CURRENT APPLICATION NUMBER: US/09/850,716A		
: CURRENT FILING DATE: 2001-05-07		
: NUMBER OF SEQ ID NOS: 440		
: SOFTWARE: FastSeq for Windows Version 3.0		
: SEQ ID NO 344		
: LENGTH: 516		
: TYPE: PRT		
: ORGANISM: Homo sapiens		
US-09-850-716A-344		
Query Match	100.0%;	Score 2751; DB 10; Length 516;
Best Local Similarity	100.0%;	Pred. No. 1.6e-220;
Matches 516; Conservative	0;	Mismatches 0; Indels 0; Gaps 0
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1 MSQSTQTNEFLSPFEVFOHIMDFLEOPICSVOPIDLFNFDEPSESDATNKIEISMDCIRMQ		60
OY	DSLSDDPMWPQYTNGILNSMDQIQONSSSTSPYNTDHAONSVTAPSPYAOSTTFDAL	120
61 DSLSDDPMWPQYTNGILNSMDQIQONSSSTSPYNTDHAONSVTAPSPYAOSTTFDAL		120
Db	61 DSLSDDPMWPQYTNGILNSMDQIQONSSSTSPYNTDHAONSVTAPSPYAOSTTFDAL	120
OY	121 SPSPAIPBSNDYPGPHSFVDVSFQOOSTAKSATWTYSTELKRLKYCOIAKTCPIQIKVMTPP	180
121 SPSPAIPBSNDYPGPHSFVDVSFQOOSTAKSATWTYSTELKRLKYCOIAKTCPIQIKVMTPP		180
Db	121 SPSPAIPBSNDYPGPHSFVDVSFQOOSTAKSATWTYSTELKRLKYCOIAKTCPIQIKVMTPP	180
OY	181 PGAGVITRAMPYYKKAHEHTVEVKRPKNHELSEFNEGQIAPPSHLIRVBGNSHAQYEDP	240
181 PGAGVITRAMPYYKKAHEHTVEVKRPKNHELSEFNEGQIAPPSHLIRVBGNSHAQYEDP		240
Db	181 PGAGVITRAMPYYKKAHEHTVEVKRPKNHELSEFNEGQIAPPSHLIRVBGNSHAQYEDP	240

Qy	24	ITGRSVIVDPYRPPOVGEFTTIVLKNPNCSSCVGGMRRPILITVLETRPDGVIGRR	3000
Db	241	ITGRSVIVDPYRPPOVGEFTTIVLKNPNCSSCVGGMRRPILITVLETRPDGVIGRR	3000
Qy	301	FEARICACPRDRKADEDISIRKQVSDSTKNGDGTRPFRONTGHIOMTSIKKRRSPDE	3600
Db	301	FEARICACPRDRKADEDISIRKQVSDSTKNGDGTRPFRONTGHIOMTSIKKRRSPDE	3600
Qy	361	LTFLPVRGRETYYMLIKIKESLELMQYLPQHTIEFRQOQOQOHLLQKOTSIQSPSSY	4200
Db	361	LTFLPVRGRETYYMLIKIKESLELMQYLPQHTIEFRQOQOQOHLLQKOTSIQSPSSY	4200
Qy	421	GNSSPPLINKNSMNKLPSVSQILINPOQRNALPTTIPDGMGANTPMWGTHPMAGDNGL	4800
Db	421	GNSSPPLINKNSMNKLPSVSQILINPOQRNALPTTIPDGMGANTPMWGTHPMAGDNGL	4800
Qy	481	SPTQALPPPLSMPSSTHCTPPPPYPTDCSIYAIMQV	516
Db	481	SPTQALPPPLSMPSSTHCTPPPPYPTDCSIYAIMQV	516

RESULT 3
 US-09-897-778-344
 ; Sequence 344, Application US/09897778
 ; Patent No. US20020147143A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tonglong
 ; APPLICANT: Marnierakis, Margarita
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Vedrick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Matanabe, Yoshihiro
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Peckham, David W.
 ; APPLICANT: Fanger, Neil
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.455C16
 ; CURRENT APPLICATION NUMBER: US/09/897,778
 ; CURRENT FILING DATE: 2001-06-28
 ; NUMBER OF SEQ ID NOS: 467
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 344
 ; LENGTH: 516
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-897-778-344

Query Match	100.0%	Score 2751	DB 10	Length 516
Best Local Similarity	100.0%	Pred. No. 1,66-220		
Matches	516	Conservative	0	Mismatches 0; Indels 0; Gaps 0
Qy	1	MSOSTQTEEFSPSEVFGHIMDFLEDPICISVOPIDINFVDESESDATNKKIEISMDCIRMQ	60	
Db	1	MSOSTQTEEFSPSEVFGHIMDFLEDPICISVOPIDINFVDESESDATNKKIEISMDCIRMQ	60	
Qy	61	DSLDSDPMPQYTNGLNLSMDQIQIONSSSTSPYNTQHAQNSVTAPSPYAQSPSTFDAL	120	
Db	61	DSLDSDPMPQYTNGLNLSMDQIQIONSSSTSPYNTQHAQNSVTAPSPYAQSPSTFDAL	120	
Qy	121	SPSPAIPSNPTYPCGPHSFDVSFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPRP	180	
Db	121	SPSPAIPSNPTYPCGPHSFDVSFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPRP	180	
Qy	181	POGAVIRAMPYKKAHEHTEVYKKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP	240	
Db	181	POGAVIRAMPYKKAHEHTEVYKKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP	240	
Qy	241	ITGQSVLYVPEPQVGTFTTLYLVNFCNCSVCVGAMRRPLLIVLTETDGOVLGRRC	300	
Db	241	ITGQSVLYVPEPQVGTFTTLYLVNFCNCSVCVGAMRRPLLIVLTETDGOVLGRRC	300	

QY	301	FEARCAACPGDRKKADEDSIRKQOVS	DSKNNDDGTRKPRRQNTHG	IOmS	SIKKRRSPDE	360
Db	301	FEARCAACPGRRKKADEDSIRKQOVS	DSKNNDDGTRKPRRQNTHG	IOmS	SIKKRRSPDE	360
QY	361	LLYLPVRGRETYEMLLIKESLEL	MQYLPOHTIETYRQOQOOO	HOHLKOTIS	OSPSSY	420
Db	361	LLYLPVRGRETYEMLLIKESLEL	MQYLPOHTIETYRQOQOOO	HOHLKOTIS	OSPSSY	420
QY	421	GNSSPPLKNKMSMNKLPSVSQ	LINQORNALPTTTPDGMG	ANIIPMAGTHMPYAGDMNGI		480
Db	421	GNSSPPLKNKMSMNKLPSVSQ	LINQORNALPTTTPDGMG	ANIIPMAGTHMPYAGDMNGI		480
QY	481	SPTQALPPLLSMPSTSHCTPP	PPYPTDGSIVIMQV			516
Db	481	SPTQALPPLLSMPSTSHCTPP	PPYPTDGSIVIMQV			516

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RESULT 4
US-09-735-705-339
Sequence 339, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yastir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRF
ORGANISM: Homo sapiens
US-09-735-705-339

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[illegible]

Db	301	FEARLCACBGRKRAKDEDSIRKQOVS	STKNGDGTRRPFRONTNGIOMTSIKRRSPDDE	360
QY	361	LLYLEVRGREIYEMLLIKIKESLELMQYL	PQHTIETERYRQOQOQOQHLLQOTSISQSSSY	420
Db	361	LLYLEVRGREIYEMLLIKIKESLELMQYL	PQHTIETERYRQOQOQOQHLLQOTSISQSSSY	420
QY	421	GNSSPPLKNMNSMKNLPYSQ	LINPOQRNALPTTIPDGMGANIPMNGTHMPAAGDNGL	480
Db	421	GNSSPPLKNMNSMKNLPYSQ	LINPOQRNALPTTIPDGMGANIPMNGTHMPAAGDNGL	480
QY	481	SPTQALPPLPSMPSSTSHCTPPPPYP	PDGCSIV 511	
Db	481	SPTQALPPLPSMPSSTSHCTPPPPYP	PDGCSIV 511	

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RESULT 5
US-09-850-716A-339
; Sequence 339, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-339

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Query Match	98.9%	Score 2722	DB 10	Length 641
Best Local Similarity	100.0%	Pred. 5.5e-218		
Matches 511	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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Db	1	MSQSTQTNWFLSPEVFOIHWFLERDPIGVOPIDLFVDEPSESDATNKEIISMDCIRMQ	60	
QY	61	DSDSLDEPMPOYTNLGLINSMDOQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSSTFDAL	120	
Db	61	DSDSLDEPMPOYTNLGLINSMDOQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSSTFDAL	120	
QY	121	SPSPAIPEBNTDYPGSHSPFDSVFSQOOSTKSAWMTYSTELKTKLYCOIAKTCPIQIIVMTMP	180	
Db	121	SPSPAIPEBNTDYPGSHSPFDSVFSQOOSTKSAWMTYSTELKTKLYCOIAKTCPIQIIVMTMP	180	
QY	181	PGAVIYRAMPYKKRAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVEDP	240	
Db	181	PGAVIYRAMPYKKRAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVEDP	240	
QY	241	ITGRQSVLVPEPPOVGTETFTTVLYNFMCNSSCVGMMRRPILIIIVTLETRDQVYLGRRG	300	
Db	241	ITGRQSVLVPEPPOVGTETFTTVLYNFMCNSSCVGMMRRPILIIIVTLETRDQVYLGRRG	300	
QY	301	FEARICACPGDRKRADEDSIRKQOVS DSTKNGDGTKRPRONTHTGIOMTSIKKRRSPDDE	360	
Db	301	FEARICACPGDRKRADEDSIRKQOVS DSTKNGDGTKRPRONTHTGIOMTSIKKRRSPDDE	360	
QY	361	LLYLPVGRRETYEMLKIKESLELMQVLPQHTIETVROOQOQOHOHLLOKQTSIOSPASSY	420	
Db	361	LLYLPVGRRETYEMLKIKESLELMQVLPQHTIETVROOQOQOHOHLLOKQTSIOSPASSY	420	
QY	421	GNSSPPLKNKMSMNKLPSVSOLINQOQENALPTTIPDGMGANIPMGTTHMPMADDMNGL	480	
Db	421	GNSSPPLKNKMSMNKLPSVSOLINQOQENALPTTIPDGMGANIPMGTTHMPMADDMNGL	480	
QY	481	SPQOALPPLPLSMSTSHCTPPPPYPTDCSIV	511	

Db 481 SPTQALPPLSMSTSHCTPPPYPTDCSIV 511

RESULT 6

US-09-897-778-339
; Sequence 339, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ. ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-897-778-339

Query Match 98.9%; Score 2722; DB 10; Length 641;
Best Local Similarity 100.0%; Pred. No. 5.5e-218;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTOTNEFLSEVPHQIMDFLEQPCISQVPIDLNVDPSDGDATNKIEISMDCTRQ 60
DB 1 MSOSTOTNEFLSEVPHQIMDFLEQPCISQVPIDLNVDPSDGDATNKIEISMDCTRQ 60
QY 61 DSDLSPPMPOQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSSFTDAL 120
DB 61 DSDLSPPMPOQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSSFTDAL 120
QY 121 SPSPALPSNTDYGPHSFVDSFOOSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPP 180
DB 121 SPSPALPSNTDYGPHSFVDSFOOSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPP 180
QY 181 POGAVIRAMVYKKAHEVTEVYKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 181 POGAVIRAMVYKKAHEVTEVYKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITGROSVLVYEPPOVGTETFTVLYNFMNCSSCVGNNRRPILITVLETRDGOVLGRRC 300
DB 241 ITGROSVLVYEPPOVGTETFTVLYNFMNCSSCVGNNRRPILITVLETRDGOVLGRRC 300
QY 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTAKRPFRONTHGLOMTSIIKKRRSPDDE 360
DB 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTAKRPFRONTHGLOMTSIIKKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKQTSIOSPSSY 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKQTSIOSPSSY 420
QY 421 GNSSPPLKNKNSNKLPSVSQILNPOORNALPTTTPDGGANIPMWGTHMPAGDMNGL 480
DB 421 GNSSPPLKNKNSNKLPSVSQILNPOORNALPTTTPDGGANIPMWGTHMPAGDMNGL 480
QY 481 SPTQALPPLSMSTSHCTPPPYPTDCSIV 511
DB 481 SPTQALPPLSMSTSHCTPPPYPTDCSIV 511

RESULT 7

US-09-735-705-342
; Sequence 342, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ. ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-735-705-342

Query Match 98.7%; Score 2714; DB 9; Length 680;
Best Local Similarity 99.8%; Pred. No. 2.8e-217;
Matches 510; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTOTNEFLSEVPHQIMDFLEQPCISQVPIDLNVDPSDGDATNKIEISMDCTRQ 60
DB 40 MSOSTOTNEFLSEVPHQIMDFLEQPCISQVPIDLNVDPSDGDATNKIEISMDCTRQ 99
QY 61 DSDLSPPMPOQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSSFTDAL 120
DB 100 DSDLSPPMPOQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSSFTDAL 129
QY 121 SPSPALPSNTDYGPHSFVDSFOOSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPP 180
DB 121 SPSPALPSNTDYGPHSFVDSFOOSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPP 219
QY 160 SPSPALPSNTDYGPHSFVDSFOOSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPP 219
DB 160 SPSPALPSNTDYGPHSFVDSFOOSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPP 219
QY 181 POGAVIRAMVYKKAHEVTEVYKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 220 POGAVIRAMVYKKAHEVTEVYKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDP 279
QY 241 ITGROSVLVYEPPOVGTETFTVLYNFMNCSSCVGNNRRPILITVLETRDGOVLGRRC 300
DB 280 ITGROSVLVYEPPOVGTETFTVLYNFMNCSSCVGNNRRPILITVLETRDGOVLGRRC 339
QY 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTAKRPFRONTHGLOMTSIIKKRRSPDDE 360
DB 340 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTAKRPFRONTHGLOMTSIIKKRRSPDDE 399
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKQTSIOSPSSY 420
DB 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKQTSIOSPSSY 459
QY 421 GNSSPPLKNKNSNKLPSVSQILNPOORNALPTTTPDGGANIPMWGTHMPAGDMNGL 480
DB 460 GNSSPPLKNKNSNKLPSVSQILNPOORNALPTTTPDGGANIPMWGTHMPAGDMNGL 519
QY 481 SPTQALPPLSMSTSHCTPPPYPTDCSIV 511
DB 520 SPTQALPPLSMSTSHCTPPPYPTDCSIV 550

RESULT 8

US-09-850-716A-342
; Sequence 342, Application US/09850716A

Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
TYPE: PR1
ORGANISM: Homo sapiens
US-09-850-716A-342

Query Match 98.7%; Score 2714; DB 10; Length 680;
Best Local Similarity 99.8%; Pred. No. 2.8e-217;
Matches 510; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTQNEFLSPVFOHIMDFLEQPCISVOPIDLNFVDEPSEDAATKIEISMDCIQRMQ 60
DB 40 MSOSTQNEFLSPVFOHIMDFLEQPCISVOPIDLNFVDEPSEDAATKIEISMDCIQRMQ 99
QY 61 DSDLSDPWMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTPDAL 120
DB 100 DSDLSDPWMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTPDAL 159
QY 121 SPSPAISSNDYPCGPHSFVDFQOOSTAKSATWTSTELKLYCOIACTCPIQIKVMP 180
DB 160 SPSPAISSNDYPCGPHSFVDFQOOSTAKSATWTSTELKLYCOIACTCPIQIKVMP 219
QY 181 POGAVIRAMPYKKAHEVTEYVKKCPNHLSREFNEGOIAPPSHLIRVGNSHAQYVDP 240
DB 220 POGAVIRAMPYKKAHEVTEYVKKCPNHLSREFNEGOIAPPSHLIRVGNSHAQYVDP 279
QY 241 ITGROSULVYEPPOVGTETFTVLYNFMCNSSCVGMMRRPILIIIVLETEDGOVLGRRC 300
DB 280 ITGROSULVYEPPOVGTETFTVLYNFMCNSSCVGMMRRPILIIIVLETEDGOVLGRRC 339
QY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRFRONTGHIQWTSIKRRSPDE 360
DB 340 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRFRONTGHIQWTSIKRRSPDE 399
QY 361 LLYLPVGRRETYEMMLIKESLELMQYLPQHTIETVYRQOQOQHLLQKQTSIQSPSSY 420
DB 400 LLYLPVGRRETYEMMLIKESLELMQYLPQHTIETVYRQOQOQHLLQKQTSIQSPSSY 459
QY 421 GNSSPPLKNNKSNKLSVSQLINPOORNALPTTIPDGKGANIPMGTHMPMAGDMNGL 480
DB 460 GNSSPPLKNNKSNKLSVSQLINPOORNALPTTIPDGKGANIPMGTHMPMAGDMNGL 519
QY 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511
DB 520 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 550

RESULT 9
US-09-897-778-342
Sequence 342, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedavick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 342
LENGTH: 680
TYPE: PR1
ORGANISM: Homo sapiens
US-09-897-778-342

Query Match 98.7%; Score 2714; DB 10; Length 680;
Best Local Similarity 99.8%; Pred. No. 2.8e-217;
Matches 510; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTQNEFLSPVFOHIMDFLEQPCISVOPIDLNFVDEPSEDAATKIEISMDCIQRMQ 60
DB 40 MSOSTQNEFLSPVFOHIMDFLEQPCISVOPIDLNFVDEPSEDAATKIEISMDCIQRMQ 99
QY 61 DSDLSDPWMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTPDAL 120
DB 100 DSDLSDPWMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTPDAL 159
QY 121 SPSPAISSNDYPCGPHSFVDFQOOSTAKSATWTSTELKLYCOIACTCPIQIKVMP 180
DB 160 SPSPAISSNDYPCGPHSFVDFQOOSTAKSATWTSTELKLYCOIACTCPIQIKVMP 219
QY 181 POGAVIRAMPYKKAHEVTEYVKKCPNHLSREFNEGOIAPPSHLIRVGNSHAQYVDP 240
DB 220 POGAVIRAMPYKKAHEVTEYVKKCPNHLSREFNEGOIAPPSHLIRVGNSHAQYVDP 279
QY 241 ITGROSULVYEPPOVGTETFTVLYNFMCNSSCVGMMRRPILIIIVLETEDGOVLGRRC 300
DB 280 ITGROSULVYEPPOVGTETFTVLYNFMCNSSCVGMMRRPILIIIVLETEDGOVLGRRC 339
QY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRFRONTGHIQWTSIKRRSPDE 360
DB 340 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRFRONTGHIQWTSIKRRSPDE 399
QY 361 LLYLPVGRRETYEMMLIKESLELMQYLPQHTIETVYRQOQOQHLLQKQTSIQSPSSY 420
DB 400 LLYLPVGRRETYEMMLIKESLELMQYLPQHTIETVYRQOQOQHLLQKQTSIQSPSSY 459
QY 421 GNSSPPLKNNKSNKLSVSQLINPOORNALPTTIPDGKGANIPMGTHMPMAGDMNGL 480
DB 460 GNSSPPLKNNKSNKLSVSQLINPOORNALPTTIPDGKGANIPMGTHMPMAGDMNGL 519
QY 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511
DB 520 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 550

RESULT 10
US-09-735-705-343
Sequence 343, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735.705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
TYPE: PRN
ORGANISM: Homo sapiens
US-09-735-705-343

Query Match 86.5%; Score 2379; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.2e-189;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDOQIONGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTFALSPSPALPSN 129
DB 15 PQTNLGLNSMDOQIONGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTFALSPSPALPSN 74
QY 130 TDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPPGAVIRAM 189
DB 75 TDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPPGAVIRAM 134
QY 190 PYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRSVLV 249
DB 135 PYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRSVLV 194
QY 250 PYEPPOVGEFTTVLYNFMCNSSCVGAMNRPILLIIVTLETROGVYGRRCFARICACP 309
DB 195 PYEPPOVGEFTTVLYNFMCNSSCVGAMNRPILLIIVTLETROGVYGRRCFARICACP 254
QY 310 GRKRADEDSIRKQOYSDSTKNGDGTKRPRONTHTGIOMTSIKRRSPDDELLYLVRGR 369
DB 255 GRKRADEDSIRKQOYSDSTKNGDGTKRPRONTHTGIOMTSIKRRSPDDELLYLVRGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETRYROQOQOHOHLQKTSIOSPSSYGNSSPPLNK 429
DB 315 EYEMLLKIKESLELMQYLPQHTIETRYROQOQOHOHLQKTSIOSPSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQILNQORNALPPTIIPDGMGANIPMGTHMPAGDMGLSPTQALPPP 489
DB 375 MNSMNLKPSVSQILNQORNALPPTIIPDGMGANIPMGTHMPAGDMGLSPTQALPPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVRIKOV 516
DB 435 LSMSTSHCTPPPPYPTDCSIVRIKOV 461

RESULT 11

US-09-850-716A-343
Sequence 343, Application US/09850716A
Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kaios, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850.716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
TYPE: PRN
ORGANISM: Homo sapiens
US-09-850-716A-343

Query Match 86.5%; Score 2379; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.2e-189;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDOQIONGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTFALSPSPALPSN 129
DB 15 PQTNLGLNSMDOQIONGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTFALSPSPALPSN 74
QY 130 TDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPPGAVIRAM 189
DB 75 TDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPPGAVIRAM 134
QY 190 PYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRSVLV 249
DB 135 PYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRSVLV 194
QY 250 PYEPPOVGEFTTVLYNFMCNSSCVGAMNRPILLIIVTLETROGVYGRRCFARICACP 309
DB 195 PYEPPOVGEFTTVLYNFMCNSSCVGAMNRPILLIIVTLETROGVYGRRCFARICACP 254
QY 310 GRKRADEDSIRKQOYSDSTKNGDGTKRPRONTHTGIOMTSIKRRSPDDELLYLVRGR 369
DB 255 GRKRADEDSIRKQOYSDSTKNGDGTKRPRONTHTGIOMTSIKRRSPDDELLYLVRGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETRYROQOQOHOHLQKTSIOSPSSYGNSSPPLNK 429
DB 315 EYEMLLKIKESLELMQYLPQHTIETRYROQOQOHOHLQKTSIOSPSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQILNQORNALPPTIIPDGMGANIPMGTHMPAGDMGLSPTQALPPP 489
DB 375 MNSMNLKPSVSQILNQORNALPPTIIPDGMGANIPMGTHMPAGDMGLSPTQALPPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVRIKOV 516
DB 435 LSMSTSHCTPPPPYPTDCSIVRIKOV 461

RESULT 12

US-09-897-778-343
Sequence 343, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Marnetakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedicak, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Pecham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897.778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 343
LENGTH: 461
TYPE: PRN
ORGANISM: Homo sapiens
US-09-897-778-343

Query Match 86.5%; Score 2379; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.2e-189;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDOQIONGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTFALSPSPALPSN 129
DB 15 PQTNLGLNSMDOQIONGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTFALSPSPALPSN 74
QY 130 TDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPPGAVIRAM 189
DB 75 TDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPPGAVIRAM 134
QY 190 PYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRSVLV 249

```

Db      135 PYVKAKEHVEVYVRCRPNHLSREFNEQIAPPSHLIRVEGNSHAQYVEDDITGRQSVLV 194
      250 PYEPPOVGETTEFTVLYNFMCMSSCVGNNRRPILIIYLETLRDGOVLGRRCFEARICACP 309
      195 PYEPPOVGETTEFTVLYNFMCMSSCVGNNRRPILIIYLETLRDGOVLGRRCFEARICACP 254
Qy      310 GRDKRADSDSIRKQOVSDSTKNGDGTKRPFQONTHGLOMTSIRKRRSPDDELIVPVGR 369
      255 GRDKRADSDSIRKQOVSDSTKNGDGTKRPFQONTHGLOMTSIRKRRSPDDELIVPVGR 314
Qy      370 EYEMLLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
      315 EYEMLLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Db      430 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPPP 489
      375 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPPP 434
Qy      490 LSMSTSHCTPPPPYPTDCSTIV 516
      435 LSMSTSHCTPPPPYPTDCSTIV 461

```

RESULT 13

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US-09-735-705-338
; Sequence 338, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-338

```

```

Query Match      84.8%; Score 2333; DB 9; Length 586;
Best Local Similarity 99.3%; Pred. No. 1.2e-185;
Matches 439; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      70 PÖYTNGLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAOPSSPTFDALSPSPALPSN 129
      15 PÖYTNGLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAOPSSPTFDALSPSPALPSN 74
Db      130 TDYGPSPFDVSVFOOOSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 189
      75 TDYGPSPFDVSVFOOOSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 134
Qy      190 PYVKAKEHVEVYVRCRPNHLSREFNEQIAPPSHLIRVEGNSHAQYVEDDITGRQSVLV 249
      135 PYVKAKEHVEVYVRCRPNHLSREFNEQIAPPSHLIRVEGNSHAQYVEDDITGRQSVLV 194
Qy      250 PYEPPOVGETTEFTVLYNFMCMSSCVGNNRRPILIIYLETLRDGOVLGRRCFEARICACP 309
      195 PYEPPOVGETTEFTVLYNFMCMSSCVGNNRRPILIIYLETLRDGOVLGRRCFEARICACP 254
Db

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Qy      310 GRDKRADSDSIRKQOVSDSTKNGDGTKRPFQONTHGLOMTSIRKRRSPDDELIVPVGR 369
      255 GRDKRADSDSIRKQOVSDSTKNGDGTKRPFQONTHGLOMTSIRKRRSPDDELIVPVGR 314
Qy      370 EYEMLLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
      315 EYEMLLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Db      430 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPPP 489
      375 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPPP 434
Qy      490 LSMSTSHCTPPPPYPTDCSTIV 511
      435 LSMSTSHCTPPPPYPTDCSTIV 456
Db

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RESULT 14

```

US-09-850-716A-338
; Sequence 338, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: McNeill, Michael D.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-338

```

```

Query Match      84.8%; Score 2333; DB 10; Length 586;
Best Local Similarity 99.3%; Pred. No. 1.2e-185;
Matches 439; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      70 PÖYTNGLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAOPSSPTFDALSPSPALPSN 129
      15 PÖYTNGLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAOPSSPTFDALSPSPALPSN 74
Db      130 TDYGPSPFDVSVFOOOSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 189
      75 TDYGPSPFDVSVFOOOSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 134
Qy      190 PYVKAKEHVEVYVRCRPNHLSREFNEQIAPPSHLIRVEGNSHAQYVEDDITGRQSVLV 249
      135 PYVKAKEHVEVYVRCRPNHLSREFNEQIAPPSHLIRVEGNSHAQYVEDDITGRQSVLV 194
Qy      250 PYEPPOVGETTEFTVLYNFMCMSSCVGNNRRPILIIYLETLRDGOVLGRRCFEARICACP 309
      195 PYEPPOVGETTEFTVLYNFMCMSSCVGNNRRPILIIYLETLRDGOVLGRRCFEARICACP 254
Db      310 GRDKRADSDSIRKQOVSDSTKNGDGTKRPFQONTHGLOMTSIRKRRSPDDELIVPVGR 369
      255 GRDKRADSDSIRKQOVSDSTKNGDGTKRPFQONTHGLOMTSIRKRRSPDDELIVPVGR 314
Qy      370 EYEMLLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
      315 EYEMLLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Db      430 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPPP 489
      375 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPPP 434
Qy      490 LSMSTSHCTPPPPYPTDCSTIV 511
      435 LSMSTSHCTPPPPYPTDCSTIV 456
Db

```

Db 435 LSMSTSHCTPPPTDCSIV 456

RESULT 15

US-09-897-778-338
: Sequence 338. Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 338
: LENGTH: 386
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-897-778-338

Query Match 84.88; Score 2333; DB 10; Length 586;
Best Local Similarity 99.38; Pred. No. 1.2e-185;
Matches 439; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 70 PÖYTNGLNSMOQIÖNSSSTSPYNTDHAÖNSVTAPSPYADSSFTDALSPSPATPSN 129
Db 15 PÖYTNGLNSMOQIÖNSSSTSPYNTDHAÖNSVTAPSPYADSSFTDALSPSPATPSN 74
QY 130 TDYPGPHSPDVSFQÖSSTAKSATWTYSTEKLKLYCQIAKTCPIQIKVMTPPÖGAVIRAM 189
Db 75 TDYPGPHSPDVSFQÖSSTAKSATWTYSTEKLKLYCQIAKTCPIQIKVMTPPÖGAVIRAM 134
QY 190 PVYKKAHVTEVYKRCPNHLSREFNÖGÖIAPPSHLIRVGNSHAQYVEDPITGRÖSVLY 249
Db 135 PVYKKAHVTEVYKRCPNHLSREFNÖGÖIAPPSHLIRVGNSHAQYVEDPITGRÖSVLY 194
QY 250 PYEPPOVGTFTTYLVNFMÖNSSCVGÖMNRPILITVLTETRDÖQVYGRRCFEARICACP 309
Db 195 PYEPPOVGTFTTYLVNFMÖNSSCVGÖMNRPILITVLTETRDÖQVYGRRCFEARICACP 254
QY 310 GRDRKADEDSIRKÖQVSDSTKNGDGTKRPRÖNTHGIÖMTSIRKRSRSPDELLYLPVGR 369
Db 255 GRDRKADEDSIRKÖQVSDSTKNGDGTKRPRÖNTHGIÖMTSIRKRSRSPDELLYLPVGR 314
QY 370 EYEMELKIKESLEMQYLPHÖTIEYRÖQÖQÖHÖHLÖKÖTISÖSSSYGNSSPPLNK 429
Db 315 EYEMELKIKESLEMQYLPHÖTIEYRÖQÖQÖHÖHLÖKÖTISÖSSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSÖLINPÖQRNALPTPTIPDGMÖNIPMÖGTHMPMAGDMNGLSPTÖALPP 489
Db 375 MNSMNLKPSVSÖLINPÖQRNALPTPTIPDGMÖNIPMÖGTHMPMAGDMNGLSPTÖALPP 434
QY 490 LSMSTSHCTPPPTDCSIV 511
Db 435 LSMSTSHCTPPPTDCSIV 456

Search completed: August 7, 2003, 09:57:07
Job time : 24.0296 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:03 ; Search time 16.268 Seconds

(without alignments)
3050.350 Million cell updates/sec

Title: US-09-538-106-14

Perfect score: 2751

Sequence: 1 MSQSTQNEFLSPVEFGHIV.....HCRPPPPYPTDCSIVRIIMOV 516

Scoring table:

BLOSUM62.
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR_76: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	847.5	30.8	396	1 JH0631	cellular tumor ant
2	777.5	28.3	363	1 A29376	cellular tumor ant
3	764.5	27.8	367	1 S02193	cellular tumor ant
4	740	26.9	386	1 S51648	cellular tumor ant
5	735	26.7	391	1 S02192	cellular tumor ant
6	719	26.1	396	1 JH0633	cellular tumor ant
7	718	26.1	393	1 DNH053	cellular tumor ant
8	717	26.1	390	1 DNMS53	cellular tumor ant
9	714.5	26.0	393	1 S06594	cellular tumor ant
10	703.5	25.6	381	2 S38824	cellular tumor ant
11	703.5	25.6	393	1 J06176	tumor suppressor p
12	699.5	25.4	391	2 J06193	cellular tumor p
13	259.5	9.4	77	2 I46226	cellular tumor ant
14	144.5	5.3	1621	2 T15264	hypothetical prote
15	140	5.1	1520	1 TVFEA	protein-tyrosine k
16	135.5	4.9	1081	2 S66736	transcription acti
17	135.5	4.9	2578	2 A56922	transcription fact
18	135	4.9	925	2 T19361	hypothetical prote
19	130.5	4.7	628	2 S19150	hypothetical prote
20	129	4.7	964	2 T41547	hypothetical prote
21	128.5	4.7	2529	2 A56923	transcription fact
22	127.5	4.6	628	2 S01955	hypothetical prote
23	127.5	4.6	963	2 T40290	hypothetical prote
24	126.5	4.6	628	2 J00110	hypothetical prote
25	126.5	4.6	1051	2 G59436	hypothetical prote
26	126.5	4.6	1062	2 G86325	KIAA1304 protein l
27	126	4.6	590	2 G44068	hypothetical prote
28	126	4.6	2897	2 B48666	cell proliferation
29	126	4.6	3256	2 A48666	cell proliferation

30	125	4.5	724	2 T47149	hypothetical prote
31	125	4.5	799	2 JH0797	castor protein - f
32	123	4.5	1572	2 S45251	SNF2alpha protein
33	122.5	4.5	969	2 T15446	hypothetical prote
34	122	4.4	864	2 H85335	hypothetical prote
35	122	4.4	864	2 T04518	hypothetical prote
36	120.5	4.4	901	2 J06093	dead ringer nuclea
37	120	4.4	561	2 T14792	hypothetical prote
38	120	4.4	832	2 S36230	hypothetical prote
39	120	4.4	1211	2 T42230	hypothetical prote
40	119.5	4.3	596	2 T03908	Af4 protein - mous
41	119.5	4.3	1706	2 I84499	hypothetical prote
42	119.5	4.3	1819	2 T32008	zinc finger protei
43	118.5	4.3	513	2 T41011	hypothetical prote
44	118.5	4.3	884	2 T40690	hypothetical prote
45	118	4.3	792	2 T26050	hypothetical prote

ALIGNMENTS

RESULT 1

Query Match	30.8%; Score 847.5; DB 1; Length 396;
Best Local Similarity	45.4%; Pred. No. 1,1e-52;
Matches	181; Conservative 61; Mismatches 102; Indels 55; Gaps 10;
QY	11 LSPVEYQHIMDFLEQPGICVQPIDLNFVDESEDAATNKIEISMDCIMQSDSLDPMMP 70
DB	12 LSOESFEDLM-----KMNINLVAVQPPETE-----SMV 39
QY	71 QYINGLANSMDQIQNGSSSTPYNTDHAQNSVTAPSPYAQPS-STFDALS-PSPAIPS 128
DB	40 GYDNF---MMEAPLQ-----VEFPSSLEFVSATPPAPQPSISTLDGSPPTSTVPT 87
QY	129 NTDPYGPSPFVDSFOQSSSTAKSATWTYSTELKIKICQIAKCPIDIKWTPPGQAVIRA 188
DB	88 TSDYFAGLGFQIRFQSSSTAKSVCTTYTPDLKLKFCQIAKCPVIVVDHPPPAVYRA 147
QY	189 MPVYKAAHYEVYKRCNHELSPENQGLAPSHLIRVEGNSHAQYVEDEPTGRQSVL 248
DB	148 LAIYKLLSDVADVVRCPHQHSTSENNGP-APRHLVRAVEGNSQSEYMEQDNTLRHSVL 206
QY	249 VPYEPVQGTFTTYLYNFMKNSSCVGMNRRPILIIYTLTRDQVLYGRCFEAKRICAC 308
DB	207 VPYEPVQGSCTTYLYNFMKNSSCVGMNRRPILIIYTLTRDQVLYGRCFEAKRICAC 266
QY	309 PGRDKADEDSIRKQ--VSDSTKNGSGTKRPFG-NTHGLOMSTIKKRS---PPDE 360
DB	267 PGRDKTEINLKQOETTLTKTPPAQGIKRAKAEASLPADQPSAKTKTSSPAVSDE 326
QY	361 LLYLPVGRGRETVEMLKIKESLELMQVYPOHTIETTYRQO 399
DB	327 IYTLQIRGEKEYEMLKRFNDSLELVPADADKTRCK 365

```

RESULT 2
A29376
cellular tumor antigen p53 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A29376; S61531; S72313; I51639
R:Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.
Oncogene 1, 71-78, 1987
A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein
A:Reference number: A29376; MUID:88143684; PMID:2830576
A:Molecule type: mRNA
A:Residues: 1-363 <SCD>
A:Cross-references: EMBL:X05191; NID:964961; PIDN:CAA28821.1; PID:964962
R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.
Oncogene 9, 109-120, 1994
A:Title: Overexpression of wild-type p53 interferes with normal development in Xenopus
A:Reference number: I51639; MUID:94134403; PMID:8302570
A:Accession: S61531
A:Molecule type: mRNA
A:Residues: 1-293, 295-363 <HOE>
A:Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514
R:Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knoechel, W.
submitted to the EMBL data library, March 1994
A:Accession: S72313
A:Molecule type: mRNA
A:Residues: 1-51, 'S', 53-70, 72-293, 295-363 <HOW>
A:Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F.150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F.362/Binding site: phospho-yl-RNA (Ser) (covalent) #status predicted

Query Match      28.3%, Score 777.5; DB 1; Length 363;
Best Local Similarity 42.5%; Pred. No. 9,16-48;
Matches 171; Conservative 55; Mismatches 95; Indels 81; Gaps 11;

OY      2  SOSTQTNEFLSPVEFONHMFLEQPI-----CSYQPIDLNFDEDESGATKIKIISDCI  57
Db      4  SSETGMDDPLSOFETFDIMSLPPDLQTVTRLDNLNLS-EPDPY-----LAADMT  52

OY      58  RMQDSDLSDDPMPQYTNGLNLSMDQQLQNGSSSTSPYNTDHAQNSVTAQSPAPSTF  117
Db      53  VLQE-----GLMGN-----AVPIYT-  67

OY      118 DALSPRAIPENTYIPRGHSFDVFSQSSSTAKSATWYTFELKLLCYOIAKTCIQIKVM  177
Db      68  -----SCAVPSTDYAGKYGLDLPQONGAKSVTCYSPRLNLFQOLATCPILRVVE  122

OY      178 TPPEGAATVIRAMPYVYKKAHEHYEVVRCRPNIELREFNEGOIAPSHLIRVGNSHAOYV  237
Db      123 SPPRGSLRATATYKKKSEHAVEVYKRCRPHNERVEGE-DAAPSHLMRQGNLQAYM  181

OY      238 EDPIITGROSVLYPRPEPVQTEFTTYLYLNFMCNCCVCGAMRRPILITVLETRDGOYLG  297
Db      182 EDVNSGRSHVCPYPEGPGVTECTTYLYNYMCNCCSGMGAMRRPILITVLETRDGOYLG  241

OY      298 RRCFEARACAPGDRKAKDEDS-IRKQOVSDSTNGSGTKRPFQONNH--GIQWTSIKKR  354
Db      242 RRCFEARACAPGDRKRIEEDNYTKKKGKLGSKG-----RELHHPSSSEPPLEPKR  292

OY      355 R---SPDELLYLPEVGRETYEMDLKIKESLELQAYLPQNTI  393
Db      293 LVVVDDDEBEITLRIKGRSRYEMIKLNDALDELQESLDDQKV  334

```

cellular tumor antigen p53 - chicken
N.Alternate names: nuclear oncprotein p53
C.Species: Gallus gallus (chicken)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
J.Accession: S02193
R.Sousai, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P.
A.Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncprotein.
A.Reference number: S02193; MUID:89083584; PMID:3060861
A.Accession: S02193
A.Molecule type: mRNA
A.Residues: 1..367 <SD>
A.Cross-references: EMBL:X13057; NID:G63740; PID:NCAA1456.1; PID:G63741
C:Superfamily: cellular tumor antigen p53
C.Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosphoprotein; zinc finger
F.I66/I64,I24/I28/Binding site: zinc (Zn), His, Cys, Gln #status predicted
F.I66/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 27.8%; Score 764.5; DB 1; Length 367;
Best Local Similarity 44.6%; Pred. No. 7,7e+47;
Matches 169; Conservative 50; Mismatches 105; Indels 55; Caps 10;

DQ 11 LSP-EVPGHINDPLEGPICVPIDLNFVDPSDGAFTNKTEISMDCIROMDSLSBPM 69
||| || | : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 9 LEPTVEFDLMSLMPY---SMQL-----PLPESHNMWELS---PLEPSDPPEPP 54

DY 70 PQYNLTGLTNSMDOIQINGSSSTPYNTDHQNVSVAAPSYAQPSSTFDALSPSPAIPSN 129
||| || | : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 55 PPPLPL-----AAAAAAAAAAAPPPLNP--TPPAASPVVPIST 85

DY 130 TDYGPHSFDYSFOOSTASTATWTYTELKLYCQIAKTCPIOTIKMTPPPOGANIVRAM 169
||||| || | : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 86 EDVGDDPFRRGVFEAGAKSVCTCYSPVLNVKYCRILAKCPVOVRVVAVAPGGSSLRAV 145

DY 190 PVYKAHEVTENVVKRCPRHELSEFRNGSQLAPSRLIRVGSNSHAQYVEEPITRGOSLV 249
||||| || | : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 146 AVYKKSEHAVAEVVKRPCHHERCGGGGTGC-LAPAQHLLRVESGNPKARHHDETTKRHSVV 204

DY 250 PYEYPQVGEFFETFLVNYFMNCNSSCVGMNNRRPJLIITYLETRDGQYLGRCCFEARICAC 309
||||| || | : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 205 PEYPEEVSGDCDTVALYNMCNCSMGMMNRRIILTILLBGQGOLLGRCRFERYVCACP 264

DY 310 GRDKRADEDSRKOQVSDSKTNKGDL-TKPFRONTHTGIOMTSIKRKRSRDDDELTYLPVR 367
||||| || | : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 265 GRDRKEIEENFK-----RGAGGAVAKRAMSPPEAPEPK-KRYLANDNDETIFYLOVR 316

DY 368 GREYEMLTKTESLETLMQ 386
||| || | : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 317 GRRTYEMKLKETNEALQLAE 335

RESULT 4
S51648
cellular tumor antigen p53 - bovine
N.Alternate names: tumor-suppressor protein p53
C.Species: Bos primigenius taurus (cattle)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
J.CAccession: S51648
R.Dequiedt, F.; Willems, L.; Burny, A.; Ketmann, R.
submitted to the EMBL Data Library, September 1994
A.Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and its
A.Reference number: S51648
A.Accession: S51648
A>Status: preliminary
A:Molecule type: mRNA
A.Residues: 1..386 <DED>
A.Cross-references: EMBL:X81704; NID:G602332; PID:NCAA57348.1; PID:G602333
C:Key words: apoptosis; cell division control; DNA binding; homotetramer; phosphoprote
F.I66/I71,I23/I25/Binding site: zinc (Zn), His, Cys, Gln #status predicted
F.I385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 26.9%; Score 740; DB 1; Length 386;

[illegible]

```

RESULT 5
S02192      cellular tumor antigen p53 - rat
N:Alternate names: gene p53 protein; nuclear oncoprotein p53
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02192; S41149
R:Soussi, T.; de Fromental, C.C.; Breugnot, C.; May, E.
A>Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A:Reference number: 502192; MUID:89083585; PMID:3060862
A:Accession: 502192
A:Molecule type: mRNA
A:Residues: 1-391 <SOU>
A:Cross-references: EMBL:X13058; NID:956828; PIDN:CA431457.1; PID:956829
R:Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A>Title: Structure of the rat p53 tumor suppressor gene.
A:Reference number: S41149; MUID:93181268; PMID:8441680
A:Accession: S41149
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173; 'W', 175-391 <HUL>
A:Cross-references: EMBL:L07909
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:
A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F:174,177,336,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
Query Match          26.7%   Score 735; DB 1; Length 391;
Best Local Similarity 38.3%; Pred. No. 1,1e-44;
Matches 171; Conservative 72; Mismatches 134; Indels 70; Gaps 13;

OY    2  SQSTQINEF-LSPVEFGHWDFLEOPICSVAPDILNFVDESEDGATNKIEISMDCIQM 60
      ||| : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    4  SQSDMSTELPSQETFFSCLMKRL--PPDDILP-----TTATGSPNSME----- 44

OY    61 DSDSLDMMPQYTNGLGISMDQIONGSSSTSYNTDHQNSTAAFSPYAPSFDAL 120
      ||| : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    45 -----DLFLPDV-AELLEGEELQVSAPPAOEGTE-----APPVAASATWPL 91

121 SPSPAISNDTPGPHSFDSFOQSSTAASKATWTYSTELKLKYLCOIAKTCPITQIKVTWP 180

```

Db	92	SSS--VP	SOKT	YOG	ANG	FH	GL	FG	LS	GA	SV	MC	TS	IS	LN	KL	FO	QA	LT	CV	OL	AM	VT	ST	149									
Qy	181	POGA	VI	RA	MP	AV	YK	KA	HE	TE	VE	VK	RC	PN	HE	LS	RE	NE	GO	-I	AP	SH	L	RV	EG	NS	HA	OY	VED	239				
Db	150	PE	BT	RA	MA	AI	YK	KS	QH	ME	TE	VR	RC	PN	HE	---	RC	SD	GO	GL	AR	PO	HL	IR	VB	EN	PA	VE	LD	206				
Qy	240	PI	TR	GO	SV	LV	PI	EP	PO	VG	TE	FT	TY	LV	LM	CNS	SC	YG	GN	RR	PI	LI	YT	LE	TR	GO	VI	GR	299					
Db	207	RO	FR	SH	SV	VV	PE	PP	EV	GS	DY	TT	HY	KW	CNS	SC	GG	NN	RR	PI	LI	IT	LE	DS	CN	LL	GR	266						
Qy	300	CE	FA	RI	CA	CP	GR	DR	KA	DE	DS	IR	KO	OV	SO	ST	KM	GD	ST	KR	PP	ON	TH	GI	OM	TS	IK	RR	P	358				
Db	267	SE	VE	RV	CA	CP	GR	DR	KE	EN	FR	KK	BE	CH	EP	EL	PS	GA	KAL	PT	---	SS	PQ	OK	K	PL	322							
Qy	359	DE	LL	Y	P	VC	RE	TE	Y	EM	L	K	ES	LE	MO	Y	P	OH	TI	ET	Y	R	O	O	O	O	H	L	L	O	K	OTS	IPS	418
Db	323	GE	Y	T	L	K	I	R	O	R	E	F	E	M	F	E	L	N	A	L	E	L	---	D	A	R	A	E	S	G	359			
Qy	419	SY	GN	SS	P	L	N	K	---	M	S	N	K	L	P	S	V	S	O	L	442													
Db	360	S	R	A	H	S	S	P	P	K	T	K	G	O	S	T	S	R	K	K	P	I	M	I	K	Y	386							

QY	Db	Query Match	Best Local Similarity	Matches 154:	Conservative 59:	Mismatches 127:	Indels 34:	Gaps 6:
QY	11	LSPEVQHIMDFLOPICSVQPIDLNFVDEPSEEDGATNKRIEISMDICRMODSLDSDPMWP 70	26.18; Score 719; DB 1; Length 396;	41.28; Pred. No. 1.5e-43;				
Db	14	LSQETFSDLMKLL-----PPNNVLSI-----LBSDSIEELFL 46						
QY	71	QYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIFSNT 130						
Db	47	SENVAQWLEDEGELALQSSAAAAAPAPAAEDPVAETPAPVASAPATWPLSSS--VPSYK 104						
QY	131	DYRPHSPFDVSGQSSATKATWTYSPELKKLYQIAKTCGICQIKWMPPRQGVATIRAP 190						
Db	105	TYQSDYIGFRGLFHSIGTAKSVTCIYSPSLNKLFCQLAKTCIPQVLWVSTSTPPGRTVRAMA 164						
QY	191	VYKKAHEVTEVVKRCPHNELSRPNEGQIAPPSHLIRVEGNSHAQYVEDPIYTRQSVLP 250						
Db	165	IYKRLQYMTVEVRCRPHHERSE--GDC-LAPQRLIRVEGNSHAQYLEDKQTFRHSVVP 222						
QY	251	YEPQVQTEETFTVLYNMCNCSQVCGNNRRPILITVLEFRDQGVLETRQCFEATICACPG 310						
Db	223	YEPEVQSDCTTHYNTNMCNCSQVCGNNRRPILITVLEFRDQGVLETRQCFEATICACPG 282						
QY	311	RRRAADSDSIRKQVQSVSTKNGDCTKRRPFRONTGIIQMTSIRKRSFDDLELLYPVGRE 370						

Db 283 RDRTEKRNFKGCEPCELPKSAKRALPTNT---SSSPQPKRKTLIDGEXYTLKINGOE 339
QY 371 TYEMLKIKESIEL 384
::: : : : :
Db 340 RKMFOELNFAEL 353

RESULT 7
DNHUS3
cellular tumor antigen p53 [validated] - human
N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppressor
C:Species: Homo sapiens (man)
C:Date: 05-Oct-1968 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C:Accession: A52224; A43073; J04336; S40773; S42669; A22837; A55060; A25397; S424905; I58354; I78850; I52681; S60153
R:Lamb, P.; Crawford, L.
Mol. Cell. Biol. 6, 1379-1385, 1986
A:Title: Characterization of the human p53 gene.
A:Reference number: A25224; MUID:87064416; PMID:2946935
A:Accession: A25224
A:Molecule type: DNA
A:Residues: 1-393 <LAMB>
A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AA59987.1; PIT
R:Buchanan, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
Gene 70, 245-252, 1988
A:Title: A variation in the structure of the protein-coding region of the human p53 gene
A:Reference number: J04336; MUID:89108008; PMID:2905688
A:Accession: A43073
A:Molecule type: DNA
A:Residues: 1-393 <BUC2>
A:Cross-references: EMBL:M22898; NID:g189474
A:Note: This 72-Avg allele appears to be about 5 times more frequent than the 72-Pro allele
A:Accession: J04336
A:Molecule type: DNA
A:Residues: 1-71, 'P', 73-393 <BUC2>
A:Cross-references: EMBL:M22898; NID:g189474; PIDN:AA59988.1; PID:g189476
R:Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.
Submitted to the EMBL Data Library, August 1990
A:Reference number: S40773
A:Accession: S40773
A:Molecule type: DNA
A:Residues: 1-393 <CHU>
A:Cross-references: EMBL:X54156; NID:g35213; PIDN:CA438095.1; PID:g35214
R:Melishewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, S.
EMBO J. 3, 3257-3262, 1984
A:Title: Isolation and characterization of a human p53 cDNA clone: expression of the human p53
A:Reference number: S42669; MUID:85126934; PMID:6396087
A:Accession: S42669
A:Molecule type: mRNA
A:Residues: 101-393 <MK11>
A:Cross-references: EMBL:X01405; NID:g35215; PIDN:CA42652.1; PID:g642241
R:Zakut-Houri, R.; Bielenz-Tadmor, B.; Givol, D.; Oren, M.
EMBO J. 4, 1251-1255, 1985
A:Title: Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.
A:Reference number: A22837; MUID:85230577; PMID:4006916
A:Accession: A22837
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-393 <ZAK>
A:Cross-references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CA426306.1; PID:g35210
Mol. Cell. Biol. 5, 1601-1610, 1985
R:Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tumor antigen p53
A:Reference number: A55060; MUID:85267676; PMID:3894933
A:Accession: A55060
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-272, 'H', 274-393 <HAK>
A:Cross-references: GB:R03199; NID:g189478; PIDN:AA59989.1; PID:g189479
R:Harbisi, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Aral, N.; Rotter, V.
Mol. Cell. Biol. 6, 4650-4656, 1986
A:Title: Molecular basis for heterogeneity of the human p53 protein.
A:Reference number: A93086; MUID:87089826; PMID:3025664

A:Accession: A25397
A:Molecule type: mRNA
A:Residues: 1-78, 'T', 80-393 <HAR1>
A:Cross-references: EMBL:M14694; NID:g339813; PIDN:AA61211.1; PID:g339814
A:Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
A:Accession: B25397
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-78, 'T', 80-393 <HAR2>
A:Cross-references: EMBL:M14695; NID:g339815; PIDN:AA61212.1; PID:g339816
A:Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
R:Malashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
Mol. Cell. Biol. 7, 961-963, 1987
A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.
A:Reference number: S42452; MUID:87144273; PMID:3547088
A:Accession: S42452
A:Molecule type: DNA
A:Residues: 66-71, 'P', 73-79 <MK12>
A:Experimental source: clone lambda C113
A:Note: 72-Cys was also found, and appears to represent a polymorphism
A:Accession: S42453
A:Molecule type: DNA
A:Residues: 66-79 <MK13>
A:Experimental source: clone J6K
R:Farrell, P.J.; Allen, G.J.; Shanahan, F.; Vonsden, K.H.; Crook, T.
EMBO J. 10, 2879-2887, 1991
A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
A:Reference number: I38082; MUID:92007731; PMID:1915267
A:Accession: I38082
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189, 'LSTLSSEKKEIVSWTMTETLFDIYVWCNPSRLRLALT', 'VPSSTTTCVTPANAA' <F01>
A:Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433
A:Note: deletion of a C nucleotide causes a frameshift at position 566
A:Accession: I38083
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-192, 'R', 194-393 <F02>
A:Cross-references: EMBL:X60011; NID:g506434; PIDN:CAA42626.1; PID:g506435
A:Accession: I38084
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-245, 'T', 247-393 <F04>
A:Cross-references: EMBL:X60013; NID:g506438; PIDN:CAA42628.1; PID:g506439
A:Accession: I38086
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-236, 'I', 238-393 <F05>
A:Cross-references: EMBL:X60014; NID:g506440; PIDN:CAA42629.1; PID:g506441
A:Accession: I38087
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F06>
A:Cross-references: EMBL:X60015; NID:g506442; PIDN:CAA42630.1; PID:g506443
A:Accession: I38088
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
A:Cross-references: EMBL:X60016; NID:g506444; PIDN:CAA42631.1; PID:g506445
A:Accession: I38089
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F08>
A:Cross-references: EMBL:X60017; NID:g506446; PIDN:CAA42632.1; PID:g506447
A:Accession: I38090
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
A:Cross-references: EMBL:X60018; NID:g506448; PIDN:CAA42633.1; PID:g506449

A:Accession: 138091
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212, 'Q', 214-393 <P10>
 A:Cross-references: EMBL:X60019; NID:g506450; PIDN:CAA2634.1; PID:g506451
 A:Accession: 138092
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-253, 'D', 255-393 <P11>
 A:Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA2635.1; PID:g506453
 A:Note: all sequences submitted to the EMBL/genbank/DBJ databases June 1991
 R:Rutledge, P.A.; Barrett, J.C.; Wiseman, R.W.
 Nucleic Acids Res. 19, 6977, 1991
 A:Title: An Alu polymorphism intragenic to the TP53 gene.
 A:Reference number: 138093; MUID:92107726; PMID:1762941
 A:Accession: 138093
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-393 <F07>
 A:Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
 R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakatani, T.
 Cancer Res. 51, 5800-5805, 1991
 A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell line
 A:Reference number: A44905; MUID:92034678; PMID:1933850
 A:Accession: A44905
 A:Molecule type: DNA
 A:Residues: 246-247, 'W', 249-250 <YAM>
 A:Cross-references: GB:S63157; NID:g237829; PIDN:AA20140.1; PID:g237830
 A:Note: sequence extracted from NCBI Backbone (NCBI:63157, NCBI:63158)
 R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
 Oncogene 6, 1067-1071, 1991
 A:Title: Use of the single strand conformation polymorphism technique and PCR to detect
 A:Reference number: 158354; MUID:91296386; PMID:1646702
 A:Accession: 158354
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 244-247, 'W', 249-252 <HEN1>
 A:Cross-references: GB:S41969; NID:g1679931; PIDN:AA19324.1; PID:g232814
 A:Accession: 178850
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 274-277, 'S', 279-282 <HEN2>
 A:Cross-references: GB:S41977; NID:g1679932; PIDN:AA19325.1; PID:g232816
 R:Chow, V.T.; Quek, R.H.; Tock, E.P.C.
 Cancer Lett. 73, 141-148, 1993
 A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphobla
 A:Reference number: 152681; MUID:94036762; PMID:8221626
 A:Accession: 152681
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 327-331, 'D', 333-393 <CHO>
 A:Cross-references: GB:S66666; NID:g436292; PIDN:AA28601.1; PID:g436293
 A:Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymph
 R:Peterson, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
 Mol. Gen. Genet. 249, 425-431, 1995
 A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragme
 A:Reference number: 560151; MUID:96133682; PMID:8552047
 A:Accession: 560151
 A:Molecule type: DNA
 A:Residues: 3-44 <PET>
 R:Dang, C.V.; Lee, W.M.F.
 J. Biol. Chem. 264, 18019-18023, 1989
 A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, N-myc, p53, HSP70,

Query Match 26.1%; Score 718; DB 1; Length 393;
 Best Local Similarity 38.4%; Pred. No. 1.7e-43;
 Matches 163; Conservative 69; Mismatches 132; Indels 60; Gaps 12;

11 LSPFQHIWFLQPGICVGPIDLPFDEPSEDAATKIKLSMCIKMOQSDLSDPMP 70
 14 LQFETSDMLKLP-----NNVLSPLPSOAMDMLSPDIDQWFTL--DP--- 58

71 QYTNGLINSMDOQIQNGSSSTPYNTDHAQNSVYAPSPYAPSSSTFDALSP----SPA 126
 59 -----GPDAPRMPAPAPR--VAPAP--AAPTAAPAPASWLLSSV 97
 127 PSNTDYPGPHSFVDSFOQSTAKSATYTWSTELKLYQIAKTCPIQIKVMPPOGAVI 186
 98 PSQKTYGSGYGRFLGFLHSGTAKSVTCYSPALNMFQIAKTCVQLMVDSTPPGTRV 157
 167 RAMPYKKAENHTEVVRKCPNHLRENEGIAAPSHLIRNGSHQYVDPITGQS 246
 158 RAMLYKQSQHNTKEVVRCPNHE--RCSDSODLAPQHLIRVEGMLRYEVLDDRTFRHS 215
 247 VLVPYEPVOVGTEFTVLYNFMCSGVMRRPILITVLETEDGQVLRGRCPEARIC 306
 216 VVPEYEPPEVSGDCITTHYNKCNSSGGMRRILITLEDSSGNLGNSTEVAVC 275
 276 ACPGRDRRTREENLRKKGEPHHELPPGSTKRALPNNT-----SSPQPKKPLDGEYFTLQ 331
 307 ACPGRDRKADEDSIRKQVSDSTKNGDCTKRPFRONTGCIOMTSIRKRRSP--DDELYLP 365
 366 VGRGTYEMLKIKESLELMQYLP-----QHT--IEYRQOQOQHHLQKQTSIQ 415
 332 IGRGRFEMFRELNALLELKDQAQKGEPSGSHSHLSKKGQSTSHKKLMFR--TE 388
 416 SPSS 419
 389 GPD 392

RESULT 8

DNMS53

cellular tumor antigen p53 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000

C:Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703

R:Biernz, B.; Zakut-Houri, R.; Gliwyl, D.; Oren, M.

EMBO J. 3, 2179-2183, 1984

A:Title: Analysis of the gene coding for the murine cellular tumor antigen p53.

A:Reference number: A22739; MUID:85027173; PMID:6092064

A:Accession: A22739

A:Molecule type: DNA

A:Residues: 1-134, 'V', 136-390 <BIE>

A:Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1; PID:g871421; GB:X01237;

R:Chumakov, P.M.

Bioorg. Khim. 13, 1691-1694, 1987

A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.

A:Reference number: S06336; MUID:88221682; PMID:3329909

A:Accession: S06336

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-134, 'V', 136-390 <CHD>

R:Zakut-Houri, R.; Oren, M.; Biernz, B.; Lavie, V.; Hazum, S.; Gliwyl, D.

Nature 306, 594-597, 1983

A:Title: A single gene and a pseudogene for the cellular tumor antigen p53.

A:Reference number: A02684; MUID:84068204; PMID:6646235

A:Accession: A02684

A:Molecule type: mRNA

A:Residues: 1-159, 'H', 161-167, 'G', 169-233, 'T', 235-390 <ZAK>

A:Cross-references: GB:X01237; GB:X01700; NID:g53575

R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

Mol. Cell. Biol. 6, 3232-3239, 1986

A:Title: Immunologically distinct p53 molecules generated by alternative splicing.

A:Reference number: S38822; MUID:87064640; PMID:3023970

A:Accession: S38822

A:Molecule type: mRNA

A:Residues: 1-390 <ARA1>

A:Cross-references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1; PID:g200199

A:Accession: S38823

A:Molecule type: mRNA

A:Residues: 1-167, 'G', 169-233, 'T', 235-390 <ARA2>

A:Cross-references: EMBL:M13873

R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

C:Superfamily: Drosophila protein-tyrosine kinase abl; protein kinase homology; SH2 homod
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transforming p
F:211-260/Domain: SH3 homology <SH3>
F:271-363/Domain: SH2 homology <SH2>
F:386-646/Domain: protein kinase homology <KIN>
F:394-402/Region: protein kinase ATP-binding motif
F:417/Active site: Lys #status predicted

Query Match		5.1%; Score 140; DB 1; Length 1520;
Best Local Similarity		21.2%; Pred. No. 0.13;
Matches 120; Conservative		71; Mismatches 230; Indels 146; Gaps 24;
Qy	26	PICSVQPIDL-----NFVDEPSEDEGATNKIEIMCIRMQDSLDSDPMWPQYTNLGLL 78
Db	608	PGCPPEVYDLMRQCQWQMDATDRPTFKSIHHALE-----HMFQESSITEAVEKQ-----L 656
Qy	79	NSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYQAPSSFTFDALSPSP-----AIP 127
Db	657	NANATSSASSAPSTSGVATGGGATTTAAAGCASSSATAASLSLTPOVMVKGLPGGQALT 716
Qy	128	SNTDYPGPFSFQSSSTAKSATWTYSTEK-----KLYCOIAKTCPIQIKVMTPPP 181
Db	717	PNAHNDPHQ-----QAASTPMSETGSTYKLSFTSSQGGKGNVQMRRTTNKQKQAPPP 771
Qy	182	QGAVIRAM---PVYKKAHVTEVVKRC-----PNHELSEFNEGQIAPPSHLIRVEGNS 232
Db	772	KRTSLSSSRDSTYREEDPAN---ARCNFIDDLSTNGLARDINS-----LTQRYDS 819
Qy	233	HAQVDEPITGRQSVLPVPEPPQV-GTEFTTVLYNFMCNSSCVCGMNRRLIIVTLETR 291
Db	820	ETDPAADPDTDATGDSLEQSLSQVIAAPVTNKMQHSLSHSGGGGGIGIPRSSQQHSFKRP 879
Qy	292	DG-OVLGRCRCFEARICACPGDRKADEDSIRKQVSDSTKNGDCTKRPFRON-----TH 344
Db	880	TGTPVGNRGLETR-----QSKRSQHSQAPGPGPSTQPHGNGNGVVTSAH 926
Qy	345	GIQMTSIKKRRSPDELLY--LPVGRGRETVEMLKIKESLELMQYLPQHTIETYRQOQQ 402
Db	927	PITVGALDVMMVKQVNNRYGTLF-KGARIGAYLDSLEDSSEAPALP-----972
Qy	403	QHQLLOKQTSIQSPSSYGNSSPPLNKMNSMKNLPSVSQILINPOQ---RNALTPTTIPDG 459
Db	973	-----ATAPSLPPANGHATPPAARLN-----PKASP-IPPOQMIRSNSSGGVTQNN 1018
Qy	460	MGANIPMW-----GTHMPM-----AGDMNGLSPTQA-----LPPPLS 491
Db	1019	AAASLNKLQRHRTTEGTMTTFSSFRAGGSSSPKRSASGVASGVQALANLEFPPLD 1078
Qy	492	M---PSTSHCTPPPPPTDCSIVRIWQ 515
Db	1079	LPPPPPEEGGPPPPPPAPESAVQAIQ 1105

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Job time : 19.268 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:32:13 ; Search time 9.15074 seconds
(without alignments)
2651.784 Million' cell updates/sec

Title: US-09-538-106-14

Perfect score: 2751

Sequence: 1 MSOSTOTNEFLSPVFOHIW.....HCTPPPPYPTDCSIVRIWQV 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1464.5	53.2	636	1 P73_HUMAN	O15350 homo sapien
2	1457.5	53.0	637	1 P73_CERAE	Q9XSK8 cercopithec
3	847.5	30.8	396	1 P53_ONCMY	P25035 oncornynchu
4	819.5	29.8	369	1 P53_BARBU	Q9W678 barbus barb
5	805.5	29.3	373	1 P53_BRARE	P79734 brachydanio
6	795	28.9	376	1 P53_ICTPU	O93379 ictalurus p
7	777.5	28.3	363	1 P53_XENLA	P07193 xenopus lae
8	776	28.2	367	1 P53_TETMU	Q9W679 tetradodon m
9	771	28.0	386	1 P53_PIG	Q9TUB2 sus scrofa
10	770	28.0	386	1 P53_FELCA	P41685 felis silve
11	764.5	27.8	367	1 P53_CHICK	P10360 gallus gall
12	758.5	27.6	381	1 P53_CANFA	Q29537 canis fami
13	746.5	27.1	352	1 P53_ORYLA	P79820 oryzias lat
14	740	26.9	386	1 P53_BOVIN	Q29628 bos taurus
15	738	26.8	391	1 P53_WARMO	Q36006 marmota mon
16	735	26.7	391	1 P53_RAT	P10361 rattus norv
17	732.5	26.6	393	1 P53_CAVPO	Q9WUR6 cavia porce
18	730	26.5	393	1 P53_TUPGB	Q9TAL1 tupata glii
19	729	26.5	382	1 P53_SHEEP	P51664 ovis aries
20	719	26.1	396	1 P53_MESAU	Q00366 mesocricetu
21	718	26.1	366	1 P53_PLAFE	O12946 platichthys
22	718	26.1	393	1 P53_HUMAN	P04637 homo sapien
23	717	26.1	390	1 P53_MOUSE	P02340 mus musculu
24	715.5	26.0	393	1 P53_MACFA	P56423 macaca fasc
25	714.5	26.0	393	1 P53_CERAE	P13481 cercopithec
26	713.5	25.9	393	1 P53_WACMU	P56424 macaca mula
27	710.5	25.8	342	1 P53_XIPHE	O57538 xiphophorus
28	709.5	25.8	342	1 P53_XIPHA	Q92143 xiphophorus
29	707.5	25.7	393	1 P53_CRIGR	O09185 cricetus
30	699.5	25.4	391	1 P53_RABIT	Q95330 oryctolagus
31	696	25.3	314	1 P53_SPEBE	O64662 spermophilu
32	689.5	25.1	280	1 P53_HORSE	P79892 equus caball
33	591.5	21.5	207	1 P53_EQUAS	Q29480 equus asinu

ALIGNMENTS

RESULT 1

ID	P73_HUMAN	STANDARD;	PRT;	636 AA.
AC	O15350; O15351; Q9NTK8;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor protein p73 (p53-like transcription factor) (p53-related protein).			
GN	TP73 OR P73.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).			
RC	TISSUE-Colon.			
RX	MEDLINE-97433090; PubMed-9288759;			
RA	Kagnad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A., Minty A., Chonnet H., Lelias J.-M., Dumont X., Ferrara P., McKeon F., Caput D.;			
RA	"Monoallelically expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers.";			
RL	Cell 90:809-819(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE-99289209; PubMed-10362363;			
RA	Yoshikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagiwara K., Harris C.C.;			
RA	"Mutational analysis of p73 and p53 in human cancer cell lines.";			
RL	Oncogene 18:3415-3421(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE-98389621; PubMed-9721206;			
RA	Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B., Jenkins R., Smith D.I., Liu W.;			
RA	"Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions.";			
RL	Genomics 51:359-363(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).			
RC	TISSUE-Neuroblastoma;			
RX	MEDLINE-99021697; PubMed-9802988;			
RA	De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M., Annichiarico-Petruzzelli M., Leviero M., Melino G.;			
RA	"Two new p73 splice variants, gamma and delta, with different transcriptional activity.";			
RL	J. Exp. Med. 188:1763-1768(1998).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).			
RC	TISSUE-Breast cancer, Hepatoma, Lymphocytes, and Skin;			
RX	MEDLINE-99310938; PubMed-10381648;			
RA	De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G., Costanzo A., Leviero M., Knight R.A.;			
RA	"Additional complexity in p73: induction by mitogens in lymphoid cells and identification of two new splicing variants epsilon and zeta.";			

Cell Death Differ. 6:389-390(1999).
 [6] SEQUENCE FROM N.A. (ISOFORM KAPPA).
 RA. Thomas D.; (WAY-2000) to the EMBL/GenBank/DBJ databases.
 RL Submitted (WAY-2000) to the EMBL/GenBank/DBJ databases.
 [7] PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
 RX MEDLINE-99318135; PubMed-10391251;
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Kharbada S., Weichselbaum R., Kufe D.;
 RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
 to DNA damage.";
 RL Nature 399:814-817(1999).
 [8] ERRATUM.
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Kharbada S., Weichselbaum R., Kufe D.;
 RL Nature 400:792-792(1999).
 [9] FUNCTION.
 RX MEDLINE-99217940; PubMed-10203277;
 RA Kaelin W.G. Jr.;
 RT "The emerging p53 gene family.";
 RL J. Natl. Cancer Inst. 91:594-598(1999).
 [10] STRUCTURE BY NMR OF 439-506.
 RX MEDLINE-99380160; PubMed-10449409;
 RA Chi S.W., Aved A., Arrowsmith C.H.;
 RT "Solution structure of a conserved C-terminal domain of p73 with
 structural homology to the SAM domain.";
 RL EMBO J. 18:4438-4445(1999).
 CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
 CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
 CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
 CC PROTEIN.
 CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
 CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
 CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
 CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
 CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=7;
 CC Name=Alpha;
 CC IsoId=O15350-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=O15350-2; Sequence=VSP_006539;
 CC Name=Gamma;
 CC IsoId=O15350-3; Sequence=VSP_006540, VSP_006541;
 CC Note-The splicing of exon 11 results in a frameshift from the
 CC original reading frame;
 CC Name=Delta;
 CC IsoId=O15350-4; Sequence=VSP_006542, VSP_006543;
 CC Name=Epsilon;
 CC IsoId=O15350-5; Sequence=VSP_006544, VSP_006545;
 CC Note-The splicing of exon 11 results in a frameshift from the
 CC original reading frame. The splicing of exon 13 reverts the
 CC reading frame to the sequence of isoform Alpha;
 CC Name=Zeta;
 CC IsoId=O15350-6; Sequence=VSP_006546;
 CC Name=Kappa;
 CC IsoId=O15350-7; Sequence=VSP_006538;
 CC TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
 CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
 CC -1- INDUCTION: NOT INDUCED BY DNA DAMAGE.
 CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
 CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
 CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
 CC -1- CELL: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE
 CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
 CC IN HUMAN CANCERS. IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
 CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Y11416; CAA72220.1; -;
 DR EMBL; Y11416; CAA72221.1; -;
 DR EMBL; Y11416; CAA72219.1; -;
 DR EMBL; AF077628; AAC61887.1; -;
 DR EMBL; AF077616; AAC61887.1; JOINED.
 DR EMBL; AF077617; AAC61887.1; JOINED.
 DR EMBL; AF077618; AAC61887.1; JOINED.
 DR EMBL; AF077619; AAC61887.1; JOINED.
 DR EMBL; AF077620; AAC61887.1; JOINED.
 DR EMBL; AF077621; AAC61887.1; JOINED.
 DR EMBL; AF077624; AAC61887.1; JOINED.
 DR EMBL; AF077625; AAC61887.1; JOINED.
 DR EMBL; AF077626; AAC61887.1; JOINED.
 DR EMBL; AF077627; AAC61887.1; JOINED.
 DR EMBL; AF079094; AAD39696.1; -;
 DR EMBL; AF079082; AAD39696.1; JOINED.
 DR EMBL; AF079083; AAD39696.1; JOINED.
 DR EMBL; AF079084; AAD39696.1; JOINED.
 DR EMBL; AF079085; AAD39696.1; JOINED.
 DR EMBL; AF079086; AAD39696.1; JOINED.
 DR EMBL; AF079087; AAD39696.1; JOINED.
 DR EMBL; AF079088; AAD39696.1; JOINED.
 DR EMBL; AF079089; AAD39696.1; JOINED.
 DR EMBL; AF079090; AAD39696.1; JOINED.
 DR EMBL; AF079091; AAD39696.1; JOINED.
 DR EMBL; AF079092; AAD39696.1; JOINED.
 DR EMBL; AF079093; AAD39696.1; JOINED.
 DR PDB; 1COK; 17-AUG-99.
 DR PDB; 1DXS; 08-AUG-01.
 DR TRANSFAC; T04931; -;
 DR Genew; HGNC:12003; TP73.
 DR MIM; 601990; -;
 DR GO; GO:0003700; F:transcription factor activity; TAS.
 DR GO; GO:0008630; P:induction of apoptosis by DNA damage; TAS.
 DR GO; GO:0006298; P:mismatch repair; TAS.
 DR InterPro; IPR002117; P53.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR ProDom; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Transcription regulation; Activator; DNA-binding; Anti-oncogene;
 KW Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing;
 KW 3D-structure.
 FT DOMAIN 1 46 TRANSACTIVATION (BY SIMILARITY).
 FT DOMAIN 1 55 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 287 304 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 346 435 MEDIATES OLIGOMERIZATION (POTENTIAL).
 FT DOMAIN 168 171 POLY-PRO.
 FT DOMAIN 391 394 POLY-GLN.
 FT DOMAIN 483 486 POLY-PRO.
 FT DOMAIN 131 310 DNA-BINDING (POTENTIAL).
 FT MOD_RES 99 99 PHOSPHORYLATION (BY ABL) (IN ISOFORM
 FT BETA).
 FT VARSPIC 282 282 G -> GNTCRHWVLCGRGLSRPVLQGPSG (in
 FT isoform Kappa).
 FT FTID=VSP_006538.
 FT SELTGCGPCNCEYFTFSOGLSQIYHLNLTIEDLGALKIPE
 FT QYRMTWIRGLQDKQGHDYSTAQQLLRSSNRAATISGSGE
 FT LQQRVMEAVFRVHTITIPNRGGPGGPDWADFGDLP
 FT DCKARKQPIKEETAEIH -> RTWGP (in isoform


```
Query Match      53.2%; Score 1464.5; DB 1; Length 636;
Best Local Similarity 57.4%; Pred. No. 4.1e-91;
Matches 303; Conservative 60; Mismatches 114; Indels 51; Gaps 15;

QY 1 MSQSTQTFNEFLSPE---VFQHIWDFLEQPCISQVQIDLNFVDEPSEDGATNKI-----EIS 53
Db 1 MAQSTTT-----SPDGGTTTFEHLWSSLEP-----DSTYFDLPQSSRGNNVVGTTDSS 48

QY 54 MDCIRMODSLSDPMWQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQP 113
Db 49 MDVTHLEGMTTS-----VMAQFNLLSSTMDQMSRAASASPYTPEHAA-SVPTHSPYAQP 102

QY 114 SSTFDALSPSPAIPSNNTDYPGPHSFVDFVQSSSTAKSATWYSTELKLYCOIAKTCPIQ 173
Db 103 SSTFDTMSPAVPISNTDYPGPHFEVTFQSSSTAKSATWYSPLLKLYCOIAKTCPIQ 162

QY 174 IKVMTPPQGAIVIRAMPYKKAHVTEVVKRCPNHELREFNEGQIAPPSHLIRVEGNH 233
Db 163 IKVSTRPPPPGFAIRAMPYKKAHVTDVVKRCPNHELGRDFNEGQAPASHLIRVEGNL 222

QY 234 AQYVEDPITGRQSVLVPYEPPOVGTFTVLYNFMCMNSCVCVGMNRRPILLIIVTLETRDG 293
Db 223 SQYVDDPVTGRQSVVVVYEPPOVGTFTVLYNFMCMNSCVCVGMNRRPILLIIVTLETRDG 282

QY 294 QVLGRRCFEARICACGRDRKADEDSIRKQV--SDSTKNGDGTGRPRQNTHTGIQM--T 349
Db 283 QVLGRSFEGRICACGRDRKADEHDYREQALNESSAKNGAASKRAFQSPPAVPAALGA 342

QY 350 SIKRRSPDDDELLYLPVRGRTYEMLLKIKESLELMQVLPQHTIETVYRQOQQOQHLLQ 409
Db 343 GVKRRRHDDEDTYYLQVRGRENFEILMKLESLELMELVLPQPLVDSYRQOQQ-----LLQ 397

QY 410 KOTSIQSPSSYGNSSPPLNKN-SMNKLPSYSOLIN--PQORNALTPTTIPDGMGANIPM 466
Db 398 RPSHLQ-PPSYGVLSPMKNVHGYNQLVSPVQPPPHSSAATNMLGVPVGG-----M 452

QY 467 MGTH---WPMAGDMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 511
Db 453 LNNHGHAVPANGEMSSHSAQ-----SMVSGSHCTPPPPYHADPSLV 494

RESULT 2
P73_CERAE
ID P73_CERAE STANDARD; PRT; 637 AA.
AC Q9XSK8; Q9TSO9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor protein p73 (p53-like transcription factor) (p53-related protein).
GN TP73 OR P73.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=Kidney;
RA Caput D.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN
CC (BY SIMILARITY).
CC -!- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Alpha;
```



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Db 4 SSETGMDPLSQETFDLWSLLPDLQVTVTCRLDNLNLS-EFFDYP-----LAADMT 52
QY 58 RQMSDLSLDPMPQVNTLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTF 117
Db 53 VLQE-----GLMGN-----AVPTVT- 67
QY 118 DALSPSPAIPNTDYPGPHSFDVFSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVM 177
Db 68 -----SCAVPSTDYAGRYGLQDFQNGTAKSVCTYSTPELNKLFQCLAKTCLLVRE 122
QY 178 TTPPGQAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGQIAPSHLIRVEGNSHAQYV 237
Db 123 SPPRGSLIRATAYIKKSEHVAEVVKRCPHRSVPEGE-DAAPPShLMRVEGLQAYVM 181
QY 238 EDITGROSILVPEYEPQVGTFTVLYNFCMNSCVGMNRRPILITVLTETRGQVIG 297
Db 182 EDVNSGRHSCVPEYEPQVGTFTVLYNFCMNSCVGMNRRPILITVLTETRGQVIG 241
QY 298 RCFPEARICACPGRRKADSDS-TRKQVSDSTKNGDGTGRPFRTNTH--GIQMTSTIKR 354
Db 242 RCFEVRVACPGRRRTEEDNYTKRGLKPSGK-----RELAPPSSEPPLPKR 292
QY 355 R---SPDELLYLVRGRETYEMLLKIKESLELMQYLPQHTI 393
Db 293 LVVVDDDEEFTLRKGRSRYEMIKKUNDALEQESLDQKV 334

RESULT 8
P53_TETMU
ID P53_TETMU STANDARD; PRT; 367 AA.
AC Q9W679;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Tetraodon murex (Congo puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphs; Tetraodontiformes;
OC Tetraodontidae; Tetraodontia; Tetraodon.
OX NCBI_TaxID=94908;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-Ovary;
RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
RT "Evolutionary conservancy of p53 gene sequences in fish.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
CC EMBL; AF071571; AAD34213.1;
CC HSP; P04637; ITUP.
CC InterPro: IPR002117; P53.
CC Pfam; PF00870; P53; 1.

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DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD02681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 86 273 OLIGOMERIZATION.
FT DOMAIN 308 337 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 342 363 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 288 301 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 366
SQ SEQUENCE 367 AA; 41266 MW; AC10EEEF2F59CFD CRC64;

Query Match
Best Local Similarity 28.2%; Score 776; DB 1; Length 367;
Matches 165; Conservative 53; Mismatches 105; Indels 64; Gaps 7;

QY 11 LSPEVFOHMFLEQPCISVQPIDLNFVDEFSDEGATNKIEISMDICIRMQDSLDSPMPWP 70
Db 10 LSQDTFQDLWDVNSAP-----PIS-----TIQTAALNEAWP 41
QY 71 QYTNLGLL-NSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAISN 129
Db 42 AERQNMCMNCFMDSFTNEALFNLLP-----EPPSRDGANSSSPTVPVT 84
QY 130 TDYPPGHSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPGQAVIRAM 189
Db 85 TDYPGEGFKLRFQKSGTAKSVTSTYSEILNKLYCOLAKTSILVEVLGKDPMPGAVLRAT 144
QY 190 PVYKKAHVTEVVKPCPNHLSREFNEGQIAPSHLIRVEGNSHAQYVEDPITGROSILV 249
Db 145 AIYKTEHVAEVRRCRPHQ-----NEDSAEHRSHLIRMEGSAQYFEHPHTRQSVTV 199
QY 250 PYEPPQVCTEFTVLYNFCMNSCVGMNRRPILITVLTETRGQVLCGRFCFARICACP 309
Db 200 PYEPPQVCTEFTVLYNFCMNSCVGMNRRPILITVLTETRGQVLCGRFCFARICACP 259
QY 310 GRDKKADSDSIRKQVSDSTKNGDGTGRPFRTNTHGIQMTSTIKRRS-----PDDELLY 363
Db 260 GRDKKTEETNSTKMQ-----NDAKDAKRRKSVTPPTSTIKKSKTASSAEDNNVEYT 312
QY 364 LPVRGRETYEMLLKIKESLELMQYLPQ 390
Db 313 LQIRGRKRYEMLLKIKESLELMQYLPQ 390

RESULT 9
P53_PIG
ID P53_PIG STANDARD; PRT; 386 AA.
AC Q9TUB2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99422034; PubMed=10490836;
RA Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;
RT "Nucleotide sequence of the porcine p53 cDNA, and the detection of
RT recombinant porcine p53 expressed in vitro with a variety of p53
RT antibodies.";
RL Oncogene 18:5005-5009(1999).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.

```

```
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
CC EMBL; AF098067; AF04620.1; -.
CC HSSP; P04637; 1C26.
CC InterPro: IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PR00386; P53SUPPRESSOR.
CC ProDom; PD002681; P53; 2.
CC PROSITE; PS00348; P53; 1.
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
CC Nuclear protein; Phosphorylation; Apoptosis.
CC FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
CC FT DNA_BIND 94 285 BY SIMILARITY.
CC FT DOMAIN 318 349 OLIGOMERIZATION.
CC FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
CC FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
CC SIMILARITY).
CC FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
CC SEQUENCE 386 AA; 42862 MW; A4C3D88E8DF55162 CRC64;
CC -----
Query Match 28.0%; Score 771; DB 1; Length 386;
Best local similarity 40.3%; Pred. No. 8.3e-45;
Matches 166; Conservative 68; Mismatches 124; Indels 54; Gaps 9;
QY 11 LSPEVFOHLEQPCISQVPIDLNFVDEPSEDGATNKIEISMDICRMQSDLSLPPMP 70
DB 14 LSQETSDLWKLPE-----NNLSSELSLAANVNDLLSP---- 48
QY 71 QYTNGLLNSMDQIQNGSSSTPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPATPSNT 130
DB 49 -----VTNWLNDENPDASRVAP-----PAATAPAPAPAPATSWPL--SSFVPSQK 93
QY 131 DYPGPHSFVDSFOQSSTAKSATWYTYSTELKLYCQIAKTCPTQIKYNTWTPPGQAVTRAMP 190
DB 94 TYFGSYDFRLGFLHSGTAKSVCTYSPALNKLFCQLAKTCPVQLWYSSPPFPTRYRAMA 153
QY 191 VYKKAHEVYVVKRCNHELSEFNGEQIAPPSSLIRVGNSHAQVVEDPITGRQSVLPV 250
DB 154 IYKSEYEVYVRCRPHHRESSDYSQ-LAPQHLIRVEGNLRAEVLDDNTRFRHSVVVP 212
QY 251 YEPQVQTEFTVLYNFMNCSSCVGMNRRPILIVLTETRGQVILGRRCFEARICACPG 310
DB 213 YEPVEVSGDCTTHYFMNCSSCMGMNRRPILITILEDASGNLLGRNSFEVRVCACPG 272
QY 311 ROKKADSDSRKQVSDSTKNGDGTFRPFQNTHTGQMTSICKRRSPDELLYLPVRGE 370
DB 273 RDRTEENFLKKGSCPCPPPGSTKRALPTST---SSSPVQKKPLDGEYFTLQIRGRE 329
QY 371 TYEMLLKIKESLELMOYLPHQHTIYRQ--QQQQOQHLLQKQTSQSPSSY 420
DB 330 RFEMFRELDALELKD-----AQTAARESGENRAHSHLKSXKG--QSPSRH 373
RESULT 10
P53_FELCA STANDARD; PRT; 386 AA.
ID P53_FELCA
```

```
AC P41685;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR TRF53.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RX MEDLINE=94333960; PubMed=8056458;
RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y.,
RA Watarai T., Goitsuka R., Tsujimoto H., Hasegawa A.;
RT "Cloning of feline p53 tumor-suppressor gene and its aberration in
RT hematopoietic tumors.";
RL Int. J. Cancer 58:602-607(1994).
RN [2]
RP SEQUENCE OF 34-354 FROM N.A.
RX MEDLINE=94114699; PubMed=8286534;
RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watarai T., Goitsuka R.,
RA O'Brien S.J., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning and chromosomal mapping of feline p53 tumor
RT suppressor gene.";
RL J. Vet. Med. Sci. 55:801-805(1993).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; D26608; BAA05653.1; -.
CC HSSP; P04637; 1OLG.
CC InterPro: IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PR00386; P53SUPPRESSOR.
CC ProDom; PD002681; P53; 1.
CC PROSITE; PS00348; P53; 1.
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
CC Nuclear protein; Phosphorylation; Apoptosis.
CC FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
CC FT DNA_BIND 94 285 BY SIMILARITY.
CC FT DOMAIN 318 349 OLIGOMERIZATION.
CC FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
CC FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
CC SIMILARITY).
CC FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
CC FT CONFLICT 285 285 K -> R (IN REF. 2).
SQ SEQUENCE 386 AA; 42692 MW; D08B43BA1BC8EB78 CRC64;
Query Match 28.0%; Score 770; DB 1; Length 386;
```



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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U57306; AAC60146.1; -.
CC DR EMBL; AF003949; AAD01195.1; -.
CC DR EMBL; AF003950; AAD01196.1; -.
CC DR HSSP; P04637; IYCS.
CC DR InterPro; IPR002117; P53.
CC DR Pfam; PF00870; P53; 1.
CC DR PRINTS; PD002681; P53; 1.
CC DR PROSITE; PS00348; P53; 1.
CC DR PROSITE; PS00348; P53; 1.
CC KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
CC Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.
CC FT DOMAIN 1 48 TRANSCRIPTION ACTIVATION (ACIDIC).
CC FT DNA_BIND 87 273 BY SIMILARITY.
CC FT DOMAIN 302 331 OLIGOMERIZATION.
CC FT DOMAIN 334 350 BASIC (REPRESSION OF DNA-BINDING).
CC FT DOMAIN 283 295 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT MOD_RES 351 351 PHOSPHORYLATION (BY SIMILARITY).
CC FT VARIANT 91 S -> T.
CC FT CONFLICT 22 22 MISSING (IN REF. 1).
CC SQ SEQUENCE 352 AA; 39753 MW; 196868A66351BFF5 CRC64;

Query Match 27.1%; Score 746.5; DB 1; Length 352;
Best Local Similarity 43.1%; Pred. No. 3.3e-43;
Matches 163; Conservative 54; Mismatches 92; Indels 69; Gaps 10;

Qy 16 FOHLWDLFQICVQPIDLNFVDEPSDGDGATNKEIEMDCIRMQDSDLSPPMPQYNL 75
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
14 FOELWETVSY- -PLETLSTPTVNEPTGSW-----VATGDMFLDQDLS-----55
Qy 76 GLNMSDQIQONGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDALSPALPSTNDYPGP 135
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
56 --GTFDDKI-----FDIP---IEPVINEVNPPTVPTVTDYPGS 91
Qy 136 HSFDVFSQQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPGAVTRAMPVYKKA 195
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
92 YELELRFQKSTAKSATVSTYSETLNLKLYCQLAKTSIEVRSKPEPKGAILRATAVYKKT 151
Qy 196 EHVEVYKRCNPHELSREFNEGQIAPPSHLLRVGNSHAQVDEPITGRQSVLYPEPPQ 255
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
152 EHADVVRRCPHQ-----NEDSVHRSHLRVSGSLAQFEDPYTKRQSVTVPEPPQ 206
Qy 256 VGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVGLRCFEARICACPGDRKA 315
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
207 PGSEMTTLLSYMCNCSGCMGNRRPILITLTET-EGVLGRRCFEVRICACPGDRKT 265
Qy 316 DEDSIRKQVSDSTKNGDGTGRPRQNTGHQMTSIKRRS-----PDDELLYLVRG 368
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
266 EESRQKTPK-----KRKYTPNT-----SSSRKKKSHSGEEDNREVFHFYVG 311
Qy 369 RETYEMLLKIKESLELMQ 386
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
312 RERIEFLKKINDGLELLE 329

RESULT 14
P53_BOVIN
ID P53_BOVIN STANDARD; PRT; 386 AA.
AC Q29628;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Bos taurus (Bovine), and
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913, 9915;
RP [1]
SEQUENCE FROM N.A.
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Db 123 NNLFOQLAKTCVQLWVDSPPPGTRVRAMAYIKLEHTEVVRRCPPHERSSDYSG-L 181
QY 220 APPSHLIRVEGNSHAQYVEDPITGROSVLVPVPEPPQVTEFTVLYNFMCMNSCVGGMNR 279
Db 182 APPQHLIRVEGNLRAEYLDNRFTFRHSVVVPVPEIDSECTIHYNFMCMNSCMGMNR 241
QY 280 RPLIIVTLTRDGOVLGRRCFEARICACPGDRKKADEDSIRKQOVSDSTKNGDGTKRPF 339
Db 242 RPLITITLEDSCGNLGRNSFEVRVACPGDRRTTEENLRKKGSCPEPPPRSTKRAL 301
QY 340 RONTICQIMTSIKRRSP--DDELLYLPVRGRETYEMLLKIKESLEMLQYLPQHTIETRYQ 398
Db 302 PINT-----SSSPQPKKPLDGYFTLQIRGFRYEMFRELNDALDEL-----KDALDGRP 352
QY 399 OQOQOH-QHLLQKOTSQSPSSGYNSSPPLNK 429
Db 353 GESRAHSHLKS-----KRPSFSCHKKPKMLKR 380

RESULT 15
P53_MARMO
ID P53_MARMO STANDARD; PRT; 391 AA.
AC O36006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Scuriinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97376996; PubMed=9233767;
RA Teilwein M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
RT "Partial characterization of the woodchuck tumor suppressor, p53, and
RT its interaction with woodchuck hepatitis virus X antigen in
RT hepatocarcinogenesis.";
RL Oncogene 15:327-336(1997).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -!- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AJ001022; CAA04478.1;
CC HSSP: P04637; 1TUP.
CC InterPro: IPR002117; P53.
CC Pfam: PF00870; P53; 1.
CC PRINTS: PR00386; P53SUPPRESSOR.
CC ProDom: PD002681; P53; 1.
CC PROSITE: PS00348; P53; 1.
```

```
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 100 290 BY SIMILARITY.
FT DOMAIN 323 354 OLIGOMERIZATION.
FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
FT SIMILARITY).
FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
FT SEQUENCE 391 AA; 4346 MW; ELDE5D864EA40182 CRC64;

Query Match 26.8%; Score 738; DB 1; Length 391;
Best Local Similarity 37.7%; Pred. No. 1.4e-42;
Matches 163; Conservative 70; Mismatches 121; Indels 78; Gaps 10;

QY 11 LSPEVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRQDSDLSPPMP 70
Db 14 LSQETFSDLWNLPP-----ENNVLSPVLS 38

QY 71 QYTNLGLNMDQIQNGSSSTSPYNTDHAQNSVTAPSPYQPSSTFDALSPSPA----- 125
Db 39 PMDDL-LLSSED--VENWFDK---GPDEALQMSAAPAKAPTAASTLAAPSPATSWPL 91

QY 126 ----IPSENTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKYCOIAKTCPIQKWTMPPO 182
Db 92 SSSVPSQNTYPGVYGRFLGFLHSGTAKSVTCYSPSLNKLFCQAKTQVQLWVDSTPPP 151

QY 183 GAVIRAMPVYKKAHVTVKPCNPHELSENEGQIAPPSHLIRVEGNSHAQYVEDPIT 242
Db 152 GTRVRAMAYIKKSHQMTVEVRRCPHHE--RCSDSGLAPPQHLIRVEGNLRAEYLDNR 209

QY 243 GRQSVLPVPEPPQVGTETFTVLYNFMCMNSCVGGMNRRLIITVLTETRDGOVLGRRCPE 302
Db 210 FRHSVVVPVPEVGVSECTIHYNYMCMNSCVGGMNRRLIITILEGSSGNLLGRNSFE 269

QY 303 ARICACPGDRKKADEDSIRKQOVSDSTKNGDGTKRPFPRONT-----HGQIMTSIKRRSP 357
Db 270 VRVCACPGDRDRTEENEFKR-----GEPCEPPPRSTRKRALPNGTSSSPQPKKPL 321

QY 358 DDELLYLPVRGRETYEMLLKIKESLEMLQYLPQHT-----IETVROQOQOQOHL 407
Db 322 DGEYFTLKIRGRARFEMFOELNEALEKDAQAEKPEGESRPHSPYLKSKKGSTSRHKKI 381

QY 408 LQKQTSIQSPSS 419
Db 382 IFKR---EGPDS 390

Search completed: August 7, 2003, 09:47:24
Job time : 11.1507 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:41:09 ; Search time 41.5172 Seconds
(without alignments)
3207.225 Million cell updates/sec

Title: US-09-538-106-14
Perfect score: 2751
Sequence: 1 MSQSTQTNFLSPVQFIHQ.....HCTPPPPYPTDCSIVRIWQV 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2751	100.0	555	Q9H3D3	Q9h3d3 homo sapien
2	2744	99.7	516	Q9P1B7	Q9p1b7 homo sapien
3	2722	98.9	641	Q75195	Q75195 homo sapien
4	2722	98.9	680	Q9H3D4	Q9h3d4 homo sapien
5	2714	98.7	538	Q99JD7	Q99jd7 rattus norv
6	2714	98.7	555	Q99JD8	Q99jd8 rattus norv
7	2714	98.7	555	Q99JW0	Q99jw0 mus musculu
8	2714	98.7	680	Q9UE10	Q9ue10 homo sapien
9	2685	97.6	663	Q99JUE3	Q99je3 rattus norv
10	2685	97.6	680	Q99JUP6	Q99jp6 rattus norv
11	2685	97.6	680	Q99JUP6	Q99jp6 rattus norv
12	2449	89.0	471	Q9NPH7	Q9nph7 mus musculu
13	2379	86.5	461	Q9UP26	Q9up26 homo sapien
14	2372	86.2	461	Q9P1B5	Q9p1b5 homo sapien
15	2356	85.6	461	Q9QWY9	Q9qw9 mus musculu
16	2352	85.5	461	Q99JD6	Q99jd6 rattus norv

17	2350	85.4	586	4	Q9UBV9	Q9ubv9 homo sapien
18	2350	85.4	586	4	Q9P1B4	Q9p1b4 homo sapien
19	2333	84.8	586	4	Q75080	Q75080 homo sapien
20	2327	84.6	586	11	Q89097	Q89097 mus musculu
21	2323	84.4	586	11	Q99JUE2	Q99je2 rattus norv
22	2239	81.4	582	13	Q9DEC7	Q9dec7 gallus gall
23	2185	79.4	487	4	Q9H3D2	Q9h3d2 homo sapien
24	2164	78.7	470	11	Q99JUE1	Q99je1 rattus norv
25	2164	78.7	487	11	Q99JUE0	Q99je0 rattus norv
26	2124	77.2	483	11	Q88897	Q88897 mus musculu
27	2077	75.5	416	4	Q9P1B6	Q9p1b6 homo sapien
28	1900	69.1	501	4	Q9H3P8	Q9h3p8 homo sapien
29	1813	65.9	393	4	Q75922	Q75922 homo sapien
30	1802	65.5	393	11	Q99JD9	Q99jd9 rattus norv
31	1801	65.5	356	4	Q9UP74	Q9up74 homo sapien
32	1779	64.7	457	13	Q8JHZ5	Q8jhz5 brachydanio
33	1771	64.4	576	13	Q8JFE3	Q8jfe3 brachydanio
34	1769	64.3	588	13	Q8JHZ6	Q8jhz6 brachydanio
35	1766	64.2	389	11	Q88899	Q88899 mus musculu
36	1667.5	60.6	365	13	Q98SW0	Q98sw0 xenopus lae
37	1520	55.3	641	13	Q9W664	Q9w664 barbus barb
38	1474.5	53.6	631	11	Q9JJP2	Q9jjp2 mus musculu
39	1442	52.4	590	11	Q9JJP1	Q9jjp1 mus musculu
40	1430.5	52.0	450	4	Q8TDY5	Q8tdy5 homo sapien
41	1418	51.5	284	11	Q8C826	Q8c826 mus musculu
42	1415.5	51.5	587	4	Q8TDY6	Q8tdy6 homo sapien
43	1256	45.7	514	11	Q9CU77	Q9cu77 mus musculu
44	1251	45.5	426	4	Q8NHW9	Q8nhw9 homo sapien
45	1217	44.2	232	4	Q96KR0	Q96kr0 homo sapien

ALIGNMENTS

RESULT 1

Q9H3D3	PRELIMINARY;	PRT;	555 AA.
ID	Q9H3D3; Q9UP27;		
AC	Q9H3D3; Q9UP27;		
DT	01-MAR-2001 (Tremblrel. 16, Created)		
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)		
DT	01-OCT-2002 (Tremblrel. 22, Last annotation update)		
DE	TA p63 beta.		
GN	P63.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98448095; PubMed=9774969;		
RA	Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,		
RA	Andrews N.C., Caput D., McKeon F.;		
RT	"p63, a p53 homolog at 3q27-29, encodes multiple products with		
RT	transactivating, death-inducing, and dominant-negative activities."		
RL	Mol. Cell 2:305-316(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Hagiwara K., McMenamin M.G., Harris C.C.;		
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.		
CC	-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		
CC	-!- SIMILARITY: BELONGS TO THE P53 FAMILY.		
DR	EMBL; AF124539; AAG45608.1; JOINED.		
DR	EMBL; AF124528; AAG45608.1; JOINED.		
DR	EMBL; AF124529; AAG45608.1; JOINED.		
DR	EMBL; AF124531; AAG45608.1; JOINED.		
DR	EMBL; AF124532; AAG45608.1; JOINED.		
DR	EMBL; AF124533; AAG45608.1; JOINED.		
DR	EMBL; AF124534; AAG45608.1; JOINED.		
DR	EMBL; AF124535; AAG45608.1; JOINED.		
DR	EMBL; AF124536; AAG45608.1; JOINED.		
DR	EMBL; AF124537; AAG45608.1; JOINED.		
DR	EMBL; AF075432; AAC62637.1; HSSP; P04637; LYCS.		

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DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSOR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 555 AA; 62433 MW; E22874BE7DBACBE CRC64;

Query Match 100.0%; Score 2751; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 2e-223;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVQHIEWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
DB 1 MSQSTQTNFLSPEVQHIEWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99
QY 61 DSLSLSPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 100 DSLSLSPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPALPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
DB 160 SPSPALPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 219
QY 181 PQGAVTRAMPVYKKAHVTEVVKRCPNHELRSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 220 PQGAVTRAMPVYKKAHVTEVVKRCPNHELRSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLPYEPYPQVGTETTVLYNFMCSNCGVGMNRRPILIIIVTLETRDQVGLGRC 300
DB 280 ITGRQSVLPYEPYPQVGTETTVLYNFMCSNCGVGMNRRPILIIIVTLETRDQVGLGRC 339
QY 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTGRPRQNTGHIQMTSIKKRRSPDDE 360
DB 340 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTGRPRQNTGHIQMTSIKKRRSPDDE 399
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYROQOQOQHLLQKQTSIQSPSSY 420
DB 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYROQOQOQHLLQKQTSIQSPSSY 459
QY 421 GNSPPLNKMNSMKNLPSVSQILNPOORNALPTTIPDGMGNIIPMGTHMPMAGDMNGL 480
DB 460 GNSPPLNKMNSMKNLPSVSQILNPOORNALPTTIPDGMGNIIPMGTHMPMAGDMNGL 519
QY 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIQV 516
DB 520 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIQV 555

RESULT 2
Q9PLB7 PRELIMINARY; PRT; 516 AA.
AC Q9P187;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 isoform TAP63BETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.,
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF116769; AAF43488.1; JOINED.
DR EMBL; AF116756; AAF43488.1; JOINED.
DR EMBL; AF116757; AAF43488.1; JOINED.
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DR EMBL; AF116759; AAF43488.1; JOINED.
DR EMBL; AF116760; AAF43488.1; JOINED.
DR EMBL; AF116761; AAF43488.1; JOINED.
DR EMBL; AF116762; AAF43488.1; JOINED.
DR EMBL; AF116763; AAF43488.1; JOINED.
DR EMBL; AF116764; AAF43488.1; JOINED.
DR EMBL; AF116765; AAF43488.1; JOINED.
DR EMBL; AF116766; AAF43488.1; JOINED.
DR EMBL; AF116767; AAF43488.1; JOINED.
DR HSPSP; P04637; IYCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSOR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 516 AA; 57598 MW; 07553781103738B1 CRC64;

Query Match 99.7%; Score 2744; DB 4; Length 516;
Best Local Similarity 99.8%; Pred. No. 7.2e-223;
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVQHIEWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
DB 1 MSQSTQTNFLSPEVQHIEWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
QY 61 DSLSLSPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSLSLSPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
QY 181 PQGAVTRAMPVYKKAHVTEVVKRCPNHELRSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 PQGAVTRAMPVYKKAHVTEVVKRCPNHELRSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLPYEPYPQVGTETTVLYNFMCSNCGVGMNRRPILIIIVTLETRDQVGLGRC 300
DB 241 ITGRQSVLPYEPYPQVGTETTVLYNFMCSNCGVGMNRRPILIIIVTLETRDQVGLGRC 300
QY 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTGRPRQNTGHIQMTSIKKRRSPDDE 360
DB 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTGRPRQNTGHIQMTSIKKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYROQOQOQHLLQKQTSIQSPSSY 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYROQOQOQHLLQKQTSIQSPSSY 420
QY 421 GNSPPLNKMNSMKNLPSVSQILNPOORNALPTTIPDGMGNIIPMGTHMPMAGDMNGL 480
DB 421 GNSPPLNKMNSMKNLPSVSQILNPOORNALPTTIPDGMGNIIPMGTHMPMAGDMNGL 480
QY 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIQV 516
DB 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIQV 516

RESULT 3
O75195 PRELIMINARY; PRT; 641 AA.
AC O75195;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 isoform TAP63ALPHA (P51B protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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RC TISSUE-Skeletal muscle;
RX MEDLINE=98324755; PubMed=9662378;
RA Osaka M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I.,
RA Ikawa Y., Nimura Y., Nakagawara A., Obinata M.;
RT "Cloning and functional analysis of human p51, which structurally and
RL functionally resembles p53.";
RL Nat. Med. 4:839-844(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AB016073; AAF43487.1; JOINED.
DR EMBL; AF116769; AAF43487.1; JOINED.
DR EMBL; AF116756; AAF43487.1; JOINED.
DR EMBL; AF116757; AAF43487.1; JOINED.
DR EMBL; AF116759; AAF43487.1; JOINED.
DR EMBL; AF116760; AAF43487.1; JOINED.
DR EMBL; AF116761; AAF43487.1; JOINED.
DR EMBL; AF116762; AAF43487.1; JOINED.
DR EMBL; AF116763; AAF43487.1; JOINED.
DR EMBL; AF116764; AAF43487.1; JOINED.
DR EMBL; AF116765; AAF43487.1; JOINED.
DR EMBL; AF116766; AAF43487.1; JOINED.
DR EMBL; AF116767; AAF43487.1; JOINED.
DR EMBL; AF116768; AAF43487.1; JOINED.
DR HSSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 641 AA; 72019 MW; 97AE61F66E63F618 CRC64;

Query Match 98.9%; Score 2722; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 6.9e-221;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIHQ 60
Db 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIHQ 60

Qy 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSYAQPSTFDAL 120
Db 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSYAQPSTFDAL 120

Qy 121 SPSPAIPTNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP 180
Db 121 SPSPAIPTNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP 180

Qy 121 SPSPAIPTNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP 180
Db 121 SPSPAIPTNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP 180

Qy 181 POGAVIRAMPYKKAHEVTEVVKPCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYKKAHEVTEVVKPCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240

Qy 241 ITGRQSVLVPEYPPQVGTEFTVLYNFMCNCSVGGMMNRPIIIVTLTETRDGQVGLRRC 300
Db 241 ITGRQSVLVPEYPPQVGTEFTVLYNFMCNCSVGGMMNRPIIIVTLTETRDGQVGLRRC 300

Qy 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIMTSIKRRSPDDE 360
Db 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRFRQNTHGQIMTSIKRRSPDDE 360

Qy 361 LLYLPVRCRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLQKOTSISQSPSSY 420
Db 361 LLYLPVRCRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLQKOTSISQSPSSY 420

Qy 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIHQ 60
Db 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIHQ 60

Qy 421 GNSSPPLNKMNSMKNLPSVSQLNPQORNALPTPTTIPDGMGANIPMGTHMPMAGDMNGL 480
Db 421 GNSSPPLNKMNSMKNLPSVSQLNPQORNALPTPTTIPDGMGANIPMGTHMPMAGDMNGL 480

Qy 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511
Db 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511

RESULT 4
Q9H3D4 PRELIMINARY; PRT; 680 AA.
AC Q9H3D4; Q9UP28;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE TA p63 alpha (Tumor protein p63).
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF124539; AAG45607.1; JOINED.
DR EMBL; AF124528; AAG45607.1; JOINED.
DR EMBL; AF124529; AAG45607.1; JOINED.
DR EMBL; AF124531; AAG45607.1; JOINED.
DR EMBL; AF124532; AAG45607.1; JOINED.
DR EMBL; AF124533; AAG45607.1; JOINED.
DR EMBL; AF124534; AAG45607.1; JOINED.
DR EMBL; AF124535; AAG45607.1; JOINED.
DR EMBL; AF124536; AAG45607.1; JOINED.
DR EMBL; AF124537; AAG45607.1; JOINED.
DR EMBL; AF124538; AAG45607.1; JOINED.
DR EMBL; AF075430; AAC62635.1; JOINED.
DR EMBL; BC039815; AAB39815.1; JOINED.
DR HSSP; P04637; IYCS.
DR Genew; HGNC:15979; TP63.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76795 MW; F66ECD45E87D9799 CRC64;

Query Match 98.9%; Score 2722; DB 4; Length 680;
Best Local Similarity 100.0%; Pred. No. 7.5e-221;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIHQ 60
Db 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIHQ 99
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DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR MGD; MGI:1330810; Trp63.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76760 MW; AC45DABB88F61400 CRC64;

Query Match          97.6%; Score 2685; DB 11; Length 680;
Best Local Similarity 98.4%; Pred. No. 1e-217;
Matches 503; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSQSTQTNFSLPEVFGHINDFLEQPCISVQPIDLNFVDEPSESGATNKIEISMDCIQM 60
DB 1 MSQSTQTNFSLPEVFGHINDFLEQPCISVQPIDLNFVDEPSESGATNKIEISMDCIQM 99

QY 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159

QY 121 SPSPAIISNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180
DB 121 SPSPAIISNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 219

QY 181 POGAVIRAMPYVYKAEHVTEVVKRCPNHELSEFNEGAIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPYVYKAEHVTEVVKRCPNHELSEFNEGAIAPPSHLIRVEGNSHAQYVEDP 279

QY 241 ITGRQSVLVPEYPQVGTEFTTVLYNFMNCSSCVGGMNRRLIIVITLRTDGOVLGRRC 300
DB 241 ITGRQSVLVPEYPQVGTEFTTVLYNFMNCSSCVGGMNRRLIIVITLRTDGOVLGRRC 339

QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSICKRRSPDDE 360
DB 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSICKRRSPDDE 399

QY 361 LLYLPVGRGRETYEMLLKIKESLELMQVLPQHTIETIROQOQQOHHLLQKOTSISQSSY 420
DB 361 LLYLPVGRGRETYEMLLKIKESLELMQVLPQHTIETIROQOQQOHHLLQKOTSISQSSY 459

QY 421 GNSPPLNKMNMKNLPSVSLINPQORNAITPTTIPDGMGANIPMGTHMPMAGDMNGL 480
DB 421 GNSPPLNKMNMKNLPSVSLINPQORNAITPTTIPDGMGANIPMGTHMPMAGDMNGL 519

QY 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511
DB 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 550

RESULT 11
O88898 PRELIMINARY; PRT; 680 AA.
AC O88898;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TA*p63 alpha.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9848095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL MOL. CELL 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

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CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF075436; AACG2641.1; -.
DR HSSP; P04637; LYCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76788 MW; 8DFF0284F247C68A CRC64;

Query Match          97.6%; Score 2685; DB 11; Length 680;
Best Local Similarity 98.4%; Pred. No. 1e-217;
Matches 503; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSQSTQTNFSLPEVFGHINDFLEQPCISVQPIDLNFVDEPSESGATNKIEISMDCIQM 60
DB 40 MSQSTQTNFSLPEVFGHINDFLEQPCISVQPIDLNFVDEPSESGATNKIEISMDCIQM 99

QY 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 100 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159

QY 121 SPSPAIISNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180
DB 160 SPSPAIISNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 219

QY 181 POGAVIRAMPYVYKAEHVTEVVKRCPNHELSEFNEGAIAPPSHLIRVEGNSHAQYVEDP 240
DB 220 POGAVIRAMPYVYKAEHVTEVVKRCPNHELSEFNEGAIAPPSHLIRVEGNSHAQYVEDP 279

QY 241 ITGRQSVLVPEYPQVGTEFTTVLYNFMNCSSCVGGMNRRLIIVITLRTDGOVLGRRC 300
DB 280 ITGRQSVLVPEYPQVGTEFTTVLYNFMNCSSCVGGMNRRLIIVITLRTDGOVLGRRC 339

QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSICKRRSPDDE 360
DB 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSICKRRSPDDE 399

QY 361 LLYLPVGRGRETYEMLLKIKESLELMQVLPQHTIETIROQOQQOHHLLQKOTSISQSSY 420
DB 400 LLYLPVGRGRETYEMLLKIKESLELMQVLPQHTIETIROQOQQOHHLLQKOTSISQSSY 459

QY 421 GNSPPLNKMNMKNLPSVSLINPQORNAITPTTIPDGMGANIPMGTHMPMAGDMNGL 480
DB 460 GNSPPLNKMNMKNLPSVSLINPQORNAITPTTIPDGMGANIPMGTHMPMAGDMNGL 519

QY 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511
DB 520 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 550

RESULT 12
Q9NPH7 PRELIMINARY; PRT; 471 AA.
AC Q9NPH7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 isoform Tap63delta (p51 delta protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tanl M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";

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Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF116771; AAF61624.1; -
DR EMBL; AF116769; AAF43489.1; JOINED.
DR EMBL; AF116756; AAF43489.1; JOINED.
DR EMBL; AF116757; AAF43489.1; JOINED.
DR EMBL; AF116759; AAF43489.1; JOINED.
DR EMBL; AF116760; AAF43489.1; JOINED.
DR EMBL; AF116761; AAF43489.1; JOINED.
DR EMBL; AF116762; AAF43489.1; JOINED.
DR EMBL; AF116763; AAF43489.1; JOINED.
DR EMBL; AF116764; AAF43489.1; JOINED.
DR EMBL; AF116765; AAF43489.1; JOINED.
DR EMBL; AF116766; AAF43489.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 471 AA; 52882 MW; 32EB39798FC1CE69 CRC64;

Query Match 89.0%; Score 2449; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.8e-198;
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVFOHWDLEQPCSVQPTDLNFVDEPSEDGATNKIEISMDCIQW 60
DB 1 MSQSTQTNFLSPEVFOHWDLEQPCSVQPTDLNFVDEPSEDGATNKIEISMDCIQW 60

QY 61 DSDLSDPMPQPTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMPQPTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

QY 121 SPSPALPNTDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMT 180
DB 121 SPSPALPNTDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMT 180

QY 181 PGAVTRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQVDEP 240
DB 181 PGAVTRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQVDEP 240

QY 241 ITGRQSVLPYEPYPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETRDQVLRRC 300
DB 241 ITGRQSVLPYEPYPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETRDQVLRRC 300

QY 301 FEARICACGRDKADEDSIRKQVSDSTKNGDGTGRPRQNTHTGQIQTSTIKRRSPDDE 360
DB 301 FEARICACGRDKADEDSIRKQVSDSTKNGDGTGRPRQNTHTGQIQTSTIKRRSPDDE 360

QY 361 LLYLPVRGRETVELMLKIKESLELMQYLPQHTIETYROOQOOHLLQKQTSIQSPSSY 420
DB 361 LLYLPVRGRETVELMLKIKESLELMQYLPQHTIETYROOQOOHLLQKQTSIQSPSSY 420

QY 421 GNSPPLKNMNSNKLPSVQLINPQQRNALPTTIPDGMGAN 463
DB 421 GNSPPLKNMNSNKLPSVQLINPQQRNALPTTIPDGMGAN 463

RESULT 13
Q9UP26 PRELIMINARY; PRT; 461 AA.
AC Q9UP26;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DN P63 beta.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE-98448095; PubMed-9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
SEQUENCE FROM N.A.
RP Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF075433; AAC62638.1; -
DR EMBL; AF124539; AAG45611.1; JOINED.
DR EMBL; AF124530; AAG45611.1; JOINED.
DR EMBL; AF124531; AAG45611.1; JOINED.
DR EMBL; AF124532; AAG45611.1; JOINED.
DR EMBL; AF124533; AAG45611.1; JOINED.
DR EMBL; AF124534; AAG45611.1; JOINED.
DR EMBL; AF124535; AAG45611.1; JOINED.
DR EMBL; AF124536; AAG45611.1; JOINED.
DR EMBL; AF124537; AAG45611.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51404 MW; 68B63547A46C1B05 CRC64;

Query Match 86.5%; Score 2379; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 3.7e-192;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
DB 15 PQTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74

QY 130 TQPGPHSPDVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
DB 75 TQPGPHSPDVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134

QY 190 PVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQVDEPITGRQSVLV 249
DB 135 PVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQVDEPITGRQSVLV 194

QY 250 PYEPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETRDQVLRRCFEARICACP 309
DB 195 PYEPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETRDQVLRRCFEARICACP 254

QY 310 GRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTHTGQIQTSTIKRRSPDELLYLPVGR 369
DB 255 GRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTHTGQIQTSTIKRRSPDELLYLPVGR 314

QY 370 ETYEMLLKIKESLELMQYLPQHTIETYROOQOOHLLQKQTSIQSPSSYGNSSPPLNK 429
DB 315 ETYEMLLKIKESLELMQYLPQHTIETYROOQOOHLLQKQTSIQSPSSYGNSSPPLNK 374

QY 430 MNSMKNLPSVQLINPQQRNALPTTIPDGMGANIPMMGTHMPMAGMNGLSPTQALPPP 489
DB 375 MNSMKNLPSVQLINPQQRNALPTTIPDGMGANIPMMGTHMPMAGMNGLSPTQALPPP 434

QY 490 LSPSTSHCTPPPPPTDCSIVRIWQV 516
DB 435 LSPSTSHCTPPPPPTDCSIVRIWQV 461

RESULT 14
Q9P1B5

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ID Q9P1B5 PRELIMINARY; PRT; 461 AA.
AC Q9P1B5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 Isoform delNbeta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF116769; AAF43492.1; JOINED.
DR EMBL; AF116758; AAF43492.1; JOINED.
DR EMBL; AF116759; AAF43492.1; JOINED.
DR EMBL; AF116760; AAF43492.1; JOINED.
DR EMBL; AF116761; AAF43492.1; JOINED.
DR EMBL; AF116762; AAF43492.1; JOINED.
DR EMBL; AF116763; AAF43492.1; JOINED.
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DR EMBL; AF116765; AAF43492.1; JOINED.
DR EMBL; AF116766; AAF43492.1; JOINED.
DR EMBL; AF116767; AAF43492.1; JOINED.
DR HSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR Nuclear protein.
KW Nucleic acid binding protein.
SQ SEQUENCE 461 AA; 51305 MW; 68B63547B81C1B05 CRC64;
Query Match 86.2%; Score 2372; DB 4; Length 461;
Best Local Similarity 99.8%; Pred. No. 1.5e-191;
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 70 PQTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAPSN 129
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QY 130 TDYPGHSDVDFVQSSSTAKSATWTYTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
DB 75 TDYPGHSDVDFVQSSSTAKSATWTYTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
QY 190 PVYKKAHEVTEVVKRCNPHELSEFNEGQIAPPVSHLIRVEGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKKAHEVTEVVKRCNPHELSEFNEGQIAPPVSHLIRVEGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPQVGTETFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDQVGLGRRCFEARIACAP 309
DB 195 PYEPQVGTETFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDQVGLGRRCFEARIACAP 254
QY 310 GRDKADEDSIRKQVSDSTKNGDGTGRPRQNTGHQMTSIKKRRSPDDDELLYLPVGR 369
DB 255 GRDKADEDSIRKQVSDSTKNGDGTGRPRQNTGHQMTSIKKRRSPDDDELLYLPVGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETRYRQOQQOQHLLQKQTSIQSPSSYGNSSPPLNK 429
DB 315 EYEMLLKIKESLELMQYLPQHTIETRYRQOQQOQHLLQKQTSIQSPSSYGNSSPPLNK 374
QY 430 MNSMNLPSVSQLINPOORNALPTTIPDGNGANIPMMGTHMPMAGDMNGLSPTQALPPP 489
DB 375 MNSMNLPSVSQLINPOORNALPTTIPDGNGANIPMMGTHMPMAGDMNGLSPTQALPPP 434
QY 490 LSMPSSTHCTPPPPYPPTDCSIVRIQV 516
DB 435 LSMPSSTHCTPPPPYPPTDCSIVRIQV 461
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DB 435 LSMPSSTHCTPPPPYPPTDCSIVRIQV 461
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AC Q9QWY9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DN p63 beta.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF075438; AAC62643.1; -.
DR HSP; P04637; IYCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR Nuclear protein.
KW Nucleic acid binding protein.
SQ SEQUENCE 461 AA; 51455 MW; 7613296F2F85DBC8 CRC64;
Query Match 85.6%; Score 2356; DB 11; Length 461;
Best Local Similarity 98.9%; Pred. No. 3.2e-190;
Matches 442; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 70 PQTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAPSN 129
DB 15 PQTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAPSN 74
QY 130 TDYPGHSDVDFVQSSSTAKSATWTYTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
DB 75 TDYPGHSDVDFVQSSSTAKSATWTYTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
QY 190 PVYKKAHEVTEVVKRCNPHELSEFNEGQIAPPVSHLIRVEGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKKAHEVTEVVKRCNPHELSEFNEGQIAPPVSHLIRVEGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPQVGTETFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDQVGLGRRCFEARIACAP 309
DB 195 PYEPQVGTETFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDQVGLGRRCFEARIACAP 254
QY 310 GRDKADEDSIRKQVSDSTKNGDGTGRPRQNTGHQMTSIKKRRSPDDDELLYLPVGR 369
DB 255 GRDKADEDSIRKQVSDSTKNGDGTGRPRQNTGHQMTSIKKRRSPDDDELLYLPVGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETRYRQOQQOQHLLQKQTSIQSPSSYGNSSPPLNK 429
DB 315 EYEMLLKIKESLELMQYLPQHTIETRYRQOQQOQHLLQKQTSIQSPSSYGNSSPPLNK 374
QY 430 MNSMNLPSVSQLINPOORNALPTTIPDGNGANIPMMGTHMPMAGDMNGLSPTQALPPP 489
DB 375 MNSMNLPSVSQLINPOORNALPTTIPDGNGANIPMMGTHMPMAGDMNGLSPTQALPPP 434
QY 490 LSMPSSTHCTPPPPYPPTDCSIVRIQV 516
DB 435 LSMPSSTHCTPPPPYPPTDCSIVRIQV 461
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Search completed: August 7, 2003, 09:51:38
Job time : 42.5172 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:31:28 ; Search time 30.8966 Seconds
(without alignments)
2301.535 Million cell updates/sec

Title: US-09-538-106-15

Perfect score: 2383

Sequence: 1 MSQSTQTNFLSPVFOHIW.....PKQSDVFRHKPPNRSVYP 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	2383	100.0	448	20 AAY45246 Human p51 protein
2	2383	100.0	448	20 AAY05955 Human cell regulat
3	2383	100.0	448	21 AAB11359 Human p63 protein
4	2383	100.0	448	22 AAB82128 Human protein #1 u
5	2383	100.0	448	23 AABG95127 Human oncogene p51
6	2383	100.0	448	23 AABG95137 Human oncogene p51
7	2383	100.0	448	23 AABG95143 Human oncogene p63
8	2383	100.0	448	23 AABP61911 Human lung cancer
9	2383	100.0	448	23 AAB74991 Human p53 homology

10	2383	100.0	448	24 ABUS6418 Lung cancer-associ
11	2296	96.3	483	20 AAY05961 Mouse cell regulat
12	2185	91.7	471	23 AABG95129 Human oncogene p51
13	2185	91.7	471	23 AABG95134 Human oncogene p51
14	2185	91.7	516	20 AAB05954 Human cell regulat
15	2185	91.7	516	21 AAB11363 Human p63 protein
16	2185	91.7	516	23 AABG95135 Human oncogene p51
17	2185	91.7	516	23 AABG95141 Human oncogene p63
18	2185	91.7	516	23 AABP61915 Human lung cancer
19	2185	91.7	516	23 AAB74995 Human p53 homology
20	2185	91.7	641	20 AAY45247 Human p51 protein
21	2185	91.7	641	20 AAY05953 Human cell regulat
22	2185	91.7	641	21 AAB11358 Human p63 protein
23	2185	91.7	641	22 AAB82129 Human protein #2 u
24	2185	91.7	641	23 AABG95128 Human oncogene p5B
25	2185	91.7	641	23 AABG95136 Human oncogene p51
26	2185	91.7	641	23 AABG95142 Human oncogene p63
27	2185	91.7	641	23 AABP61910 Human lung cancer
28	2185	91.7	641	23 AAB74990 Human p53 homology
29	2185	91.7	680	21 AAB11361 Human p63 protein
30	2185	91.7	680	21 AAY50997 Human KET protein.
31	2185	91.7	680	23 AABP61913 Human lung cancer
32	2185	91.7	680	23 AAB74993 Human p53 homology
33	2169	91.0	680	20 AAY05958 Human cell regulat
34	2169	91.0	680	21 AAY50998 Rat KET protein.
35	2011	84.4	393	20 AAY05957 Human cell regulat
36	2011	84.4	393	23 AABG95133 Human oncogene p51
37	2011	84.4	393	23 AABG95139 Human oncogene p63
38	1938	81.3	389	20 AAY05964 Mouse cell regulat
39	1813	76.1	416	23 AABG95130 Human oncogene p51
40	1813	76.1	461	21 AAB11362 Human p63 protein
41	1813	76.1	461	23 AABG95131 Human oncogene p51
42	1813	76.1	461	23 AABG95138 Human oncogene p63
43	1813	76.1	461	23 AABP61914 Human lung cancer
44	1813	76.1	461	23 AAB74994 Human p53 homology
45	1813	76.1	586	20 AAY05956 Human cell regulat

ALIGNMENTS

RESULT 1
AAY45246
ID AAY45246 standard; Protein; 448 AA.
XX AC AAY45246;
XX DT 07-JAN-2000 (first entry)
XX DE Human p51 protein A.
XX KW Human; p51; p53 related gene; cell proliferation; regulation; cancer;
XX LW tumour suppression; diagnosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 1..59
XX FT Domain /label= transactivation_domain
XX FT Domain 142..321
XX FT Domain /label= DNA_binding_domain
XX FT Domain 353..397
XX FT Domain /label= oligomerisation_domain
XX PN WO9950412-A1.
XX PD 07-OCT-1999.
XX PF 24-MAR-1999; 99WO-JP01512.
XX PR 27-MAR-1998; 98JP-0100467.
XX PA (SAKA) OTSUKA PHARM CO LTD.

PA (IKAW/) IKAWA Y.
XX Ikawa Y, Ikawa S, Obinata M;
XX WPI; 1999-591318/50.
DR N-PSDB; AAZ25770.
XX
XX New p53 related human gene p51, useful for diagnosis, investigation and
PT treatment of cancers and screening for potential cell proliferation
PT agents -
XX
XX Claim 1; Page 147-148; 163pp; Japanese.
XX
XX The present sequence represents a human p51 protein, which is related to
CC p53 and has cell proliferation regulation and tumour suppression
CC activity. The p51 gene can be used in the investigation, diagnosis and
CC treatment of diseases such as cancer, with which the p53 family cell
CC proliferation regulation is associated. The p51 protein may be used for
CC screening potential agonists and antagonists of its regulatory function,
CC for use as drugs,
XX
XX Sequence 448 AA;
SQ
Query Match 100.0%; Score 2383; DB 20; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQSTOTNEFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSDGNATNKIEISMDICRMQ 60
Db 1 MSQSTOTNEFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSDGNATNKIEISMDICRMQ 60
QY 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIPSTNDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPTQIKYMTTP 180
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Db 241 ITGRQSVLPYEPYPQVGTFTVLYNFMNCNSCVGMNRRPILIIIVTLETRDQVGLGRRC 300
QY 301 FEARICACGRDRKKADEDSIRKQOVSDSTKNGDGTGRPRQNTGHIQMTSIKRRSPDDE 360
Db 301 FEARICACGRDRKKADEDSIRKQOVSDSTKNGDGTGRPRQNTGHIQMTSIKRRSPDDE 360
QY 361 LLYLPVGRGRETVEMLKIKESLELMQYLPQHTIETVYRQOQQOQHLLQKHLISACFRNE 420
Db 361 LLYLPVGRGRETVEMLKIKESLELMQYLPQHTIETVYRQOQQOQHLLQKHLISACFRNE 420
QY 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448
Db 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448
RESULT 2
AAV05955
ID AAY05955 standard; Protein; 448 AA.
XX
XX AAY05955;
XX
XX 16-AUG-1999 (first entry)
XX Human cell regulatory protein p63, isoform huAp63 gamma.
XX Cell regulatory protein; p63; huAp63 gamma; Tap63 gamma;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy.

XX Homo sapiens.
OS
XX
PI WO9919357-A2.
PN
XX
XX 22-APR-1999.
PD
XX
XX 02-OCT-1998; 98WO-US21992.
PF
XX
XX 29-MAY-1998; 98US-0087216.
PR
XX
XX 15-OCT-1997; 97US-0062076.
PS
XX
XX (HARD) HARVARD COLLEGE.
PA
XX
XX McKeon F, Yang A;
PI
XX
XX WPI; 1999-277595/23.
DR
XX
XX N-PSDB; AAX58574.
DR
XX
XX New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
XX
XX
XX Claim 23; Fig 11; 161pp; English.
PS
XX
XX The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. It has been observed that the
CC intron-exon organisation is conserved between p73 and p53, and from
CC known exon and intron sizes for these 2 genes, it was possible to
CC identify new members of this gene family using a PCR-based strategy
CC of amplifying 2 exons in a conserved domain and their intervening
CC intron. The human p63 gene was localised to chromosomal position
CC 3q27-29. At least 6 different isotypes exist. Splice variants
CC differing at the C-terminus have been designated as alpha, beta and
CC gamma forms, while p63 members differing in the N-terminus are
CC designated as deltaN and TA forms, where the deltaN form lacks the
CC transactivation domain. The present sequence represents human
CC p63 isotype TA-p63 gamma. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.
XX
XX Sequence 448 AA;
SQ
Query Match 100.0%; Score 2383; DB 20; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQSTOTNEFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSDGNATNKIEISMDICRMQ 60
Db 1 MSQSTOTNEFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSDGNATNKIEISMDICRMQ 60
QY 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIPSTNDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPTQIKYMTTP 180
Db 121 SPSPAIPSTNDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPTQIKYMTTP 180
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Db 181 PQGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSSHILRVEGNSHAQYVEDP 240

Db 181 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSSHILIRVEGNSHAQYVEDP 240
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 Db 241 ITGROSVLVPYEPPOVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDGOVLGRR 300
 QY 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIKKRRSPDDE 360
 Db 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIKKRRSPDDE 360
 QY 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOOOHHLLQKHLLSACFRNE 420
 Db 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOOOHHLLQKHLLSACFRNE 420
 QY 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
 Db 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448

RESULT 3
 AAB11359
 ID AAB11359 standard; Protein; 448 AA.
 XX AAB11359;
 AC AAB11359;
 XX 21-FEB-2001 (first entry)
 DT Human p63 protein isoform #3.
 DE Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 KW vaccine; detection.
 XX Homo sapiens.
 OS WO200061612-A2.
 PN 19-OCT-2000.
 XX 03-APR-2000; 2000WO-US08896.
 PF 02-APR-1999; 99US-0285479.
 PR 17-DEC-1999; 99US-0466396.
 PR 30-DEC-1999; 99US-0476496.
 PR 10-JAN-2000; 2000US-0480884.
 PR 22-FEB-2000; 2000US-0510376.
 XX (CORI-) CORIXA CORP.
 PA Wang T, Fan L;
 XX WPI; 2000-628399/60.
 DR N-PSDB; AAC66029.
 XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
 PT protein is used for detecting and monitoring progression of lung cancer
 PT in a patient -
 XX Disclosure; Page 247-249; 261pp; English.
 PS This invention describes a novel isolated polypeptide (I) which
 XX comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.
 XX Sequence 448 AA;

Query Match 100.0%; Score 2383; DB 21; Length 448;
 Best Local Similarity 100.0%; Pred. No. 4.7e-207;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFELSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIETSMDCIRMQ 60
 Db 1 MSQSTQTNFELSPEVQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIETSMDCIRMQ 60
 QY 61 DSDLSDPMPQVYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 Db 61 DSDLSDPMPQVYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 121 SPSPAIPNTDYPGPHSFDV3FQSSSTAKSATWTYSTELKKLYCQIAKTCTPIQIKVMTTP 180
 Db 121 SPSPAIPNTDYPGPHSFDV3FQSSSTAKSATWTYSTELKKLYCQIAKTCTPIQIKVMTTP 180
 QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSSHILIRVEGNSHAQYVEDP 240
 Db 181 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSSHILIRVEGNSHAQYVEDP 240
 QY 241 ITGROSVLVPYEPPOVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDGOVLGRR 300
 Db 241 ITGROSVLVPYEPPOVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDGOVLGRR 300
 QY 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIKKRRSPDDE 360
 Db 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIKKRRSPDDE 360
 QY 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOOOHHLLQKHLLSACFRNE 420
 Db 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOOOHHLLQKHLLSACFRNE 420
 QY 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
 Db 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448

RESULT 4
 AAB82128
 ID AAB82128 standard; protein; 448 AA.
 XX AAB82128;
 AC AAB82128;
 DT 03-AUG-2001 (first entry)
 XX Human protein #1 used to produce a chimeric p53 protein.
 DE Human; cytostatic; gene therapy; p53; human tumour.
 XX Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 1..59
 FT /label= Transactivation_domain
 FT Domain 142..321
 FT /label= DNA_binding_domain
 FT Domain 353..397
 FT /label= Oligomerisation_domain
 XX JP2000354488-A.
 PN 26-DEC-2000.
 PD 09-APR-1999; 99JP-0139034.
 PF 09-APR-1999; 99JP-0139034.
 PR 09-APR-1999; 99JP-0139034.
 XX (IKAWA/) IKAWA H.
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX WPI; 2001-268293/28.
 DR N-PSDB; AAF86588.
 XX

PT Chimera gene of the p53 family, useful for gene therapy, and treatment
PT of cancer, comprises a transcription activating region and a DNA
XX binding region -
XX
XX Example 1; Page 30-32; 57pp; Japanese.
XX
CC The present invention relates to a chimera gene of p53 family encoding a
CC transcription activating region, a DNA binding region, and an oligomer
CC formation region of different p53 family proteins. The chimeric gene can
CC be used for gene therapy of p53 variant human tumours, and analysis of
CC the function of the p53 family gene. The present sequence was used in the
CC present invention.
XX
XX
SQ Sequence 448 AA;
Query Match 100.0%; Score 2383; DB 22; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQSTQTNFLSPVEVQHIWDFLEQPCVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
DB 1 MSQSTQTNFLSPVEVQHIWDFLEQPCVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
QY 61 DSDLSPPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSFDAL 120
DB 61 DSDLSPPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSFDAL 120
QY 121 SPSPAIPSNITDYPGPHSFVDFVFSQOSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPSNITDYPGPHSFVDFVFSQOSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 PQGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 PQGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSVLYPEPPQVGTFTVLYNFMCSNCGVGMNRRPILIIIVTLETRDQVGLGRR 300
DB 241 ITGROSVLYPEPPQVGTFTVLYNFMCSNCGVGMNRRPILIIIVTLETRDQVGLGRR 300
QY 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTGRPRFRQNTGHGIQMTSIRKRRSPDDE 360
DB 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTGRPRFRQNTGHGIQMTSIRKRRSPDDE 360
QY 361 LLYLPRGRETVEMLKIKESLEMLQYLPQHTIETTRQOQQOQHLLKHLLSACFRNE 420
DB 361 LLYLPRGRETVEMLKIKESLEMLQYLPQHTIETTRQOQQOQHLLKHLLSACFRNE 420
QY 421 LVEPRRETQKQSDVFFRHSKPPNRSVYP 448
DB 421 LVEPRRETQKQSDVFFRHSKPPNRSVYP 448
RESULT 5
ABG95127
ID ABG95127 standard; Protein; 448 AA.
XX
XX AC ABG95127;
XX
XX DT 04-DEC-2002 (first entry)
XX
XX DE Human oncogene p51A.
XX
KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
OS Homo sapiens.
XX

PN WO200269900-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-US06518.
XX
PR 01-MAR-2001; 2001US-272751P.
XX
PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX
PI Fritz LC, Burrows FJ;
XX
DR WPI; 2002-698710/75.
DR N-PSDB; ABS73327.
XX
PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90
PT
PS Disclosure; Page 320-321; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock
CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis, or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
XX
SQ Sequence 448 AA;
Query Match 100.0%; Score 2383; DB 23; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQSTQTNFLSPVEVQHIWDFLEQPCVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
DB 1 MSQSTQTNFLSPVEVQHIWDFLEQPCVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
QY 61 DSDLSPPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSFDAL 120
DB 61 DSDLSPPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSFDAL 120
QY 121 SPSPAIPSNITDYPGPHSFVDFVFSQOSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPSNITDYPGPHSFVDFVFSQOSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 PQGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 PQGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSVLYPEPPQVGTFTVLYNFMCSNCGVGMNRRPILIIIVTLETRDQVGLGRR 300
DB 241 ITGROSVLYPEPPQVGTFTVLYNFMCSNCGVGMNRRPILIIIVTLETRDQVGLGRR 300
QY 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTGRPRFRQNTGHGIQMTSIRKRRSPDDE 360
DB 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTGRPRFRQNTGHGIQMTSIRKRRSPDDE 360

QY 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETRYQQQQQHQHLLKHLSSACFRNE 420
 Db 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETRYQQQQQHQHLLKHLSSACFRNE 420
 QY 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448
 Db 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448

RESULT 6

ABG95137

ID ABG95137 standard; Protein; 448 AA.

XX

AC ABG95137;

XX

DT 04-DEC-2002 (first entry)

XX

DE Human oncogene p51 isoform TPap63gamma.

XX

KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.

XX Homo sapiens.

OS

XX WO200269900-A2.

PN

XX 12-SEP-2002.

XX

XX 01-MAR-2002; 2002WO-US06518.

PF

XX 01-MAR-2001; 2001US-272751P.

XX

XX (CONF-) CONFORMA THERAPEUTICS CORP.

FA

PI Fritz LC, Burrows FJ;

XX

XX WPI; 2002-698710/75.

DR

PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90

PT

XX

XX Disclosure; Page 341-342; 389pp; English.

PS

XX The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock
 CC protein (HSP)-90, or selectively treating cells expressing (II)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML;
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.

XX Sequence 448 AA;
 SR

Query Match 100.0%; Score 2383; DB 23; Length 448;
 Best Local Similarity 100.0%; Pred. No. 4.7e-207;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFSLSPVDFQHIWDFLEQPICSVQPIDNFVDEPSESGATNKIEISMD CIRMQ 60
 Db 1 MSQSTQTNFSLSPVDFQHIWDFLEQPICSVQPIDNFVDEPSESGATNKIEISMD CIRMQ 60
 QY 61 DSDLSDPMWPQYTNLGLLSNMDQQTONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 Db 61 DSDLSDPMWPQYTNLGLLSNMDQQTONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 121 SPSPAIPSNITDYPGPHSFDVSVFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVWTPP 180
 Db 121 SPSPAIPSNITDYPGPHSFDVSVFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVWTPP 180
 QY 181 PQGAVIRAMPVYKKAHVTEVYVVKRCPNHELSTREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
 Db 181 PQGAVIRAMPVYKKAHVTEVYVVKRCPNHELSTREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
 QY 241 ITGROSVLVPYEPPOVGTFTVLYNFCNCSVCVGMNRRPILIIIVTLETRDGOVLGRRC 300
 Db 241 ITGROSVLVPYEPPOVGTFTVLYNFCNCSVCVGMNRRPILIIIVTLETRDGOVLGRRC 300
 QY 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTHTGIMQTSIKKRSPDDE 360
 Db 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTHTGIMQTSIKKRSPDDE 360
 QY 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETRYQQQQQHQHLLKHLSSACFRNE 420
 Db 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETRYQQQQQHQHLLKHLSSACFRNE 420
 QY 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448
 Db 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448

RESULT 7

ABG95143

ID ABG95143 standard; Protein; 448 AA.

XX

AC ABG95143;

XX

DT 04-DEC-2002 (first entry)

XX

DE Human oncogene p63 isoform.

XX

KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.

XX Homo sapiens.

OS

XX WO200269900-A2.

PN

XX 12-SEP-2002.

XX

XX 01-MAR-2002; 2002WO-US06518.

XX

XX 01-MAR-2001; 2001US-272751P.

XX

XX (CONF-) CONFORMA THERAPEUTICS CORP.

PA

XX Fritz LC, Burrows FJ;

XX

XX WPI; 2002-698710/75.

XX

XX N-PSDB; ABS73335.

DR

XX Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90
PT
PT
XX
XX
PS Disclosure; Page 354-356; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock
CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
XX
SQ Sequence 448 AA;

Query Match 100.0%; Score 2383; DB 23; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTOTNEFLSPEVQHIWDFLEQICSVQPIDLNFVDEPSDGTATKIEISMDICRMQ 60
DB 1 MSQSTOTNEFLSPEVQHIWDFLEQICSVQPIDLNFVDEPSDGTATKIEISMDICRMQ 60
QY 61 DSDLDSPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLDSPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPATPSNTDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPATPSNTDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 PGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 PGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLYPEPPQVGTETTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDQVGLGRR 300
DB 241 ITGRQSVLYPEPPQVGTETTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDQVGLGRR 300
QY 301 FEARICACGRDKADESIRKQVSDSTKNGDGTGRPRQNTHTGQITSIKRRSPDDE 360
DB 301 FEARICACGRDKADESIRKQVSDSTKNGDGTGRPRQNTHTGQITSIKRRSPDDE 360
QY 361 LLYLPVRGETYEMLLKIKESLELMQYLPQHTIETVYRQOQQOQHOHLLOKHLLSACFRNE 420
DB 361 LLYLPVRGETYEMLLKIKESLELMQYLPQHTIETVYRQOQQOQHOHLLOKHLLSACFRNE 420
QY 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448
DB 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448

RESULT 8
ABP61911
ID ABP61911 standard; Protein; 448 AA.
XX
AC ABP61911;

XX 07-OCT-2002 (first entry)
XX Human lung cancer associated protein sequence SEQ ID NO:340.
DE
DE
KW Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200247534-A2.
XX
PD 20-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-US47576.
XX
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
PR 28-JUN-2001; 2001US-0897778.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM,
XX
DR WPI; 2002-583465/62.
DR N-PSDB; ABQ92434.
XX
XX Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT by the polynucleotides, useful in pharmaceutical compositions such as
PT vaccines and as markers to indicate the presence of lung cancer -
PS Example 2; Page 329-330; 381pp; English.
XX
XX The present invention describes isolated human lung carcinoma
CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC activity, and can be used in gene therapy and in vaccines. Compositions
CC comprising (I) or (II) can be used for stimulating an immune response of
CC a patient and for treating lung cancer in a patient. Oligonucleotides of
CC (I) can be used for detecting the presence of a cancer in a patient, by
CC obtaining a biological sample from the patient, contacting the
CC biological sample with the oligonucleotide, detecting in the sample, an
CC amount of polynucleotide that hybridises to the oligonucleotide and
CC comparing the amount of polynucleotide that hybridises to the
CC oligonucleotide to a predetermined cut-off value, and determining the
CC presence of a cancer in the patient. (I) and (II) are useful in
CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
CC indicate the presence or absence of a cancer such as lung cancer.
CC ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 448 AA;

Query Match 100.0%; Score 2383; DB 23; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTOTNEFLSPEVQHIWDFLEQICSVQPIDLNFVDEPSDGTATKIEISMDICRMQ 60
DB 1 MSQSTOTNEFLSPEVQHIWDFLEQICSVQPIDLNFVDEPSDGTATKIEISMDICRMQ 60
QY 61 DSDLDSPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLDSPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPATPSNTDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPATPSNTDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 PGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 PGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240

QY 241 ITGRQSVLPVPEPPQGVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQGVLRRC 300
 Db 241 ITGRQSVLPVPEPPQGVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQGVLRRC 300
 QY 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTGRFRQNTGHIQMTSIKKRRSPDDE 360
 Db 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTGRFRQNTGHIQMTSIKKRRSPDDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROOQOQOHHLLQKLLSACFRNE 420
 Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROOQOQOHHLLQKLLSACFRNE 420
 QY 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448
 Db 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448

RESULT 9

ID ABB74991 standard; Protein; 448 AA.

AC ABB74991;

DT 01-MAY-2002 (first entry)

XX Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:340.

DE Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

KW immune response.

XX Homo sapiens.

XX WO200200174-A2.

PN 03-JAN-2002.

PD 28-JUN-2001; 2001WO-US21065.

PR 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.

PR 21-AUG-2000; 2000US-0643597.

PR 15-SEP-2000; 2000US-0662786.

PR 09-OCT-2000; 2000US-0685696.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;

PI McNeill PD, Fanger N, Retter MW, Warnerakis M, Fanger GR;

PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;

XX WPI; 2002-090513/12.

DR N-PSDB; ABL49248.

XX Polynucleotides encoding lung tumor polypeptides, useful for treating

PT lung cancer or stimulating an immune response -

XX Example 2; Page 322-323; 374pp; English.

XX The present invention describes human lung tumour proteins. Human lung

CC tumour proteins and polynucleotides have cytostatic and immunostimulant

CC activities, and can be used in vaccine production. Compositions

CC comprising the lung tumour proteins, polynucleotides, antibodies,

CC fusion proteins, T cell populations, or antigen presenting cells that

CC express the lung tumour proteins are useful for treating lung cancer or

CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to

CC ABB75070 represent sequences used in the exemplification of the present

XX invention.

XX Sequence 448 AA;

Query Match 100.0%; Score 2383; DB 23; Length 448;

Best Local Similarity 100.0%; Pred. No. 4.7e-207;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSQSTQTFEFLSPVFOHWDLEQPCISVQPIDLNFVDEPSEDGATNKIETSMDCIRMQ 60
 Db 1 MSQSTQTFEFLSPVFOHWDLEQPCISVQPIDLNFVDEPSEDGATNKIETSMDCIRMQ 60
 QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 Db 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 121 SPSPAIPNTDYPGPHSFDVSFQSQSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180
 Db 121 SPSPAIPNTDYPGPHSFDVSFQSQSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180
 QY 181 POGAVIRAMPVYKKAHEVTEVVKRCNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 Db 181 POGAVIRAMPVYKKAHEVTEVVKRCNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 QY 241 ITGRQSVLPVPEPPQGVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQGVLRRC 300
 Db 241 ITGRQSVLPVPEPPQGVGTEFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQGVLRRC 300
 QY 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTGRFRQNTGHIQMTSIKKRRSPDDE 360
 Db 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTGRFRQNTGHIQMTSIKKRRSPDDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROOQOQOHHLLQKLLSACFRNE 420
 Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROOQOQOHHLLQKLLSACFRNE 420
 QY 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448
 Db 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448

RESULT 10

ABU56418
 ID ABU56418 standard; Protein; 448 AA.

AC ABU56418;

DT 02-APR-2003 (first entry)

DE Lung cancer-associated polypeptide #11.

XX Lung cancer-associated polypeptide; cytostatic; emphysema;

KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;

KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX WO200286443-A2.

XX 31-OCT-2002.

XX 18-APR-2002; 2002WO-US12476.

XX 18-APR-2001; 2001US-284770P.

PR 10-MAY-2001; 2001US-290492P.

PR 09-NOV-2001; 2001US-339245P.

PR 13-NOV-2001; 2001US-350666P.

PR 29-NOV-2001; 2001US-334370P.

PR 12-APR-2002; 2002US-372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Aziz N, Murray R;

XX WPI; 2003-093161/08.

DR N-PSDB; ABX76134.

XX Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer
XX
XX Claim 27; Page 196; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences AB056408-AB056745 represent lung cancer-associated
CC polypeptides of the invention.
XX
XX Sequence 448 AA;

Query Match 100.0%; Score 2383; DB 24; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQSTQTNFEFLSPEVFOHIDWLEQPCISQVQIDLNFDVDESDGATNKIELSMDCIRMQ 60
DB 1 MSQSTQTNFEFLSPEVFOHIDWLEQPCISQVQIDLNFDVDESDGATNKIELSMDCIRMQ 60
QY 61 DSDLSDPMWPQYTNLGLLNSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMWPQYTNLGLLNSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFDVSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIKWTPP 180
DB 121 SPSPALPSNTDYPGPHSFDVSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIKWTPP 180
QY 181 POGAVIRAMPYVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPYVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSVLVYPPQVQTEFTVLVNFMCNSCVGGMNRRPILIIIVTLTRDQVGLRRRC 300
DB 241 ITGROSVLVYPPQVQTEFTVLVNFMCNSCVGGMNRRPILIIIVTLTRDQVGLRRRC 300
QY 301 FEARICACGRDRKADESIKQOYSDSTKNGDGKRFPRQNTGHIQMTSIKRRSPDDE 360
DB 301 FEARICACGRDRKADESIKQOYSDSTKNGDGKRFPRQNTGHIQMTSIKRRSPDDE 360
QY 361 LLYLEVRGRETYEMLLKIKESLELMQYLPQHTIETRYQQOQOQHLLQKHLLSACFRNE 420
DB 361 LLYLEVRGRETYEMLLKIKESLELMQYLPQHTIETRYQQOQOQHLLQKHLLSACFRNE 420
QY 421 LVEPRETPKQSDVFRHSKPPNRSVYP 448
DB 421 LVEPRETPKQSDVFRHSKPPNRSVYP 448

RESULT 11
AY05961
ID AAY05961 standard; Protein; 483 AA.
XX
AC AAY05961;
XX

DT 16-AUG-1999 (first entry)
XX Mouse cell regulatory protein p63, isoform muTap63 gamma.
DE Cell regulatory protein; p63; muTap63 gamma; TA663 gamma; mouse;
XX cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy.
KW Mus sp.
OS WO9919357-A2.
XX PN 22-APR-1999.
XX PD 02-OCT-1998; 98WO-US21992.
XX PF 29-MAY-1998; 98US-0087216.
XX PR 15-OCT-1997; 97US-0062076.
XX (HARD) HARVARD COLLEGE.
XX McKeon F, Yang A;
XX WPI; 1999-277595/23.
XX N-PSDB; AAX58580.
XX New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
PT Claim 23; Fig 17; 161pp; English.
PS The present invention concerns the discovery of a new family of
XX cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
CC RACE. Sequencing of the amplification product indicated that the
CC amplified cDNA possessed a truncated N-terminus, i.e. the
CC transactivation domain was absent. Additional splice variants were
CC identified by screening a cDNA library with a probe corresponding
CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
CC variants differing at the C-terminus are designated as alpha, beta
CC and gamma forms, while p63 members differing in the N-terminus are
CC designated as deltaN and TA forms, where the deltaN form lacks the
CC transactivation domain. The present sequence represents murine
CC p53 isoform muTap63 gamma. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
CC AAY58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.
XX
SQ Sequence 483 AA;
Query Match 96.3%; Score 2296; DB 20; Length 483;
Best Local Similarity 96.9%; Pred. No. 4e-199;
Matches 434; Conservative 3; Mismatches 7; Indels 4; Gaps 1;
QY 1 MSQSTQTNFEFLSPEVFOHIDWLEQPCISQVQIDLNFDVDESDGATNKIELSMDCIRMQ 60
DB 40 MSQSTQTNFEFLSPEVFOHIDWLEQPCISQVQIDLNFDVDESDGATNKIELSMDCIRMQ 99
QY 61 DSDLSDPMWPQYTNLGLLNSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 100 DSDLSDPMWPQYTNLGLLNSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159

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Qy 121 SPSPALPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Db 160 SPSPALPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 219
Qy 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGQIAPPShLIRVEGNSHAQYVEDP 240
Db 220 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGQIAPPShLIRVEGNSHAQYVEDP 279
Qy 241 ITGRQSVLVPYEPPOVGTFTVLYNFCMNSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Db 280 ITGRQSVLVPYEPPOVGTFTVLYNFCMNSCVGGMNRRPILIIIVTLETRDGOVLGRR 339
Qy 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTFRPFRQNTHGIGIOMTSIKRRSPDDE 360
Db 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTFRPFRQNTHGIGIOMTSIKRRSPDDE 395
Qy 361 LLYLPVGRGRTYEMLLKIKESLELMQYLPQHTIETIYRQOOQOOHQHLLQKLLSACFRNE 420
Db 396 LLYLPVGRGRTYEMLLKIKESLELMQYLPQHTIETIYRQOOQOOHQHLLQKLLSACFRNE 455
Qy 421 LVEPRRETQKQSDVFFRHSKPPNRSVYP 448
Db 456 LVEPRGEAPTQSDVFFRHSNPPNHSVYP 483

RESULT 12
ABG95129
ID ABG95129 standard; Protein; 471 AA.
XX
AC ABG95129;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human oncogene p51 delta.
XX
KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
OS Homo sapiens.
XX
PN WO200269900-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-US06518.
XX
PR 01-MAR-2001; 2001US-272751P.
XX
PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX
PI Fritz LC, Burrows FJ;
XX
DR WPI; 2002-698710/75.
XX
DR N-PSDB; ABS73329.
XX
PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90
PT
XX
PS Disclosure; Page 325-327; 389pp; English.
XX
CC The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock
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CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
XX
SQ Sequence 471 AA;
Query Match 91.7%; Score 2185; DB 23; Length 471;
Best Local Similarity 94.1%; Pred. NO. 4.4e-189;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
Qy 1 MSQSTQTNFLSPVEVQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Db 1 MSQSTQTNFLSPVEVQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Qy 61 DSDLSDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDAL 120
Db 61 DSDLSDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDAL 120
Qy 121 SPSPALPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPALPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Qy 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGQIAPPShLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGQIAPPShLIRVEGNSHAQYVEDP 240
Qy 241 ITGRQSVLVPYEPPOVGTFTVLYNFCMNSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Db 241 ITGRQSVLVPYEPPOVGTFTVLYNFCMNSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Qy 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTFRPFRQNTHGIGIOMTSIKRRSPDDE 360
Db 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTFRPFRQNTHGIGIOMTSIKRRSPDDE 360
Qy 361 LLYLPVGRGRTYEMLLKIKESLELMQYLPQHTIETIYRQOOQOOHQHLLQKLLSACFRNE 420
Db 361 LLYLPVGRGRTYEMLLKIKESLELMQYLPQHTIETIYRQOOQOOHQHLLQKLLQK 410
Qy 421 LVEPRRETQKQSDVFFRHSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 13
ABG95134
ID ABG95134 standard; Protein; 471 AA.
XX
AC ABG95134;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human oncogene p51 isoform Tap63delta.
XX
KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
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XX OS Homo sapiens.
 XX PN WO200269900-A2.
 XX PD 12-SEP-2002.
 XX PF 01-MAR-2002; 2002WO-US06518.
 XX PR 01-MAR-2001; 2001US-272751P.
 XX PA (CONF-) CONFORMA THERAPEUTICS CORP.
 XX PI Fritz LC, Burrows FJ;
 XX DR WPI; 2002-698710/75.
 XX PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90
 PT
 XX
 XX PS Disclosure; Page 335-336; 389pp; English.
 XX CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock
 CC protein (HSP)-90, or selectively treating cells expressing (II)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.
 XX
 XX SQ Sequence 471 AA;
 Query Match 91.7%; Score 2185; DB 23; Length 471;
 Best Local Similarity 94.1%; Pred. No. 4.4e-189;
 Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
 QY 1 MSQSTQTNFLSPEVFOHFWLEQPCSVQPTDLNFDVDEPSDGNKIEISMDCIRMQ 60
 DB 1 MSQSTQTNFLSPEVFOHFWLEQPCSVQPTDLNFDVDEPSDGNKIEISMDCIRMQ 60
 QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDAL 120
 DB 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDAL 120
 QY 121 SPSPALPSNTDYPGPHSFDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
 DB 121 SPSPALPSNTDYPGPHSFDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
 QY 181 PGAVIRAMPVYKKAHVTVVYKRCPNHLSREFNEGQIAPPShLIRVSGNSHAQYVEDP 240
 DB 181 PGAVIRAMPVYKKAHVTVVYKRCPNHLSREFNEGQIAPPShLIRVSGNSHAQYVEDP 240
 QY 241 ITGROSLVYPPEPPQVGTFTTFLVNFMCNSCVGMNRRPILIIIVTETROGVGLGRC 300
 DB 241 ITGROSLVYPPEPPQVGTFTTFLVNFMCNSCVGMNRRPILIIIVTETROGVGLGRC 300
 QY 301 FEARICACPRDRKADEDSIRKQOVSDSTKNGDGTFRPRQNTHTGQMTSIRKRRSPDDE 360
 DB 301 FEARICACPRDRKADEDSIRKQOVSDSTKNGDGTFRPRQNTHTGQMTSIRKRRSPDDE 360

Db 301 FEARICACPRDRKADEDSIRKQOVSDSTKNGDGTFRPRQNTHTGQMTSIRKRRSPDDE 360
 QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTTETVRQOOQOHOHLQKHLSACFRNE 420
 Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTTETVRQOOQOHOHLQKHLSACFRNE 420
 QY 421 LVEPRRETQKQSDVFFRHSKPP 442
 Db 411 -----QTSIQSPSSYGNSSPP 426
 RESULT 14
 AAY05954
 ID AAY05954 standard; Protein; 516 AA.
 XX AC AAY05954;
 XX DT 16-AUG-1999 (first entry)
 XX DE Human cell regulatory protein p63, isoform huTap63 beta.
 XX KW Cell regulatory protein; p63; huTap63 beta; Tap63 beta; human;
 KW cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; therapy.
 XX OS Homo sapiens.
 XX PN WO9919357-A2.
 XX PD 22-APR-1999.
 XX PF 02-OCT-1998; 98WO-US211992.
 XX PR 29-MAY-1998; 98US-0087216.
 XX PR 15-OCT-1997; 97US-0062076.
 XX PA (HARD) HARVARD COLLEGE.
 XX PI McKeon F, Yang A;
 XX WPI; 1999-277595/23.
 XX N-PSDB; AAX58573.
 XX PT New isolated p63 cell regulatory protein for, e.g. treatment of
 XX tumours
 XX PS Claim 23; Fig 10; 161pp; English.
 XX CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. It has been observed that the
 CC intron-exon organisation is conserved between p73 and p53, and from
 CC known exon and intron sizes for these 2 genes, it was possible to
 CC identify new members of this gene family using a PCR-based strategy
 CC of amplifying 2 exons in a conserved domain and their intervening
 CC intron. The human p53 gene was localised to chromosomal position
 CC 3q27-29. At least 6 different isotypes exist. Splice variants
 CC differing at the c-terminus have been designated as alpha, beta and
 CC gamma forms, while p63 members differing in the N-terminus are
 CC designated as deltaN and TA forms, where the deltaN form lacks the
 CC transactivation domain. The present sequence represents human
 CC p63 isotype Tap63 beta. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAX58572-83) and anti-p63 antibodies of the invention can be used to

CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.

XX SQ Sequence 516 AA;
Query Match 91.7%; Score 2185; DB 20; Length 516;
Best Local Similarity 94.1%; Pred. No. 5.1e-189;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
Qy 1 MSQSTQTNFEFLSPVFOHWFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Db 1 MSQSTQTNFEFLSPVFOHWFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Qy 61 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPSTNTDYPGPHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPSTNTDYPGPHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180
Qy 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Qy 241 ITGRQSVLPVPEPPQVGTFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDQVGLGRR 300
Db 241 ITGRQSVLPVPEPPQVGTFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDQVGLGRR 300
Qy 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTHTGQVMTSIIKKRRSPDDE 360
Db 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTHTGQVMTSIIKKRRSPDDE 360
Qy 361 LLYLPVGRGRETVEMLLKIKESLELMQYLPQHTIETRYOQOQOQOHHLLQKLLSACFRNE 420
Db 361 LLYLPVGRGRETVEMLLKIKESLELMQYLPQHTIETRYOQOQOQOHHLLQKLLSACFRNE 420
Qy 421 LVEPRRETPKQSDVFFRHSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 15

AA11363
ID AAB11363 standard; Protein; 516 AA.
AC AAB11363;
XX
DT 21-FEB-2001 (first entry)
DE Human p63 protein isoform #7.
KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW vaccine; detection.
XX Homo sapiens.
OS WO200061612-A2.
PN 19-OCT-2000.
PD 03-APR-2000; 2000WO-US08896.
PF 02-APR-1999; 99US-0285479.
PR 17-DEC-1999; 99US-0466396.
PR 30-DEC-1999; 99US-0476496.
PR 10-JAN-2000; 2000US-0480884.
PR 22-FEB-2000; 2000US-0510376.
XX (CORI-) CORIXA CORP.
XX Wang T, Fan L;

XX WPI; 2000-628399/60.
DR N-PSDB; AAC66033.
XX
PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -
XX
PS Disclosure; Page 255-256; 261pp; English.
XX
CC This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.

XX SQ Sequence 516 AA;

Query Match 91.7%; Score 2185; DB 21; Length 516;
Best Local Similarity 94.1%; Pred. No. 5.1e-189;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSQSTQTNFEFLSPVFOHWFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Db 1 MSQSTQTNFEFLSPVFOHWFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Qy 61 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPSTNTDYPGPHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPSTNTDYPGPHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180
Qy 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Qy 241 ITGRQSVLPVPEPPQVGTFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDQVGLGRR 300
Db 241 ITGRQSVLPVPEPPQVGTFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDQVGLGRR 300
Qy 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTHTGQVMTSIIKKRRSPDDE 360
Db 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTHTGQVMTSIIKKRRSPDDE 360
Qy 361 LLYLPVGRGRETVEMLLKIKESLELMQYLPQHTIETRYOQOQOQOHHLLQKLLSACFRNE 420
Db 361 LLYLPVGRGRETVEMLLKIKESLELMQYLPQHTIETRYOQOQOQOHHLLQKLLSACFRNE 420
Qy 421 LVEPRRETPKQSDVFFRHSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

Search completed: August 7, 2003, 09:46:24
Job time : 31.8966 secs

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: August 7, 2003, 09:42:54 ; Search time 12.3586 Seconds
(without alignments)
1533.769 Million cell updates/sec

Title: US-09-538-106-15
Perfect score: 2383
Sequence: 1 MSQSTQTNFSLPEVQHIW.....PKQSDVFRHSKPPNRVYP 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/6C_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/6D_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2383	100.0	448	US-09-643-597-340	Sequence 340, App
2	2383	100.0	448	US-09-542-615A-340	Sequence 340, App
3	2383	100.0	448	US-09-606-421B-340	Sequence 340, App
4	2185	91.7	516	US-09-643-597-344	Sequence 344, App
5	2185	91.7	516	US-09-542-615A-344	Sequence 344, App
6	2185	91.7	516	US-09-606-421B-344	Sequence 344, App
7	2185	91.7	641	US-09-643-597-339	Sequence 339, App
8	2185	91.7	641	US-09-542-615A-339	Sequence 339, App
9	2185	91.7	680	US-09-606-421B-339	Sequence 339, App
10	2185	91.7	680	US-09-643-597-342	Sequence 342, App
11	2185	91.7	680	US-09-542-615A-342	Sequence 342, App
12	2185	91.7	680	US-09-606-421B-342	Sequence 342, App
13	2136	89.6	426	US-09-277-196-19	Sequence 19, Appl
14	1813	76.1	461	US-09-643-597-343	Sequence 343, App
15	1813	76.1	461	US-09-542-615A-343	Sequence 343, App
16	1813	76.1	461	US-09-606-421B-343	Sequence 343, App
17	1796	75.4	356	US-09-643-597-341	Sequence 341, App
18	1796	75.4	356	US-09-542-615A-341	Sequence 341, App
19	1796	75.4	356	US-09-606-421B-341	Sequence 341, App
20	1796	75.4	356	US-09-643-597-338	Sequence 338, App
21	1796	75.4	356	US-09-542-615A-338	Sequence 338, App
22	1796	75.4	356	US-09-606-421B-338	Sequence 338, App
23	1796	75.4	356	US-09-643-597-152	Sequence 152, App
24	1796	75.4	356	US-09-542-615A-152	Sequence 152, App
25	1789	75.1	586	US-09-480-884A-152	Sequence 152, App
26	1789	75.1	586	US-09-542-615A-152	Sequence 152, App
27	1789	75.1	586	US-09-606-421B-152	Sequence 152, App

28	1297.5	54.4	420	4	US-09-277-196-20	Sequence 20, Appl
29	1297.5	54.4	635	4	US-09-081-975-3	Sequence 3, Appl
30	753.5	31.6	381	4	US-09-257-580-2	Sequence 2, Appl
31	722.5	30.3	393	1	US-08-047-041A-27	Sequence 27, Appl
32	722.5	30.3	393	1	US-08-390-516C-8	Sequence 8, Appl
33	722.5	30.3	393	1	US-08-390-515A-8	Sequence 8, Appl
34	722.5	30.3	393	2	US-08-801-718-8	Sequence 8, Appl
35	717.5	30.1	362	4	US-09-603-052-2	Sequence 2, Appl
36	717.5	30.1	363	2	US-08-697-221-17	Sequence 17, Appl
37	717.5	30.1	393	1	US-08-047-041A-25	Sequence 25, Appl
38	717.5	30.1	393	1	US-08-047-041A-26	Sequence 26, Appl
39	717.5	30.1	393	1	US-08-347-792-2	Sequence 2, Appl
40	717.5	30.1	393	1	US-08-390-516C-6	Sequence 6, Appl
41	717.5	30.1	393	1	US-08-390-516C-7	Sequence 7, Appl
42	717.5	30.1	393	1	US-08-431-357-2	Sequence 2, Appl
43	717.5	30.1	393	1	US-08-390-515A-6	Sequence 6, Appl
44	717.5	30.1	393	1	US-08-390-515A-7	Sequence 7, Appl
45	717.5	30.1	393	2	US-08-795-006A-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-643-597-340
; Sequence 340, Application US/09643597
; Patent No. 6426072

GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455CII

; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 340
; LENGTH: 448

; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-643-597-340

Query Match 100.0%; Score 2383; DB 4; Length 448;

Best Local Similarity 100.0%; Pred. No. 3.6e-218;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSQSTQTNFSLPEVQHIWDFLEOPICSVOPIDLNFVDFSEDCATNKIETSMDCIRMQ 60

Db 1 MSQSTQTNFSLPEVQHIWDFLEOPICSVOPIDLNFVDFSEDCATNKIETSMDCIRMQ 60

Oy 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

Db 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

Oy 121 SPSPAISNTDYPGPHSFDVSFQSSSTAKSATWYISTELKKLYCOIATCPIQIKWTPPP 180

Db 121 SPSPAISNTDYPGPHSFDVSFQSSSTAKSATWYISTELKKLYCOIATCPIQIKWTPPP 180

Oy 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGOIAPPShLIRVEGNSHAQYVEDP 240

Db 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGOIAPPShLIRVEGNSHAQYVEDP 240

Oy 241 ITGRQSLVLPYEPQVGTEFTTVLYNFCNCSGVMNRRLPIITVLTETRDGOVLGRRC 300

|||||
Db 241 ITGROSVLVPEPPQVGTFTVLVNFMCNSSCVGMNRRPILIIIVTLETRDQVGLGRC 300
|||||
QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHTQMTSIIKKRSPDDE 360
|||||
Db 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHTQMTSIIKKRSPDDE 360
|||||
QY 361 LLYLPVRGRETVELLKIKESELMQYLPQHTIETIRYRQOQOQOHHLLQKHLLSACFRNE 420
|||||
Db 361 LLYLPVRGRETVELLKIKESELMQYLPQHTIETIRYRQOQOQOHHLLQKHLLSACFRNE 420
|||||
QY 421 LVEPRETPKQSDVFRHRSKPPNRSVYP 448
|||||
Db 421 LVEPRETPKQSDVFRHRSKPPNRSVYP 448
|||||
RESULT 2
US-09-542-615A-340
; Sequence 340, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-340

Query Match 100.0%; Score 2383; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.6e-218;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQSTQTNFLSPEVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
|||||
Db 1 MSQSTQTNFLSPEVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
|||||
QY 61 DSDLDPMMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
|||||
Db 61 DSDLDPMMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
|||||
QY 121 SPSPAIPSTNDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
|||||
Db 121 SPSPAIPSTNDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
|||||
QY 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQVDEP 240
|||||
Db 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQVDEP 240
|||||
QY 241 ITGROSVLVPEPPQVGTFTVLVNFMCNSSCVGMNRRPILIIIVTLETRDQVGLGRC 300
|||||
Db 241 ITGROSVLVPEPPQVGTFTVLVNFMCNSSCVGMNRRPILIIIVTLETRDQVGLGRC 300
|||||
QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHTQMTSIIKKRSPDDE 360
|||||
Db 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHTQMTSIIKKRSPDDE 360
|||||
QY 361 LLYLPVRGRETVELLKIKESELMQYLPQHTIETIRYRQOQOQOHHLLQKHLLSACFRNE 420
|||||
Db 361 LLYLPVRGRETVELLKIKESELMQYLPQHTIETIRYRQOQOQOHHLLQKHLLSACFRNE 420
|||||
QY 421 LVEPRETPKQSDVFRHRSKPPNRSVYP 448
|||||

|||||
Db 421 LVEPRETPKQSDVFRHRSKPPNRSVYP 448
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RESULT 3
US-09-606-421B-340
; Sequence 340, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-340

Query Match 100.0%; Score 2383; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.6e-218;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQSTQTNFLSPEVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
|||||
Db 1 MSQSTQTNFLSPEVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
|||||
QY 61 DSDLDPMMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
|||||
Db 61 DSDLDPMMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
|||||
QY 121 SPSPAIPSTNDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
|||||
Db 121 SPSPAIPSTNDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
|||||
QY 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQVDEP 240
|||||
Db 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQVDEP 240
|||||
QY 241 ITGROSVLVPEPPQVGTFTVLVNFMCNSSCVGMNRRPILIIIVTLETRDQVGLGRC 300
|||||
Db 241 ITGROSVLVPEPPQVGTFTVLVNFMCNSSCVGMNRRPILIIIVTLETRDQVGLGRC 300
|||||
QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHTQMTSIIKKRSPDDE 360
|||||
Db 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHTQMTSIIKKRSPDDE 360
|||||
QY 361 LLYLPVRGRETVELLKIKESELMQYLPQHTIETIRYRQOQOQOHHLLQKHLLSACFRNE 420
|||||
Db 361 LLYLPVRGRETVELLKIKESELMQYLPQHTIETIRYRQOQOQOHHLLQKHLLSACFRNE 420
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QY 421 LVEPRETPKQSDVFRHRSKPPNRSVYP 448
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Db 421 LVEPRETPKQSDVFRHRSKPPNRSVYP 448
|||||

RESULT 4
US-09-643-597-344
; Sequence 344, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-344

Query Match 91.7%; Score 2185; DB 4; Length 516;
Best Local Similarity 94.1%; Pred. No. 3.1e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSQSTQTFNEFLSPVFOHINDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 60
Db 1 MSQSTQTFNEFLSPVFOHINDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 60

Qy 61 DSLSLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDAL 120
Db 61 DSLSLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDAL 120

Qy 121 SPSPAIPSNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPSNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180

Qy 181 PQGAVIRAMPYVYKAEHVTEVVKPCPNHLSRENEGOIAPPSSHILIVEGNSHAQYVEDP 240
Db 181 PQGAVIRAMPYVYKAEHVTEVVKPCPNHLSRENEGOIAPPSSHILIVEGNSHAQYVEDP 240

Qy 241 ITGRQSVLVPEYPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRR 300
Db 241 ITGRQSVLVPEYPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRR 300

Qy 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTHGHIQMTSIIKRRSPDDE 360
Db 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTHGHIQMTSIIKRRSPDDE 360

Qy 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETYRQOQOQOHOHLKLLSACFRNE 420
Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETYRQOQOQOHOHLKLLSACFRNE 420

Qy 421 LVEPRRETQKQSDVFFRHRSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 5
US-09-542-615A-344
; Sequence 344, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-344

Query Match 91.7%; Score 2185; DB 4; Length 516;
Best Local Similarity 94.1%; Pred. No. 3.1e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSQSTQTFNEFLSPVFOHINDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 60
Db 1 MSQSTQTFNEFLSPVFOHINDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 60

Qy 61 DSLSLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDAL 120
Db 61 DSLSLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDAL 120

Qy 121 SPSPAIPSNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPSNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180

Qy 181 PQGAVIRAMPYVYKAEHVTEVVKPCPNHLSRENEGOIAPPSSHILIVEGNSHAQYVEDP 240
Db 181 PQGAVIRAMPYVYKAEHVTEVVKPCPNHLSRENEGOIAPPSSHILIVEGNSHAQYVEDP 240

Qy 241 ITGRQSVLVPEYPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRR 300
Db 241 ITGRQSVLVPEYPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRR 300

Qy 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTHGHIQMTSIIKRRSPDDE 360
Db 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTHGHIQMTSIIKRRSPDDE 360

Qy 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETYRQOQOQOHOHLKLLSACFRNE 420
Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETYRQOQOQOHOHLKLLSACFRNE 420

Qy 421 LVEPRRETQKQSDVFFRHRSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 6
US-09-606-421B-344
; Sequence 344, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT

```
; ORGANISM: Homo sapiens
US-09-606-421B-344

Query Match          91.7%; Score 2185; DB 4; Length 516;
Best Local Similarity 94.1%; Pred. No. 3 le-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTNFLSPEVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
DB 1 MSQSTQTNFLSPEVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
QY 61 DSDLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
DB 61 DSDLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
QY 121 SPSPAIPSNVDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPSNVDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 PGAVIRAMPVYKKAEBHVTVEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 PGAVIRAMPVYKKAEBHVTVEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSVLVYPPEPPQVGTETFTVLYNFMCSNCSVCGMNRRLIIVTLETRDGOVLGRRC 300
DB 241 ITGROSVLVYPPEPPQVGTETFTVLYNFMCSNCSVCGMNRRLIIVTLETRDGOVLGRRC 300
QY 301 FEARICACGRDRKKADEDSIRKQOVSDDTKNGDGTRKPRFRQNTGHGIOMTSIKRRSPDDE 360
DB 301 FEARICACGRDRKKADEDSIRKQOVSDDTKNGDGTRKPRFRQNTGHGIOMTSIKRRSPDDE 360
QY 361 LLYLPVGRGRETMYEMLLKIKESLELMQYLPQHTIETIRQOQOQOHHLLKHLKSACFRNE 420
DB 361 LLYLPVGRGRETMYEMLLKIKESLELMQYLPQHTIETIRQOQOQOHHLLKHLKSACFRNE 420
QY 421 LVEPRETPKQSDVFRHSKPP 442
DB 411 -----QTSIQSPSSYGNSSPP 426

RESULT 7
US-09-643-597-339
; Sequence 339, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-339

Query Match          91.7%; Score 2185; DB 4; Length 641;
Best Local Similarity 94.1%; Pred. No. 4.3e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
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QY 1 MSQSTQTNFLSPEVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
DB 1 MSQSTQTNFLSPEVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
QY 61 DSDLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
DB 61 DSDLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
QY 121 SPSPAIPSNVDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPSNVDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 PGAVIRAMPVYKKAEBHVTVEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 PGAVIRAMPVYKKAEBHVTVEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSVLVYPPEPPQVGTETFTVLYNFMCSNCSVCGMNRRLIIVTLETRDGOVLGRRC 300
DB 241 ITGROSVLVYPPEPPQVGTETFTVLYNFMCSNCSVCGMNRRLIIVTLETRDGOVLGRRC 300
QY 301 FEARICACGRDRKKADEDSIRKQOVSDDTKNGDGTRKPRFRQNTGHGIOMTSIKRRSPDDE 360
DB 301 FEARICACGRDRKKADEDSIRKQOVSDDTKNGDGTRKPRFRQNTGHGIOMTSIKRRSPDDE 360
QY 361 LLYLPVGRGRETMYEMLLKIKESLELMQYLPQHTIETIRQOQOQOHHLLKHLKSACFRNE 420
DB 361 LLYLPVGRGRETMYEMLLKIKESLELMQYLPQHTIETIRQOQOQOHHLLKHLKSACFRNE 420
QY 421 LVEPRETPKQSDVFRHSKPP 442
DB 411 -----QTSIQSPSSYGNSSPP 426

RESULT 8
US-09-542-615A-339
; Sequence 339, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-339

Query Match          91.7%; Score 2185; DB 4; Length 641;
Best Local Similarity 94.1%; Pred. No. 4.3e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
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```
QY 1 MSQSTQTNFLSPEVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
DB 1 MSQSTQTNFLSPEVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
QY 61 DSDLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
DB 61 DSDLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
QY 121 SPSPAIPSNVDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPSNVDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
```

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Qy 181 POGAVIRAMPYVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
Qy 241 ITGRQSVLVPEYPPQVGTETTVLYNPMCMSSCVGGMNRRLPILIVTLETRDGOVLGRR 300
Db 241 ITGRQSVLVPEYPPQVGTETTVLYNPMCMSSCVGGMNRRLPILIVTLETRDGOVLGRR 300
Qy 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
Db 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETIYRQOQOQOHHLLQKLLSACPRNE 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETIYRQOQOQOHHLLQKLLSACPRNE 420
Qy 421 LVEPRRETQKQSDVFRHRSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 9
US-09-606-421B-339
; Sequence 339, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-339
```

```
Query Match 91.7%; Score 2185; DB 4; Length 641;
Best Local Similarity 94.1%; Pred. No. 4.3e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSOSTQTNEFLSPVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Db 1 MSOSTQTNEFLSPVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Qy 61 DSLSLDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSLSLDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPNTDYPGPHSFDVSFQOSSTAKSATWTYTELKLYCQIAKTCPQIKVMTTP 180
Db 121 SPSPAIPNTDYPGPHSFDVSFQOSSTAKSATWTYTELKLYCQIAKTCPQIKVMTTP 180
Qy 181 POGAVIRAMPYVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
Qy 241 ITGRQSVLVPEYPPQVGTETTVLYNPMCMSSCVGGMNRRLPILIVTLETRDGOVLGRR 300
Db 241 ITGRQSVLVPEYPPQVGTETTVLYNPMCMSSCVGGMNRRLPILIVTLETRDGOVLGRR 300
Qy 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
Db 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
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Db 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETIYRQOQOQOHHLLQKLLSACPRNE 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETIYRQOQOQOHHLLQKLLSACPRNE 420
Qy 421 LVEPRRETQKQSDVFRHRSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 10
US-09-643-597-342
; Sequence 342, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-342
```

```
Query Match 91.7%; Score 2185; DB 4; Length 680;
Best Local Similarity 94.1%; Pred. No. 4.7e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSOSTQTNEFLSPVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Db 40 MSOSTQTNEFLSPVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 99
Qy 61 DSLSLDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 100 DSLSLDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
Qy 121 SPSPAIPNTDYPGPHSFDVSFQOSSTAKSATWTYTELKLYCQIAKTCPQIKVMTTP 180
Db 160 SPSPAIPNTDYPGPHSFDVSFQOSSTAKSATWTYTELKLYCQIAKTCPQIKVMTTP 219
Qy 181 POGAVIRAMPYVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
Db 220 POGAVIRAMPYVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSLIRVEGNSHAQYVEDP 279
Qy 241 ITGRQSVLVPEYPPQVGTETTVLYNPMCMSSCVGGMNRRLPILIVTLETRDGOVLGRR 300
Db 280 ITGRQSVLVPEYPPQVGTETTVLYNPMCMSSCVGGMNRRLPILIVTLETRDGOVLGRR 339
Qy 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
Db 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 399
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETIYRQOQOQOHHLLQKLLSACPRNE 420
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETIYRQOQOQOHHLLQKLLSACPRNE 449
```

QY 421 LVEPRRETPKQSDVFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465

RESULT 11

US-09-542-615A-342
; Sequence 342, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-342

Query Match 91.7%; Score 2185; DB 4; Length 680;

Best Local Similarity 94.1%; Pred. No. 4.7e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTNFEFLSPEVQFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Db 40 MSQSTQTNFEFLSPEVQFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 99
QY 61 DSDLSDPMPQYTNLGLNSMDQQTONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 100 DSDLSDPMPQYTNLGLNSMDQQTONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPAIPSNTPDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
Db 160 SPSPAIPSNTPDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Db 220 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGROSVLVPYPPQVGTFTVLNFMCSNCSVGMNRRPILIIIVTLETRDGOVLGRRC 300
Db 280 ITGROSVLVPYPPQVGTFTVLNFMCSNCSVGMNRRPILIIIVTLETRDGOVLGRRC 339
QY 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHGIQMTSIIKKRSPDDE 360
Db 340 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHGIQMTSIIKKRSPDDE 399
QY 361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYYRQOQOQOHHLLQKHLLSACFRNE 420
Db 400 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYYRQOQOQOHHLLQKHLLSACFRNE 449
QY 421 LVEPRRETPKQSDVFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465

RESULT 12

US-09-606-421B-342
; Sequence 342, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-342

Query Match 91.7%; Score 2185; DB 4; Length 680;

Best Local Similarity 94.1%; Pred. No. 4.7e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTNFEFLSPEVQFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Db 40 MSQSTQTNFEFLSPEVQFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 99
QY 61 DSDLSDPMPQYTNLGLNSMDQQTONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 100 DSDLSDPMPQYTNLGLNSMDQQTONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPAIPSNTPDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
Db 160 SPSPAIPSNTPDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Db 220 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGROSVLVPYPPQVGTFTVLNFMCSNCSVGMNRRPILIIIVTLETRDGOVLGRRC 300
Db 280 ITGROSVLVPYPPQVGTFTVLNFMCSNCSVGMNRRPILIIIVTLETRDGOVLGRRC 339
QY 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHGIQMTSIIKKRSPDDE 360
Db 340 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHGIQMTSIIKKRSPDDE 399
QY 361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYYRQOQOQOHHLLQKHLLSACFRNE 420
Db 400 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYYRQOQOQOHHLLQKHLLSACFRNE 449
QY 421 LVEPRRETPKQSDVFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465

RESULT 13

US-09-277-196-19
; Sequence 19, Application US/09277196
; Patent No. 6476206
; GENERAL INFORMATION:
; APPLICANT: Trink, Barry
; APPLICANT: Ratovitski, Edward
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: p40 Protein Acts as an Oncogene
; FILE REFERENCE: 01107.79765
; CURRENT APPLICATION NUMBER: US/09/277,196
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/079736
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-277-196-19

Query Match 89.6%; Score 2136; DB 4; Length 426;
Best Local Similarity 93.1%; Pred. No. 1e-194;
Matches 405; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

```
Qy 8 NEFLSPVFQIHWDFLEQPCISQVPIDLNFVDEPSESGATNKIEISMDCTRMQSDSLSDP 67
Db 1 SEFLSPVFQIHWDFLEQPCISQVPIDLNFVDEPSESGATNKIEISMDCTRMQSDSLSDP 60
Qy 68 MWPOYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIP 127
Db 61 MWPOYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIP 120
Qy 128 SNTDYPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPGAVIR 187
Db 121 SNTDYPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPGAVIR 180
Qy 188 AMPYKKAHVTEVVKRCNPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDPITGRQSV 247
Db 181 AMPYKKAHVTEVVKRCNPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDPITGRQSV 240
Qy 248 LVPYEPQVGTETFTVLYNFMCNSSCVGGMNRRPILLIIVTLETRDGOVLGRRCFEARICA 307
Db 241 LVPYEPQVGTETFTVLYNFMCNSSCVGGMNRRPILLIIVTLETRDGOVLGRRCFEARICA 300
Qy 308 CPGRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDELLYLPVR 367
Db 301 CPGRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDELLYLPVR 360
Qy 368 GRETYEMLLKIKESLELMQYLPOHTIETTYRQOQOQOHHLLQKLLSACFRELVEPRE 427
Db 361 GRETYEMLLKIKESLELMQYLPOHTIETTYRQOQOQOHHLLQKLLSACFRELVEPRE 427
Qy 428 TPQSDVFFRHSKPP 442
Db 405 TSMQSSSYGNSSP 419
```

RESULT 14
US-09-643-597-343
; Sequence 343, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-343

Query Match 76.1%; Score 1813; DB 4; Length 461;
Best Local Similarity 93.0%; Pred. No. 6.2e-164;
Matches 347; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

```
Qy 70 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 129
Db 15 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 74
Qy 130 TDYCPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPGAVIRAM 189
Db 75 TDYCPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPGAVIRAM 134
Qy 190 PVYKKAHVTEVVKRCNPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDPITGRQSVLV 249
Db 135 PVYKKAHVTEVVKRCNPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDPITGRQSVLV 194
Qy 250 PYEPQVGTETFTVLYNFMCNSSCVGGMNRRPILLIIVTLETRDGOVLGRRCFEARICACP 309
Db 195 PYEPQVGTETFTVLYNFMCNSSCVGGMNRRPILLIIVTLETRDGOVLGRRCFEARICACP 254
Qy 310 GRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDELLYLPVRGR 369
Db 255 GRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDELLYLPVRGR 314
Qy 370 ETYEMLLKIKESLELMQYLPOHTIETTYRQOQOQOHHLLQKLLSACFRELVEPREPRT 429
Db 315 ETYEMLLKIKESLELMQYLPOHTIETTYRQOQOQOHHLLQKLLSACFRELVEPREPRT 429
Qy 430 KQSDVFFRHSKPP 442
Db 359 IQSPSSSYGNSSP 371
```

RESULT 15
US-09-542-615A-343
; Sequence 343, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-343

Query Match 76.1%; Score 1813; DB 4; Length 461;
Best Local Similarity 93.0%; Pred. No. 6.2e-164;
Matches 347; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

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Db 15 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 74
Qy 130 TDYCPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPGAVIRAM 189
Db 75 TDYCPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPGAVIRAM 134
Qy 190 PVYKKAHVTEVVKRCNPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDPITGRQSVLV 249
Db 135 PVYKKAHVTEVVKRCNPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDPITGRQSVLV 194
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Db 195 PYEPPOVGTFTVLYNFCNSSCVGGMNRRLIIVTLETRDQGVLGRRCFEARICACP 254
QY 310 GRDRKADEDSIRKQVSDSTKNGDGTFRFRONTGHIOMTSIKKRSPDDELLYLPVGR 369
Db 255 GRDRKADEDSIRKQVSDSTKNGDGTFRFRONTGHIOMTSIKKRSPDDELLYLPVGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETYROOQOQOHOHLLOKHLLSACFRNELVEPRRTP 429
Db 315 EYEMLLKIKESLELMQYLPQHTIETYROOQOQOHOHLLOKHLLSACFRNELVEPRRTP 371
QY 430 KOSDVEFRHSKPP 442
Db 359 IQSPSSYGNSSPP 371

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Search completed: August 7, 2003, 09:54:52
Job time : 13.3586 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 7, 2003, 09:46:34 ; Search time 19.1264 Seconds
(without alignments) 2781.719 Million cell updates/sec

Title: US-09-538-106-15
 Perfect score: 2383
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues
Total number of hits satisfying chosen parameters: 451899

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published_Applications_AA:*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %			ID	Description
		Match	Length	DB		
1	2383	100.0	448	9	US-09-735-705-340	Sequence 340, App
2	2383	100.0	448	10	US-09-850-716A-340	Sequence 340, App
3	2383	100.0	448	10	US-09-897-778-340	Sequence 340, App
4	2185	91.7	516	9	US-09-735-705-344	Sequence 344, App
5	2185	91.7	516	10	US-09-850-716A-344	Sequence 344, App
6	2185	91.7	516	10	US-09-897-778-344	Sequence 344, App
7	2185	91.7	641	9	US-09-735-705-339	Sequence 339, App
8	2185	91.7	641	10	US-09-850-716A-339	Sequence 339, App
9	2185	91.7	680	10	US-09-897-778-339	Sequence 339, App
10	2185	91.7	680	9	US-09-735-705-342	Sequence 342, App
11	2185	91.7	680	10	US-09-850-716A-342	Sequence 342, App
12	2185	91.7	680	10	US-09-897-778-342	Sequence 342, App
13	2136	89.6	426	15	US-10-274-874-19	Sequence 19, Appl
14	1813	76.1	461	9	US-09-735-705-343	Sequence 343, App
15	1813	76.1	461	10	US-09-850-716A-343	Sequence 343, App

16	1813	76.1	461	10	US-09-897-778-343	Sequence 343, App
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18	1796	75.4	356	10	US-09-850-716A-341	Sequence 341, App
19	1796	75.4	356	10	US-09-897-778-341	Sequence 341, App
20	1796	75.4	356	15	US-10-274-874-2	Sequence 2, Appli
21	1796	75.4	586	9	US-09-735-705-338	Sequence 338, App
22	1796	75.4	586	10	US-09-850-716A-338	Sequence 338, App
23	1796	75.4	586	10	US-09-897-778-338	Sequence 338, App
24	1789	75.1	586	9	US-09-735-705-152	Sequence 152, App
25	1789	75.1	586	10	US-09-850-716A-152	Sequence 152, App
26	1789	75.1	586	10	US-09-897-778-152	Sequence 152, App
27	1789	75.1	586	11	US-09-466-396A-152	Sequence 152, App
28	1297.5	54.4	420	15	US-10-274-874-20	Sequence 20, Appl
29	1297.5	54.4	635	14	US-10-155-059-3	Sequence 3, Appli
30	1297.5	54.4	636	10	US-09-733-384-10	Sequence 10, Appl
31	717.5	30.1	393	9	US-09-776-695-32	Sequence 32, Appl
32	717.5	30.1	393	10	US-09-732-384-3	Sequence 3, Appli
33	717.5	30.1	393	10	US-09-860-211-9	Sequence 9, Appli
34	717.5	30.1	393	11	US-09-029-327-4	Sequence 4, Appli
35	717.5	30.1	393	11	US-09-860-286-9	Sequence 9, Appli
36	717.5	30.1	393	15	US-10-274-874-4	Sequence 4, Appli
37	717.5	30.1	393	15	US-10-160-290-2	Sequence 2, Appli
38	717.5	30.1	428	15	US-10-076-691-2	Sequence 2, Appli
39	716.5	30.1	353	15	US-10-146-473-78	Sequence 78, Appl
40	714	30.0	390	15	US-10-038-010-6	Sequence 6, Appli
41	714	30.0	401	10	US-09-968-851-34	Sequence 34, Appl
42	711	29.8	390	15	US-10-160-290-3	Sequence 3, Appli
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44	704	29.5	381	10	US-09-968-851-36	Sequence 36, Appl
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ALIGNMENTS

RESULT 1
US-09-735-705-340
; Sequence 340, Application US/09735705

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AFFILIANT: FANGEL, NELL
 :
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

1. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
2. TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

: FILE REFERENCE: 210121.455C14

FILE REFERENCE: 210121.435014
CURRENT APPLICATION NUMBER: US/09/735,705

; CURRENT FILING DATE: 2000-12-12

; NUMBER OF SEQ ID NOS: 419

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ	ID	NO	340
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; LENGTH: 448

; TYPE: PRT

ORGANISM: *Homo sapiens*

US-09-735-705-340

Query Match 100.0%; Score 2383; DB 9; Length 448;

Best Local Similarity 100.0%; Pred. No. 1e-208;

Matches	448;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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RESULT 2

US-09-850-716A-340

; Sequence 340, Application US/09850716A

; Patent No. US20020115139A1

; GENERAL INFORMATION:

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C15

; CURRENT APPLICATION NUMBER: US/09/850,716A

; CURRENT FILING DATE: 2001-05-07

; NUMBER OF SEQ ID NOS: 440

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 340

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-850-716A-340

Query Match 100.0%; Score 2383; DB 10; Length 448;
Best Local Similarity 100.0%; Pred. No. 1e-208;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTFRPRQNTGHIQMTSIIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQOHHLLQKHLLSACFRNE 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQOHHLLQKHLLSACFRNE 420
QY 421 LVEPRETPKQSDVFRHRSKPPNRSVYP 448
DB 421 LVEPRETPKQSDVFRHRSKPPNRSVYP 448

RESULT 3

US-09-897-778-340

; Sequence 340, Application US/09897778

; Patent No. US20020147143A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Marnerakis, Margarita

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Henderson, Robert A.

; APPLICANT: Peckham, David W.

; APPLICANT: Fanger, Neil

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C16

; CURRENT APPLICATION NUMBER: US/09/897,778

; CURRENT FILING DATE: 2001-06-28

; NUMBER OF SEQ ID NOS: 467

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 340

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-897-778-340

Query Match 100.0%; Score 2383; DB 10; Length 448;
Best Local Similarity 100.0%; Pred. No. 1e-208;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSQSTQTNFELSPEVFOHLDLEQIPICVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
QY 61 DSDLDPMMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLDPMMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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DB 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
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DB 181 POGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLPYEPYPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETRDQVGLGRC 300
DB 241 ITGRQSVLPYEPYPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETRDQVGLGRC 300
QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTFRPRQNTGHIQMTSIIKRRSPDDE 360
DB 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTFRPRQNTGHIQMTSIIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQOHHLLQKHLLSACFRNE 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQOHHLLQKHLLSACFRNE 420

Qy 421 LVEPRRETQKSDVFFRHSKPPNRSVYP 448
Db 421 LVEPRRETQKSDVFFRHSKPPNRSVYP 448

RESULT 4

US-09-735-705-344
; Sequence 344, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Lijun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735.705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-344

Query Match 91.7%; Score 2185; DB 9; Length 516;
Best Local Similarity 94.1%; Pred. No. 1.4e-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
Qy 1 MSQSTQTFNEFLSPVDFHINDFLEQPCISVQPIDLNFVDFSEDPGATNKIEISMDCIHQ 60
Db 1 MSQSTQTFNEFLSPVDFHINDFLEQPCISVQPIDLNFVDFSEDPGATNKIEISMDCIHQ 60
Qy 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Qy 181 PQGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSSLIRVEGNSHAQYVEDP 240
Db 181 PQGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSSLIRVEGNSHAQYVEDP 240
Qy 241 ITGRQSVLPYEPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETDRDGOVLGRRC 300
Db 241 ITGRQSVLPYEPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETDRDGOVLGRRC 300
Qy 301 FEARICACGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTHGQIOMTSIKKRRSPDDE 360
Db 301 FEARICACGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTHGQIOMTSIKKRRSPDDE 360
Qy 361 LLYLPVGRRETYEMLLIKESLELMQYLPQHTIETYRQOQOQOHHLLQKLLSACFRNE 420
Db 361 LLYLPVGRRETYEMLLIKESLELMQYLPQHTIETYRQOQOQOHHLLQKLLSACFRNE 420
Qy 421 LVEPRRETQKSDVFFRHSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 5

US-09-850-716A-344
; Sequence 344, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850.716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-344

Query Match 91.7%; Score 2185; DB 10; Length 516;
Best Local Similarity 94.1%; Pred. No. 1.4e-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
Qy 1 MSQSTQTFNEFLSPVDFHINDFLEQPCISVQPIDLNFVDFSEDPGATNKIEISMDCIHQ 60
Db 1 MSQSTQTFNEFLSPVDFHINDFLEQPCISVQPIDLNFVDFSEDPGATNKIEISMDCIHQ 60
Qy 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Qy 181 PQGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSSLIRVEGNSHAQYVEDP 240
Db 181 PQGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSSLIRVEGNSHAQYVEDP 240
Qy 241 ITGRQSVLPYEPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETDRDGOVLGRRC 300
Db 241 ITGRQSVLPYEPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETDRDGOVLGRRC 300
Qy 301 FEARICACGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTHGQIOMTSIKKRRSPDDE 360
Db 301 FEARICACGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTHGQIOMTSIKKRRSPDDE 360
Qy 361 LLYLPVGRRETYEMLLIKESLELMQYLPQHTIETYRQOQOQOHHLLQKLLSACFRNE 420
Db 361 LLYLPVGRRETYEMLLIKESLELMQYLPQHTIETYRQOQOQOHHLLQKLLSACFRNE 420
Qy 421 LVEPRRETQKSDVFFRHSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 6

US-09-897-778-344
; Sequence 344, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/897.778
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-344

; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-344

Query Match
Best Local Similarity 91.7%; Score 2185; DB 10; Length 516;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
QY 1 MSOSTQTNEFLSPEVQFQHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 1 MSOSTQTNEFLSPEVQFQHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
QY 61 DSDLSPPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSPPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 POGAVTRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVTRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLPYEPYPQVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDQVGLGRR 300
DB 241 ITGRQSVLPYEPYPQVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDQVGLGRR 300
QY 301 FEARICACPRGRKKADEDSIRKQVSDSTKNGDGTGRPRQNTHTGQMTSIRKRRSPDDE 360
DB 301 FEARICACPRGRKKADEDSIRKQVSDSTKNGDGTGRPRQNTHTGQMTSIRKRRSPDDE 360
QY 361 LLYLPVGRGETYEMLLKIKESLELMQYLPQHTIETVYRQOOQOHOHLKHLLSACFRNE 420
DB 361 LLYLPVGRGETYEMLLKIKESLELMQYLPQHTIETVYRQOOQOHOHLKHLLSACFRNE 420
QY 421 LVEPRRETQKSDVFFRHSKPP 442
DB 411 -----QTSIQSPSSYGNSSPP 426

RESULT 7
US-09-735-705-339
; Sequence 339, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339

; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-339

Query Match
Best Local Similarity 91.7%; Score 2185; DB 9; Length 641;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
QY 1 MSOSTQTNEFLSPEVQFQHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 1 MSOSTQTNEFLSPEVQFQHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
QY 61 DSDLSPPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSPPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 POGAVTRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVTRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLPYEPYPQVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDQVGLGRR 300
DB 241 ITGRQSVLPYEPYPQVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDQVGLGRR 300
QY 301 FEARICACPRGRKKADEDSIRKQVSDSTKNGDGTGRPRQNTHTGQMTSIRKRRSPDDE 360
DB 301 FEARICACPRGRKKADEDSIRKQVSDSTKNGDGTGRPRQNTHTGQMTSIRKRRSPDDE 360
QY 361 LLYLPVGRGETYEMLLKIKESLELMQYLPQHTIETVYRQOOQOHOHLKHLLSACFRNE 420
DB 361 LLYLPVGRGETYEMLLKIKESLELMQYLPQHTIETVYRQOOQOHOHLKHLLSACFRNE 420
QY 421 LVEPRRETQKSDVFFRHSKPP 442
DB 411 -----QTSIQSPSSYGNSSPP 426

RESULT 8
US-09-850-716A-339
; Sequence 339, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-339

Query Match
Best Local Similarity 91.7%; Score 2185; DB 10; Length 641;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
QY 1 MSOSTQTNEFLSPEVQFQHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 1 MSOSTQTNEFLSPEVQFQHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
QY 61 DSDLSPPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

Db 61 DSLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPTNDYDGPCHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPTNDYDGPCHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180
Qy 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSSHIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSSHIRVEGNSHAQYVEDP 240
Qy 241 ITGRQSVLVPYEPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Db 241 ITGRQSVLVPYEPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Qy 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTHG IQMTSIKKRRSPDDE 360
Db 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTHG IQMTSIKKRRSPDDE 360
Qy 361 LLYLPVRGRETYEMLLKIKESLELMQYLPOHTIETTYRQOQQOQHLLQKHLLSACFRNE 420
Db 361 LLYLPVRGRETYEMLLKIKESLELMQYLPOHTIETTYRQOQQOQHLLQKHLLSACFRNE 420
Qy 421 LVEPRRETQKQSDVFRHRSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 9

US-09-897-778-339
; Sequence 339, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Warnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-339

Query Match 91.7%; Score 2185; DB 10; Length 641;
Best Local Similarity 94.1%; Pred. No. 2e-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
Qy 1 MSQSTQTNFLSPFVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Db 1 MSQSTQTNFLSPFVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Qy 61 DSLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPTNDYDGPCHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPTNDYDGPCHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180
Qy 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSSHIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSSHIRVEGNSHAQYVEDP 240

Qy 241 ITGRQSVLVPYEPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Db 241 ITGRQSVLVPYEPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Qy 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTHG IQMTSIKKRRSPDDE 360
Db 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTHG IQMTSIKKRRSPDDE 360
Qy 361 LLYLPVRGRETYEMLLKIKESLELMQYLPOHTIETTYRQOQQOQHLLQKHLLSACFRNE 420
Db 361 LLYLPVRGRETYEMLLKIKESLELMQYLPOHTIETTYRQOQQOQHLLQKHLLSACFRNE 420
Qy 421 LVEPRRETQKQSDVFRHRSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 10

US-09-735-705-342
; Sequence 342, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, AiJun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-342

Query Match 91.7%; Score 2185; DB 9; Length 680;
Best Local Similarity 94.1%; Pred. No. 2.le-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
Qy 1 MSQSTQTNFLSPFVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Db 40 MSQSTQTNFLSPFVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 99
Qy 61 DSLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 100 DSLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
Qy 121 SPSPAIPTNDYDGPCHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180
Db 160 SPSPAIPTNDYDGPCHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 219
Qy 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSSHIRVEGNSHAQYVEDP 240
Db 220 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSSHIRVEGNSHAQYVEDP 279
Qy 241 ITGRQSVLVPYEPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Db 280 ITGRQSVLVPYEPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 339
Qy 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRFRQNTHG IQMTSIKKRRSPDDE 360

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Db 340 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTFRPQNTGHIQMTSIKKRSPDDE 399
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROOQOQOHOHLQKLLSACFRNE 420
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROOQOQOHOHLQK----- 449
Qy 421 LVEPRRTPKQSDVFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465

RESULT 11
US-09-850-716A-342
; Sequence 342, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-342
```

```
Query Match 91.7%; Score 2185; DB 10; Length 680;
Best Local Similarity 94.1%; Pred. No. 2.1e-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSQSTQTFNEFLSPEVFOHIWDFLEQIPICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
Db 40 MSQSTQTFNEFLSPEVFOHIWDFLEQIPICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99
Qy 61 DSDLDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 100 DSDLDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
Qy 121 SPSPAIPNTDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPP 180
Db 160 SPSPAIPNTDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPP 219
Qy 181 PGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Db 220 PGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
Qy 241 ITGROSVLVPYPPQVGTFTVLVNFMCNSCVGMMNRRLIIVTLTETRDGQVLRRC 300
Db 280 ITGROSVLVPYPPQVGTFTVLVNFMCNSCVGMMNRRLIIVTLTETRDGQVLRRC 339
Qy 301 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTFRPQNTGHIQMTSIKKRSPDDE 360
Db 340 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTFRPQNTGHIQMTSIKKRSPDDE 399
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROOQOQOHOHLQKLLSACFRNE 420
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROOQOQOHOHLQK----- 449
Qy 421 LVEPRRTPKQSDVFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465
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RESULT 12
US-09-897-778-342
; Sequence 342, Application US/09897778
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```
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Barrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-342

Query Match 91.7%; Score 2185; DB 10; Length 680;
Best Local Similarity 94.1%; Pred. No. 2.1e-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSQSTQTFNEFLSPEVFOHIWDFLEQIPICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
Db 40 MSQSTQTFNEFLSPEVFOHIWDFLEQIPICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99
Qy 61 DSDLDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 100 DSDLDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
Qy 121 SPSPAIPNTDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPP 180
Db 160 SPSPAIPNTDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPP 219
Qy 181 PGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Db 220 PGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
Qy 241 ITGROSVLVPYPPQVGTFTVLVNFMCNSCVGMMNRRLIIVTLTETRDGQVLRRC 300
Db 280 ITGROSVLVPYPPQVGTFTVLVNFMCNSCVGMMNRRLIIVTLTETRDGQVLRRC 339
Qy 301 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTFRPQNTGHIQMTSIKKRSPDDE 360
Db 340 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTFRPQNTGHIQMTSIKKRSPDDE 399
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROOQOQOHOHLQKLLSACFRNE 420
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROOQOQOHOHLQK----- 449
Qy 421 LVEPRRTPKQSDVFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465

RESULT 13
US-10-274-874-19
; Sequence 19, Application US/10274874
; Publication No. US20030113774A1
; GENERAL INFORMATION:
; APPLICANT: Trink, Barry
; APPLICANT: Jen, Jin
; APPLICANT: Ratovitski, Edward
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: p40 Protein Acts as an Oncogene
; FILE REFERENCE: 01107.79765
; CURRENT APPLICATION NUMBER: US/10/274,874
```

; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US/09/277,196
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079736
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-274-874-19

Query Match 89.6%; Score 2136; DB 15; Length 426;
Best Local Similarity 93.1%; Pred. No. 3.1e-186;
Matches 405; Conservative 5; Mismatches 9; Indels 16; Gaps 1;
QY 8 NEFLSPEVQHWDLEQPCISQVPIDLNFVDEPESDGTAKNIEISMDICRQDSLSDP 67
DB 1 SEFLSPEVQHWDLEQPCISQVPIDLNFVDEPESDGTAKNIEISMDICRQDSLSDP 60
QY 68 MPQVTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPPAIP 127
DB 61 MPQVTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPPAIP 120
QY 128 SNTDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIR 187
DB 121 SNTDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIR 180
QY 188 AMPVYKKAHTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSV 247
DB 181 AMPVYKKAHTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSV 240
QY 248 LVPYEPQVGTFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDQVILGRRCFEARICA 307
DB 241 LVPYEPQVGTFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDQVILGRRCFEARICA 300
QY 308 CPGDRKADEDSIRKQVSDSTKNGDGTGRFRQNTHGQIOMTSIKRRSPDDDELLYLPR 367
DB 301 CPGDRKADEDSIRKQVSDSAKNGDGTGRFRQNTHGQIOMTSIKRRSPDDDELLYLPR 360
QY 368 GRETVELLKIKESLELMQYLPQHTIETRYQQQQOQHLLQKHLLSACFRNELVEPRE 427
DB 361 GRETVELLKIKESLELMQYLPQHTIETRYQQQQOQHLLQKHLLSACFRNELVEPRE 420
QY 428 TPQSDVFFRHSKPP 442
DB 405 TSMQSSSYGNSPP 419

RESULT 14
US-09-735-705-343
; Sequence 343, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-343

Query Match 76.1%; Score 1813; DB 9; Length 461;
Best Local Similarity 93.0%; Pred. No. 9.8e-157;
Matches 347; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
QY 70 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPPAIPSN 129
DB 15 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPPAIPSN 74
QY 130 TDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 189
DB 75 TDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 134
QY 190 PVYKKAHTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKKAHTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPQVGTFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDQVILGRRCFEARICAC 309
DB 195 PYEPQVGTFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDQVILGRRCFEARICAC 254
QY 310 GDRKADEDSIRKQVSDSTKNGDGTGRFRQNTHGQIOMTSIKRRSPDDDELLYLPRGR 369
DB 255 GDRKADEDSIRKQVSDSTKNGDGTGRFRQNTHGQIOMTSIKRRSPDDDELLYLPRGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETRYQQQQOQHLLQKHLLSACFRNELVEPRETP 429
DB 315 EYEMLLKIKESLELMQYLPQHTIETRYQQQQOQHLLQKHLLSACFRNELVEPRETP 429
QY 430 KQSDVFFRHSKPP 442
DB 359 IQSPSSSYGNSPP 371

RESULT 15
US-09-850-716A-343
; Sequence 343, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-343

Query Match 76.1%; Score 1813; DB 10; Length 461;
Best Local Similarity 93.0%; Pred. No. 9.8e-157;
Matches 347; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
QY 70 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPPAIPSN 129
DB 15 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPPAIPSN 74
QY 130 TDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 189
DB 75 TDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 134

QY 190 PVYKKAHVTEVVKRCPNHELSPREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
Db |||||
QY 135 PVYKKAHVTEVVKRCPNHELSPREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
Db |||||
QY 250 PYEPQVGTFTVLYNEMCNSSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICACP 309
Db |||||
QY 195 PYEPQVGTFTVLYNEMCNSSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICACP 254
Db |||||
QY 310 GRDKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIOMTSIKRRSPDDELLYLPVGR 369
Db |||||
QY 255 GRDKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIOMTSIKRRSPDDELLYLPVGR 314
Db |||||
QY 370 EYEMLLKIKESLELMQYLPQHTIETRYQQQQQQHLLQXHLJSACFRELVEPRRTP 429
Db |||||
QY 315 EYEMLLKIKESLELMQYLPQHTIETRYQQQQQQHLLQK-----QTS 358
Db |||||
QY 430 KQSDVFFRHSKPP 442
Db |||||
QY 359 IQSPSSYGNSSPP 371
Db |||||

Search completed: August 7, 2003, 09:57:08
Job time : 20.1264 secs

Result No.	Query			DB ID	Description
	Score	Match	Length		
1	847.5	35.6	396	1 JH0631	cellular tumor ant
2	777.5	32.6	363	1 A29376	cellular tumor ant
3	764.5	32.1	367	1 S02193	cellular tumor ant
4	741.5	31.1	386	1 S51648	cellular tumor ant
5	732	30.7	391	1 S02192	cellular tumor ant
6	719.5	30.2	396	1 JH0633	cellular tumor ant
7	717.5	30.1	393	1 DNHU53	cellular tumor ant
8	715	30.0	390	1 DNM553	cellular tumor ant
9	714.5	30.0	393	1 S06594	cellular tumor ant
10	704	29.5	393	2 JC61176	tumor suppressor p
11	702	29.5	381	2 S38824	cellular tumor ant
12	699.5	29.4	391	2 JC61193	tumor suppressor p
13	259.5	10.9	77	2 I46226	cellular tumor ant
14	114.5	4.8	3942	2 T42730	Bassoon protein -
15	111.5	4.7	1819	2 T32008	hypothetical prote
16	110.5	4.6	2529	2 A56923	transcription fact
17	110	4.6	5762	2 A41819	proline-rich pepti
18	109	4.6	4273	2 C69679	polyketide synthas
19	108.5	4.6	701	1 S33709	DHR39-short protei
20	108.5	4.6	808	1 S33708	nuclear steroid/th
21	107	4.5	1691	1 D54689	protein-tyrosine-p
22	107	4.5	1894	2 C54689	protein-tyrosine-p
23	107	4.5	1912	2 A56178	protein-tyrosine-p
24	106.5	4.5	631	2 T31782	hypothetical prote
25	106.5	4.5	2578	2 A56922	transcription fact
26	105.5	4.4	395	2 A54949	syndecan precursor
27	105	4.4	384	2 I49528	hypothetical prote
28	105	4.4	766	1 S61694	floculation suppr
29	105	4.4	909	2 T06635	hypothetical prote

RESULT 2

A29376
cellular tumor antigen p53 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A29376; S61531; S72313; I51639
R:Sousi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.
Oncogene 1, 71-78, 1987
A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein
A:Reference number: A29376; MUID:88143684; PMID:2830576
A:Accession: A29376
A:Molecule type: mRNA
A:Residues: 1-363 <SOU>
C:Cross-references: EMBL:X05191; NID:g64961; PIDN:CAA28021.1; PID:g64962
R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.
Oncogene 9, 109-120, 1994
A:Title: Overexpression of wild-type p53 interferes with normal development in Xenopus laevis
A:Reference number: I51639; MUID:94134403; PMID:8302570
A:Accession: S61531
A:Molecule type: mRNA
A:Residues: 1-293,295-363 <HOE>
C:Cross-references: EMBL:X77346; NID:g468513; PIDN:CAA54672.1; PID:g468514
R:Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knoechel, W.
submitted to the EMBL Data Library, March 1994
A:Reference number: S72313
A:Accession: S72313
A:Molecule type: mRNA
A:Residues: 1-51,'S',53-70,72-293,295-363 <HOW>
C:Cross-references: EMBL:X77346; NID:g468513; PIDN:CAA54672.1; PID:g468514
C:Genetics: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F:150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 32.6%; Score 777.5; DB 1; Length 363;
Best Local Similarity 42.5%; Pred. No. 1.7e-52;
Matches 171; Conservative 55; Mismatches 95; Indels 81; Gaps 11;
QY 2 SOSTQNEPLSEVQHWFLEQPI----CSVQIDLNFDVDEPSEDGATNKIEISMDCI 57
DB 4 SSETGMDPLSQETFDLWSLLPDLQVTCTRLNLS-EFDYP-----LAADMT 52
QY 58 RMQDSLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTF 117
DB 53 VLQE-----GLMGN-----AVPTVT- 67

QY 118 DALSPSPAIPNTDYPGHSFVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKYM 177
DB 68 -----SCAVPSTDDYAGYGLQLDFQNGTAKSVCTYSPNLKLFQCLAKTCPLLRVE 122
QY 178 TTPPGQAVTRAMPYTKAEHVTEVVKRCPNHLSREFNEGQTAPPSHLIRVEGNSHAQV 237
DB 123 SPPPRGISILRAYVYKSHVAEVVKRCPPHRSVEPGE-DAAPPSPHLMRVEGNLQAYYM 181
QY 238 EDPITGRQSVLYPEPPQVGTFTTVLYNFMCSVCVGMNRRPILITVLETRDGVGLG 297
DB 182 EDVNSGRHSVCVPYEGPQVGTCTTVLYNFMCSVCVGMNRRPILITVLETRDGVGLG 241
QY 298 RRCFEARICACPRDKADEDS-IRKQOVSDTKNGDGTKRPRQNTH--GIQMTSIKRK 354
DB 242 RRCFEVRVACPGDRRTEDNTYKRGKLPKSGK-----RELAHPSPSEPLPKKR 292
QY 355 R---SPDDELLYLPVGRRTYEMLLKIKESLELMQVLPQHTI 393
DB 293 LVVVDDDEEFTLRIGKRSRYEMIKKLNDALEQLSLOQKY 334

RESULT 3

S02193

cellular tumor antigen p53 - chicken
N:Alternate names: nuclear oncoprotein p53
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02193
R:Sousi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P.
Nucleic Acids Res. 16, 11383, 1988
A:Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.
A:Reference number: S02193; MUID:89083584; PMID:3060861
A:Accession: S02193
A:Molecule type: mRNA
A:Residues: 1-367 <SOU>
C:Cross-references: EMBL:X13057; NID:g63740; PIDN:CAA31456.1; PID:g63741
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F:161,164,224,228/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 32.1%; Score 764.5; DB 1; Length 367;
Best Local Similarity 44.6%; Pred. No. 1.8e-51;
Matches 169; Conservative 50; Mismatches 105; Indels 55; Gaps 10;
QY 11 LSP-EVFOHIWDFLEQICSVQPIDLNFDVDEPSEDGATNKIEISMDCI RMQDSLDSPMW 69
DB 9 LEPTVFMDLNSMLPY----SMOQL-----PLPEDHSNWQELS-----PLESPDPPPPPP 54
QY 70 PQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
DB 55 PPPLPL-----AAAAAPPPLNPP--TPPRAAPSPVPVST 85
QY 130 TDYPGHSFVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
DB 86 EDYGGDFDFRGVFEAGTAKSVCTYSPVLNKKVYCLAKPCPVQVRGVAPPSPSSLRV 145
QY 190 PVYKAEHVTEVVKRCPNHLSREFNEGQTAPPSHLIRVEGNSHAQYVEDPTTGRQSVLV 249
DB 146 AVYKSEHVAEVRRCPPHRCGGGTG--LAPAQHLIRVEGNSHAQYHDETTKRHSVVV 204
QY 250 PYEPQVGTFTTVLYNFMCSVCVGMNRRPILITVLETRDGVGLRRCFEARICACP 309
DB 205 PYEPPEVSGDCTVLYNFMCSVCVGMNRRPILITVLETRDGVGLRRCFEARICACP 264
QY 310 GDRKADDEDSIRKQOVSDTKNGDG--TKRPRQNTHGIQMTSIKRKSPDELLYLPVR 367
DB 265 GDRKIEENFRK-----RGAGGVAKRAMSPTEAPPK-KRVLNPDNEIFYLQVR 316
QY 368 GREYEMLLKIKESLELMQ 386
DB 317 GRRYEMLKINEALQLAE 335

RESULT 4

S51648
cellular tumor antigen p53 - bovine
N:Alternate names: tumor-suppressor protein p53
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S51648
R:Dequiedt, F.; Willem, L.; Burny, A.; Kettmann, R.
submitted to the EMBL Data Library, September 1994
A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and it
A:Reference number: S51648
A:Accession: S51648
A:Molecule type: mRNA
A:Residues: 1-386 <DEO>
C:Cross-references: EMBL:X81704; NID:g602332; PIDN:CAA57348.1; PID:g602333
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprote
F:168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 31.1%; Score 741.5; DB 1; Length 386;

[illegible]

RESULT 6

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Query Match          30.2%; Score 719.5; DB 1; Length 396;
Best Local Similarity 38.1%; Pred. No. 6e-48;
Matches 162; Conservative 67; Mismatches 145; Indels 51; Gaps 8

Qy 11 LSPVFQHIWDFLEQPCISQPIDLNFVDEPSEDGATNKIEISMDICRMQSDLSLDPMPW 70
Db 14 LSQETFDLWKLL-----PNNVLST-----LPSSDSEEEUFL 46
Qy 71 QYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSYAQPSTFDFALSPSPAI 130
Db 47 SENVAGWLEDPGEALQGSAAAPAAAPAEEDPVAETPAPVASAPATPWLSS--VPSVK 104
Qy 131 DYPGPHFDVYFQOSSTAKSATWYSTELKKLYCOIAKTCPIQIKWTPPPQGVIRAMP 190
Db 105 TYQGDYGFRLGFLHSGTAKSVTCYSPSLNKLFCQAKLTCPVQMLVSTPPPGTVRMA 164
Qy 191 VYKAEHVTEVVKPCNHELSEFNEGQIAPSHLIRVEGNSHAQYVEDPITGROSLVP 250
Db 165 IYKQLQYTEVVRRCPHRSSE--GDG--LAPQHLIRVEGNHABYLDKQTFHRSVVP 222
Qy 251 YEPQVGEFTVLYNFWCMSSCVGGMNRRPILITVLTEDRGQGVIGRCRFEARICAPG 310

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A:Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F08>
A:Cross-references: EMBL:X60017; NID:g506446; PIDN:CAA42632.1; PID:g506447
A:Accession: I38090
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
A:Cross-references: EMBL:X60018; NID:g506448; PIDN:CAA42633.1; PID:g506443
A:Accession: I38091
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212, 'Q', 214-393 <F10>
A:Cross-references: EMBL:X60019; NID:g506450; PIDN:CAA42634.1; PID:g506451
A:Accession: I38092
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-253, 'D', 255-393 <F11>
A:Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453
A:Note: all sequences submitted to the EMBL/GenBank/DBJ databases June 1991
R:Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.
Nucleic Acids Res. 19, 6977, 1991
A:Title: An Alu polymorphism intragenic to the TP53 gene.
A:Reference number: I38093; MUID:92107726; PMID:1762941
A:Accession: I38093
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-393 <FUT>
A:Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakatani, T.
Cancer Res. 51, 5800-5805, 1991
A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell line
A:Reference number: A44905; MUID:92034678; PMID:1933850
A:Accession: A44905
A:Molecule type: DNA
A:Residues: 246-247, 'W', 249-250 <YAM>
A:Cross-references: GB:563157; NID:g337829; PIDN:AAB20140.1; PID:g337830
A:Note: sequence extracted from NCBI backbone (NCBIN:63157, NCBIp:63158)
A:Note: mutation from a liver metastasis of a gastric cancer
R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
Oncogene 6, 1067-1071, 1991
A:Title: Use of the single strand conformation polymorphism technique and PCR to detect
A:Reference number: I58354; MUID:91296386; PMID:1648702
A:Accession: I58354
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 244-247, 'W', 249-252 <HEN1>
A:Cross-references: GB:541969; NID:g1679931; PIDN:AAB19324.1; PID:g232814
A:Accession: I78850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 274-277, 'S', 279-282 <HEN2>
A:Cross-references: GB:541977; NID:g1679932; PIDN:AAB19325.1; PID:g232816
R:Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1993
A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphoblastoid cell line
A:Reference number: I52681; MUID:94036762; PMID:8221626
A:Accession: I52681
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 327-331, 'DQTSFKENC' <CHO>
A:Cross-references: GB:566666; NID:g436292; PIDN:AAB28601.1; PID:g436293
A:Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymphoblastoid cell line
R:Petersen, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
Mol. Gen. Genet. 249, 425-431, 1995
A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragment
A:Reference number: S60151; MUID:96133682; PMID:8552047
A:Accession: S60151
A:Molecule type: DNA
A:Residues: 3-44 <PET>
R:Dang, C.V.; Lee, W.M.F.
J. Biol. Chem. 264, 18019-18023, 1989
A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, N-myc, p53, HSP70,

Query Match 30.1%; Score 717.5; DB 1; Length 393;
Best Local Similarity 41.2%; Pred. No. 8.4e-48;
Matches 156; Conservative 60; Mismatches 116; Indels 47; Gaps 9;
QY 11 LSPVFOHIWDFLEOPICSVQPDLDNFVDPSESDGATNKIEISMDCTRMQDSLSDDPMPW 70
DB 14 LSOETFSDLKLLPE-----NNVSLPLSQAMDDMLSLPDDIEQWFTF--DP--- 58
QY 71 QYTNLGLLMDQIQNGSSSTSPYNTDHAQNSVTAPSPVAOPSSSTFDALSP----SPA 126
DB 59 -----GPEAPRMPFAAPR--VAPAP-AAPAPAPAPAPSWPLSSV 97
QY 127 PSNTDYPGPHSFDVSFOQSTAKSATWTYSTEKLKLYCQIAKTCPIQIKVMTPPQGA 186
DB 98 PSQKTYQGSYGFRLGFLHSGTAKSVTCYSPALNKMFCQLAKTQVGLWVDSTPPGTRV 157
QY 187 RAMPVYKAEHVTEVVKRCPNHELRSFNEQIAPPSHLIRVEGNSHAQVVEDITGRQS 246
DB 158 RAMAIYKOSQHMTVEVRRCPPHHE--RCSDSGLAPQPHLIRVEGNLRYEYLDLDRNTRHS 215
QY 247 VLVPYEPQVQTEFTTVLYNFMCSVCGVMNRRLIIVTLETRDQVGLGRRRCFEARIC 306
DB 216 VVVPYEPVGSQDCTTHYNYMCSGCMGNNRRPILITITLEDSSGNLGRNSFEVRVC 275
QY 307 ACPGRDRKADEDSIRKQOVSSTKNGDGTKRPFQNTHTGIMTSIKKRRSP-DDELLYLP 365
DB 276 ACPGRDRRTTEENLRKKGEPHHELPGSTKRALPNNT-----SSSPQPKKKPLDGEYFTLQ 331
QY 366 VRGRETTEMLLKESLEL 384
DB 332 IGRERFEMPRELNEALEL 350
RESULT 8
DNMS53
cellular tumor antigen p53 - mouse
N:Alternate names: oncoprotein p53
C:Species: Mus musculus (house mouse)
C>Date: 28-Aug-1985 #sequence.revision 04-Oct-1996 #text.change 11-May-2000
C:Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
R:Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
EMBO J. 3, 2179-2183, 1984
A:Title: Analysis of the gene coding for the murine cellular tumour antigen p53.
A:Reference number: A22739; MUID:85027173; PIDN:CAA25420.1; PID:g871421; GB:X01237;
A:Accession: A22739
A:Molecule type: DNA
A:Residues: 1-134, 'V', 136-390 <BIE>
A:Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1; PID:g871421; GB:X01237;
R:Chumakov, P.M.
Bioorg. Khim. 13, 1691-1694, 1987
A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.
A:Reference number: S06336; MUID:88221682; PMID:3329909
A:Accession: S06336
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-134, 'V', 136-390 <CHU>
R:Zakut-Houri, R.; Oren, M.; Bienz, B.; Lavie, V.; Hazum, S.; Givol, D.
Nature 306, 594-597, 1983
A:Title: A single gene and a pseudogene for the cellular tumour antigen p53.
A:Reference number: A02684; MUID:84068204; PMID:6646235
A:Accession: A02684
A:Molecule type: mRNA
A:Residues: 1-159, 'H', 161-167, 'G', 169-233, 'I', 235-390 <ZAK>
A:Cross-references: GB:X01237; GB:X01700; NID:g53575
R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
Mol. Cell. Biol. 6, 3232-3239, 1986
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
A:Reference number: S38822; MUID:87064640; PMID:3023970
A:Accession: S38822
A:Molecule type: mRNA
A:Residues: 1-390 <ARAI>
A:Cross-references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1; PID:g200199
A:Accession: S38823

C:Genetics:

A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: liver; tumor

Query Match 29.5%; Score 704; DB 2; Length 393;

Best Local Similarity 38.6%; Pred. No. 9.3e-47;
Matches 165; Conservative 69; Mismatches 134; Indels 60; Gaps 11;

Qy 11 LSPVFOHINDFLEQPTCSVQPIDLNFVDEPSEDAATKIEISMDICRMDSLDSPM-- 68

Db 14 LSQETFDLWKLK-----PPNVLSTLPSSDS-----IEELFUSEVTG 52

Qy 69 WPOYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIP 127

Db 53 WLEDSGGAL-----QGVAAAAAAT-----AEDPVTEPAPVASAPATPWLSS--VP 98

Qy 128 SNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVIR 187

Db 99 SYKTFQGDYGFRLGFLHSGTAKSTCTYSTSLNKLFCQLAKTCVPQLVWVNSTPPPGTRVR 158

Qy 188 AMPYKKAHVTEVVKCPNHELSEFNEGOIAPPISHLIRVEGNSHAQYVEDPITGQSV 247

Db 159 AMAYKKLQYTWVVRCPHERSEGD--SLAPPQHLIRVEGNSHAQYVEDPITGQSV 216

Qy 248 LVPYEPPOVGTFTVLYNMCNSSCVGGMNRRPILITVLETRDGVGLRRCFEARICA 307

Db 217 VVPYEPPEVSGDCTTIHYNMCNSSCVGGMNRRPILITVLETRDGVGLRRCFEARICA 276

Qy 308 CPGRDRKADEDSIRKQVSDSTKNGDGTGKRPFRONTGHIQMTSITKRRSPDDELLYLPR 367

Db 277 CPGRDRTEKNEKFOKGEPCPELPPKSAKRALPTNT---SSSPPPKKTLTLDGEYFTLKIR 333

Qy 368 GREYEMLLKTESLEMLQVLPQHTIE-----TYRQQQQQOHOHLKHLLSACFERNEL 421

Db 334 GHERKMFQELNEALELKDQAASKGSDNGAHSSYLSKKGQASRLKLM----- 385

Qy 422 VEPRRETP 429

Db 386 ---KREGP 390

RESULT 11

S38824

cellular tumor antigen p53, minor splice form - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S38824; S35478

R:Araki, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

Mol. Cell. Biol. 6, 3232-3239, 1986

A:Title: Immunologically distinct p53 molecules generated by alternative splicing.

A:Reference number: S38822; MUID:87064640; PMID:3023970

A:Accession: S38824

A:Molecule type: mRNA

A:Residues: 1-381 <RAN>

A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203.

R:Han, K.A.; Kulesz-Martin, M.F.

Nucleic Acids Res. 20, 1979-1981, 1992

A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different tiss

A:Reference number: S35478; MUID:92253421; PMID:1579500

A:Accession: S35478

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-381 <HAN>

A:Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203

A:Note: The nucleotide sequence was submitted to the EMBL data Library, July 1988

C:Comment: This sequence, produced by alternative splicing of the tenth intron, lacks th

s not known.

C:Superfamily: cellular tumor antigen p53

C:Keywords: alternative splicing; phosphoprotein; zinc

F:1-44/Domain: transcription activation #status predicted <TRA>

F:16-26/Region: conserved region I

F:99-289/Domain: DNA-binding core #status predicted <DBC>

F:108-121/Region: L1 loop

F:114-139/Region: conserved region II

F:160-192/Region: L2 loop

F:168-178/Region: conserved region III

F:231-252/Region: conserved region IV

F:233-248/Region: L3 loop

F:267-283/Region: conserved region V

F:313-319/Region: nuclear location signal

F:319-357/Region: tetramer association

F:7, 9, 12, 18, 23, 37/Binding site: phosphate (Ser) (covalent) #status predicted

F:173, 176, 235, 239/Binding site: zinc (Cys, His, Cys) #status predicted

F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted

Query Match 29.5%; Score 702; DB 2; Length 381;

Best Local Similarity 40.4%; Pred. No. 1.3e-46;

Matches 159; Conservative 58; Mismatches 113; Indels 64; Gaps 11;

Qy 2 SQTQTNEF-LSPEVFOHINDFLEQPTCSVQPIDLNFVDEPSEDAATKIEISMDICRMQ 60

Db 7 SQSDISLEPLSQETFSGLMKLL-----PPED-----ILSPHC----- 40

Qy 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDA 119

Db 41 ---MDDLPLPQ-----DVEEFEGPSEALRVSGAPAAQDPVETPGPVA----- 81

Qy 120 LSPSPA-----IPSNTPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTC 171

Db 82 --PAPATPWPPLSSFPVSKTYGNGYGHFGFLQSGTAKSVMTYSPPLNKLFLQAKTCP 139

Qy 172 IQIKVMTPPGAGVIRAMPYVYKKAHVTEVVKCPNHELSEFNEGO-IAPPSHLIRVEG 230

Db 140 VQLWVSATPPAGSVRAMAIYKSKHMTVEVVRCPHHE---RCSDDGDLAPQHLIRVEG 196

Qy 231 NSHAQYVEDPITGQSVLVPYEPPOVGTFTVLYNMCNSSCVGGMNRRPILITVLET 290

Db 197 NLYPEYLEDRTGFRHSVVVYEPPEAGSEYTHYKMCNSSCVGGMNRRPILITVLET 256

Qy 291 RDGVLGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTGKRPFRONTGHIQMTS 350

Db 257 --SGNLLGRDSEVRVACACPGDRRTEENFRKKEVLCPELPGPSAKRALPTCT---SASP 313

Qy 351 IKRRSPDDELLYLPRVGRRETYEMLLKIKESLEL 384

Db 314 PQKKPLDGEYFTLKIRGRKRFEMFRELNEALEL 347

RESULT 12

JC6193

tumor suppressor p53 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000

C:Accession: JC6193

R:Le Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.

Gene 185, 169-173, 1997

A:Title: cDNA cloning and immunological characterization of rabbit p53.

A:Reference number: JC6193; MUID:97208869; PMID:9055811

A:Accession: JC6193

A:Molecule type: mRNA

A:Residues: 1-391 <LEA>

A:Cross-references: EMBL:X90592; NID:gl532043; PIDN:CAA62216.1; PID:gl532044

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: tumor

Query Match 29.4%; Score 699.5; DB 2; Length 391;

Best Local Similarity 40.7%; Pred. No. 2.1e-46;

Matches 156; Conservative 59; Mismatches 111; Indels 57; Gaps 10;

Qy 11 LSPEVFOHINDFLEQPTCSVQPIDLNFVDEPSEDAATKIEISMDICRMQSDLSDPMPW 70

Db 14 LSQETFDLWKLK---PENNLITTSILN-----PPVD-----DLLSAED----- 48


```

Query Match      4.8%; Score 114.5; DB 2; Length 3942;
Best Local Similarity 21.2%; Pred. No. 9.4;
Matches 113; Conservative 61; Mismatches 190; Indels 169; Gaps 25;

QY      1  MSQSTQTNFLSPVEQHTWDFLEQPI-----CSVQPIDLNFVDEPSED----- 44
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2038  LGQGLYGSFTD---LRHPTDLLSHPLRRYSVSNITYSDHRYGPRGDAVGFEASLAQ 2094

QY      45  -GATNKKIEISMDCIRMQSDSLSDPMWPQVTNGLLNSMDQQ-Q-LQNGSSSTSP-----YNTD 98
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2095  YGATTAREISRMG-----AALNSMDQYGRGHRGGSGGPPOLVQYQPO 2135

```

DB 2136 HGP-GLSAPGGLAPLRSGLTGNTYPEGQPS-----PGNLAQYGPAAQSQATAVRQLLPSTAT 2191

QY 153 -----WYSTEELKUYCQIAKTCPTQIK---VMTPPQGAIVTRAMPVYKKASHVTEVK 203

Db 2192 VRAADGMIST-----INTPIATLPTTTPASVLRPWVGGMYR-----PYVSGGVTT 2239

204	QY	RCFNGHLSREFNQGJLAP	-----PSHLIRYEGNSHAQIVLDFPLIGKQSVLVPLFE	FPQWG	237
2240	Db	AVPLTSLTR	---VPMIAPRVPLGAGLYRYPAPRF	-----PIA	SSVPPAEGPVYLK
258	QY	TEFTTVLYNFMNCSSCVGGMNRRPILI	IVTLTRDQGVLGRRRCFEARICACPG	-----	310
2288	Db	KPAAT	-----KASGAGGPPRPDELPAAGVAREEP	FTTAPAVIKEAPVAPAGCPAPPPP	2340

```
QY      :  
-----KURKADELSLRKKVSDSTANGDIGTRKPPFRQNTHGIQ   347  
          :: |:: |||||  
  
Db    2341 GOKPAGEAAGSGSVLSPASEKEEASDROKQOE-----Q   2379  
          :: |:: |||||  
  
QY    348 MTSIKRRRDPDELILPV-----RRETYEMLLKIKESLELMQLPQHETIET   395  
        : ::: |:: |:: |:: |:: |:: |:: |:: |::
```

[illegible]

hypothetical protein K10G6.3 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

R:Davidson, S.; Wohlmann, P.; Mullen, G.
submitted to the EMBL Data Library, July 1997
A:Description: the sequence of *C. elegans* cosmid K1066.
A:Reference number: Z21111
A:Accession: T32008
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA

A; Cross-references: EMBL:AF015669; PIDN:AA866098.1; GSPDB:GN0020; CESP:K10G6.3
A; Experimental source: strain Bristol N2; clone K10G6
C; Genetics:
A; Gene: CESP:K10G6.3
A; Map position: 2
A; Introns: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3

Query match	4.7%	Score 111.5	DB 2	Length 1815

Search completed: August 7, 2003, 09:53:26
Job time : 18.1241 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 7, 2003, 09:32:13 ; Search time 7.94483 Seconds
(without alignments)
2651.784 Million cell updates/sec

Title: US-09-538-106-15

Perfect score: 2383

Sequence: 1 MSQSTQTFNEFLSPVFOHIW.....PKQSDVFFRRHSKPNRSVYP 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

* Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1297.5	54.4	636	1 P73_HUMAN	Q15350 homo sapien
2	1296.5	54.4	637	1 P73_CERAE	Q9XSK8 cercopithec
3	847.5	35.6	396	1 P53_ONCMY	P25035 oncorhynchu
4	819.5	34.4	369	1 P53_BARBU	Q9W678 barbus barb
5	805.5	33.8	373	1 P53_BRARE	P79734 brachydanio
6	800	33.6	376	1 P53_ICTPU	Q93379 ictalurus p
7	777.5	32.6	363	1 P53_XENLA	P07193 xenopus lae
8	776	32.6	367	1 P53_TETMO	Q9W679 tetraodon m
9	770	32.3	386	1 P53_FELCA	P41685 felis silve
10	767	32.2	386	1 P53_PIG	Q9TUB2 sus scrofa
11	764.5	32.1	367	1 P53_CHICK	P10360 gallus gall
12	753.5	31.6	381	1 P53_CANFA	Q29537 canis famil
13	746.5	31.3	352	1 P53_ORVLA	P79820 oryzias lat
14	741.5	31.1	386	1 P53_BOVIN	Q29628 bos taurus
15	736	30.9	391	1 P53_MARMO	P10361 marmota mon
16	732	30.7	391	1 P53_RAT	Q1361 rattus norv
17	730.5	30.7	391	1 P53_CAVPO	Q9WUR6 cavia porce
18	729.5	30.6	393	1 P53_TUPGB	Q9TAL1 tupaja glis
19	727.5	30.5	382	1 P53_SHEEP	P51664 ovis aries
20	719.5	30.2	396	1 P53_MESAU	Q00366 mesocricetu
21	718	30.1	366	1 P53_PLAFA	O12946 platichthys
22	717.5	30.1	393	1 P53_HUMAN	P04637 homo sapien
23	715.5	30.0	393	1 P53_MACFA	P56423 macaca fasc
24	715	30.0	390	1 P53_MOUSE	P02340 mus musculu
25	714.5	30.0	393	1 P53_CERAE	P13481 cercopithec
26	713.5	29.9	393	1 P53_MACMU	P56424 macaca mula
27	710.5	29.8	342	1 P53_XIPHE	O57538 xiphophorus
28	709.5	29.8	342	1 P53_XIPMA	Q92143 xiphophorus
29	708	29.7	393	1 P53_CRIGR	O09185 cricetus
30	699.5	29.4	391	1 P53_RABIT	Q95330 oryctolagus
31	696	29.2	314	1 P53_SPERE	Q64662 spermophilu
32	689.5	28.9	280	1 P53_HORSE	P79892 equus caball
33	591.5	24.8	207	1 P53_EQUAS	Q29480 equus asinu

ALIGNMENTS

RESULT 1

P73_HUMAN
ID P73_HUMAN STANDARD; PRT; 636 AA.
AC O15350: O15351; Q9NTK8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor protein p73 (p53-like transcription factor) (p53-related
DE protein).
DE TP73 OR P73.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE-Colon;
RX MEDLINE=97433090; PubMed=9288759;
RA Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A.,
RA Minty A., Chalton P., Lelias J.-M., Dumont X., Ferrara P., McKeon F.,
RA Caput D.;
RT "Noncallelically expressed gene related to p53 at 1p36, a region
RT frequently deleted in neuroblastoma and other human cancers.";
RL Cell 90:809-819(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=99289209; PubMed=10362363;
RA Yoshikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagiwara K.,
RA Harris C.C.;
RT "Mutation analysis of p73 and p53 in human cancer cell lines.";
RL Oncogene 18:3415-3421(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=98389621; PubMed=9721206;
RA Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B.,
RA Jenkins R., Smith D.I., Liu W.;
RT "Genomic organization and mutation analysis of p73 in
RT oligodendrogliomas with chromosome 1 p-arm deletions.";
RL Genomics 51:359-363(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).
RC TISSUE-Neuroblastoma;
RX MEDLINE=99021697; PubMed=9802988;
RA De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,
RA Annichiarico-Petruzzelli M., Leviero M., Melino G.;
RT "Two new p73 splice variants, gamma and delta, with different
RT transcriptional activity.";
RL J. Exp. Med. 188:1763-1768(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).
RC TISSUE-Breast cancer, Hepatoma, Lymphocytes, and Skin;
RX MEDLINE=99310938; PubMed=10381648;
RA De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G.,
RA Costanzo A., Leviero M., Knight R.A.;
RT "Additional complexity in p73: induction by mitogens in lymphoid cells
RT and identification of two new splicing variants epsilon and zeta.";

34 117.5 4.9 5147 1 PCLO_HUMAN Q9Y6V0 homo sapien
35 111.5 4.7 808 1 PTFB_DROME Q05192 drosophila
36 109 4.6 4273 1 PKSM_BACSU P40872 bacillus su
37 107 4.5 1912 1 PTPD_HUMAN P23468 homo sapien
38 106.5 4.5 513 1 MX13_MOUSE Q8BGT6 mus musculu
39 106 4.4 490 1 FXN3_HUMAN Q00409 homo sapien
40 105.5 4.4 395 1 SDC_DROME P49415 drosophila
41 105.5 4.4 5085 1 PCLO_RAT Q91KS6 rattus norv
42 105 4.4 766 1 SFL1_YEAST P20134 saccharomyc
43 104.5 4.4 1703 1 SNF2_YEAST P22082 saccharomyc
44 103.5 4.3 1507 1 SIMA_DROME Q24167 drosophila
45 103 4.3 1533 1 Y586_HUMAN Q9BVV6 homo sapien


```
Query Match 54.4% Score 1297.5; DB 1; Length 636;
Best Local Similarity 61.4%; Pred. No. 8.7e-89;
Matches 258; Conservative 47; Mismatches 84; Indels 31; Gaps 9;

QY 1 MSQSTQTNFLSPE---VFQIHWDFLEQPCISQVQIDNLFVDEPSEDGATNKI---EIS 53
DQ 1 MAQSTAT-----SPDGGTTTFFHLWSSLEP-----DSTYFDLPQSSKGNNEVVGTTDSS 48

QY 54 MDCIRMQDSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQP 113
DQ 49 MDVHFLEGMTTS-----VMAQFNLLSMTDQMSRAASAPYTPHAA--SVPTHSPPYAQP 102

QY 114 SSTFDALSPSPAIPTNDYDGPFFHFEVTFQSSSTAKSATWTYSPELAKLYCQIAKTCPIQ 173
DQ 103 SSTFDMSPAVPISNTDYPGPHFEVTFQSSSTAKSATWTYSPLLKLYCQIAKTCPIQ 162

QY 174 IKVMTPPQGAIVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNH 233
DQ 163 IKVSTPPPGTAIRAMPVYKKAHVTDVVKRCPNHELGRDFNEGQSPASHLIRVEGNL 222

QY 234 AQYVEDPITGRQSVLVPYEPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDG 293
DQ 223 SQYVDDPVTGRQSVVVPYEPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDG 282

QY 294 QVLRGRCFEARICACPGDRKADEDSIRKQV--SDSTKNGDGTFRPQNTHTGQM--T 349
DQ 283 QVLRGRRSEGRICACPGDRKADEDSIRKQV--SDSTKNGDGTFRPQNTHTGQM--T 349

QY 350 SIKRRSPDDELLYLPVRGRTYEMLLKIKESLELMQYLPOHTTETTRQOQO--QOHOHL 407
DQ 343 GVKRRHGDEDTYYLQVRGRENFEILMKLESLELMELVPOPLVDYSYRQOQOQLLRPSHL 402

RESULT 2
ID P73_CERAE STANDARD; PRT; 637 AA.
AC Q9XSK8; Q9TSQ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor protein p73 (p53-like transcription factor) (p53-related
protein).
GN TP73 OR P73.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=Kidney;
RA Caput D.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN
CC (BY SIMILARITY).
CC -!- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=Q9XSK8-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=Q9XSK8-2; Sequence=VSP_006537;
CC -!- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
-----

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or send an email to license@isb-sib.ch).
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EMBL; Y11419; CAA72224.1; -
EMBL; Y11419; CAA72225.1; -
HSP; O15350; ICK.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
Pfam; PF00536; SAM; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOM; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Transcription regulation; Activator; DNA-binding; Anti-oncogene;
Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing.
VARSPIC 495 637
SFLGLGCPNCEIVETSGLOSIYHLQNTLTDGLAKLPIE
QYRTIWRGLQDLKQGHYDGAQAQQLLRSSNAAISIGSG
ELQKRVMEAVHVRVRRITIPNRRGGPGADENADPFDL
PCKARKQPIKEEFTEAEIH -> RTWGP (in isoform
Beta).
/FTid=VSP_006537.
SQ SEQUENCE 637 AA; 69630 MW; 7CB200B919C970A CRC64;

Query Match 54.4%; Score 1296.5; DB 1; Length 637;
Best Local Similarity 61.2%; Pred. No. 1e-88;
Matches 257; Conservative 48; Mismatches 84; Indels 31; Gaps 9;

QY 1 MSQSTQTNFLSPE---VFQIHWDFLEQPCISQVQIDNLFVDEPSEDGATNKI---EIS 53
DQ 1 MAQSTTT-----SPDGGTTTFFHLWSSLEP-----DSTYFDLPQSSKGNNEVVGTTDSS 48

QY 54 MDCIRMQDSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQP 113
DQ 49 MDVHFLEGMTTS-----VMAQFNLLSMTDQMSRAASAPYTPHAA--SVPTHSPPYAQP 102

QY 114 SSTFDALSPSPAIPTNDYDGPFFHFEVTFQSSSTAKSATWTYSPELAKLYCQIAKTCPIQ 173
DQ 103 SSTFDMSPAVPISNTDYPGPHFEVTFQSSSTAKSATWTYSPLLKLYCQIAKTCPIQ 162

QY 174 IKVMTPPQGAIVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNH 233
DQ 163 IKVSAAPPPTAIRAMPVYKKAHVTDVVKRCPNHELGRDFNEGQSPASHLIRVEGNL 222

QY 234 AQYVEDPITGRQSVLVPYEPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDG 293
DQ 223 SQYVDDPVTGRQSVVVPYEPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDG 282

QY 294 QVLRGRCFEARICACPGDRKADEDSIRKQV--SDSTKNGDGTFRPQNTHTGQM--T 349
DQ 283 QVLRGRRSEGRICACPGDRKADEDSIRKQV--SDSTKNGDGTFRPQNTHTGQM--T 349

QY 350 SIKRRSPDDELLYLPVRGRTYEMLLKIKESLELMQYLPOHTTETTRQOQO--QOHOHL 407
DQ 343 GVKRRHGDEDTYYLQVRGRENFEILMKLESLELMELVPOPLVDYSYRQOQOQLLRPSHL 402

RESULT 3
ID P53_ONCMY STANDARD; PRT; 396 AA.
AC P25035;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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QY 143 QOSTAKSARWTSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAMPVYKKAHVTEV 202
Db 78 POSGTSVCTSYSSDLNKLFCQAKTCPQVMVNVAPPQGSVIRATAIYKKSHEVAEV 137
QY 203 KRCPNHLSREFNEGQIAPSHLIRVGNHQAQVVEDPIICRQSVLPVYPPQVGTFTT 262
Db 138 RRCPPHRTPD-DGG-LAPAAHLIRVGNHQAQVVEDPIICRQSVLPVYPPQVGTFTT 195
QY 263 VLYNFMNCSGVMGMRPILIIIVTLETRDQVLRRCFEARICACPRDKADEDSIRK 322
Db 196 VLYNFMNCSGVMGMRPILIIIVTLETRDQVLRRCFEARICACPRDKADEDSIRK 255
QY 323 QQVSDSTKNGD---GTVKRF-RQNTGHIQMTSIRKRR---SPDDELLYLPVGRGTYE 373
Db 256 DQ---EFKTLDKIPANSKSLTKDSTSVPRPEGSKKAKLSSGSDIEIYTLQVRGKRYE 312
QY 374 MLKKIKESLELMQYLPQHTIETRYQQ 399
Db 313 MLKKINDSLELSVDVPPSEMDRYNQK 338

RESULT 5
P53_BRARE
ID - P53_BRARE STANDARD; PRT; 373 AA.
AC P79734; Q90440;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR DRP53.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97344388; PubMed=9200835;
RA Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
RA Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;
RT "Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
RL expression during embryogenesis.";
RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
RN [2]
RP SEQUENCE OF 140-212 FROM N.A.
RA Winge P.;
RN Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and PAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U60804; AAB40617.1; -
CC EMBL; U46593; ABA97408.1; -
CC HSP; P04637; ITUP.
CC ZFIN; ZDB-GENE-990415-270; tp53.
CC InterPro; IPR002117; P53.
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DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 70 260 BY SIMILARITY.
FT DOMAIN 301 332 OLIGOMERIZATION.
FT DOMAIN 345 366 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 280 296 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 372 372 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 373 AA; 41899 MW; AC7AB724FA6B61FF CRC64;

Query Match 33.8%; Score 805.5; DB 1; Length 373;
Best Local Similarity 53.9%; Pred. No. 1.3e-52;
Matches 158; Conservative 42; Mismatches 82; Indels 11; Gaps 4;

QY 112 QPSSTFDALSPSPAIPNTDYPGPHSFDSVFSQOSTAKSATWTSTELKLYCQIAKTC 171
Db 55 QPST---LPPTSTVPETSDYPGDHGFRLRFPQSGTAKSVTCTYSPDLNKLFCQAKTC 110
QY 172 IQIKVMTPPQGAIVRAMPVYKKAHVTEVVKRCNPNHLSREFNEGQIAPSHLIRVEGN 231
Db 111 QVMYDVAPPQGSVVRATAIYKKSHEVAEYVRCPPHHE--RTPGDNLAPAGHLIRVEGN 168
QY 232 SHAOYVEDPIICRQSVLPVYPPQVGTFTTLYNFMNCSGVMGMRPILIIIVTLETR 291
Db 169 QRANYREDNITLRHSVFVPEAPQGAETVTLNFMNCSGVMGMRPILIIIVTLETR 228
QY 292 DQVGLRRCFEARICACPRDKADEDSIRK-QQVSDSTKNGDGTKRPFQNTGHIOM-- 348
Db 229 EGQLLRGSFEVRCVACPCPRDKRTEESNFKKQDKTKMAKTTTGTKRSLVKSSSATLRP 288
QY 349 --TSIKARRSPDDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQ 399
Db 289 EGSKKAKGSSDSEIFTQVRGRERYEILKINDSLELSVDVPPSEMDRYNQK 341

RESULT 6
P53_ICTPU
ID - P53_ICTPU STANDARD; PRT; 376 AA.
AC O93379;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (tumor suppressor p53).
GN TP53 OR P53.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9907179; PubMed=9854815;
RA Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
RT "Identification and characterization of the tumor suppressor p53 in
channel catfish (Ictalurus punctatus)".;
RL Comp. Biochem. Physiol. 120B:675-682(1998).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and PAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC
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Db 94 TYPGDFRGLGFLHSGTAKSVCTCTSPALNKLFCQLAKTCPVQLWVSPPPGTRVRAMA 153
Qy 191 VYKKAHVTEVVKRCPNHELSEFNEQGIAPPSSHLIRVEGNSHAQYVEDPTTGROSLVP 250
Db 154 IYKSEVTEVVKRCPNHELSEFNEQGIAPPSSHLIRVEGNSHAQYVEDPTTGROSLVP 212
Qy 251 YEPPQVGTFTVLYNFMCMSCVGGMNRRLPILITVLETRDGOVLGRRCFEARIACPG 310
Db 213 YEPEVGSDDCTIHYNFMCMSCVGGMNRRLPILITVLETRDGOVLGRRCFEARIACPG 272
Qy 311 RDRKADEDSIRKQOVSDSTNGDGTGKPRFRONTHGHIOMTSIKKRRSPDDELLYLVPVGR 370
Db 273 RDRTEENFLKQSGPEPPPGSTKRALPTSTSSSPVQKKPLDGEYFTLQIRGE 329
Qy 371 TYEMLLKIKESLEMLQYLPQHTIETIRO--QOOQOHOHLQKHLLSACFRNELVEPRRET 428
Db 330 RFEMFRELDALDKD-----AQTAESGENRAHSHLSK-----KGQS 369
Qy 429 PKOSDVFFRHSKP 441
Db 370 PS-----RHKKP 376

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RESULT 11

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P53_CANFA
ID P53_CANFA STANDARD; PRT; 367 AA.
AC P10360;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (tumor suppressor p53).
GN TP53.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPAFAS;
RX MEDLINE=89083584; PubMed=3060861;
RA Soussi T.;
RT "Nucleotide sequence of a cDNA encoding the chicken p53 nuclear
  oncoprotein."
RL Nucleic Acids Res. 16:11383-11383(1988).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
  growth arrest or apoptosis depending on the physiological
  circumstances and cell type. Involved in cell cycle regulation as
  a trans-activator that acts to negatively regulate cell division
  by controlling a set of genes required for this process. One of
  the activated genes is an inhibitor of cyclin-dependent kinases.
  Apoptosis induction seems to be mediated either by stimulation of
  BAX and FAS antigen expression, or by repression of Bcl-2
  expression (by similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
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  or send an email to license@isb-sib.ch).
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CC EMBL; X13057; CAA31456.1; -.
CC PIR; S02193; S02193.
CC HSSP; P04637; 1TUP.
CC InterPro; IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PR00386; P53SUPPRESSR.

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DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 30 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 87 278 BY SIMILARITY.
FT DOMAIN 308 339 OLIGOMERIZATION.
FT DOMAIN 347 364 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 292 306 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 366 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 367 AA; 40169 MW; FC37D0FDF9195B6 CRC64;

Query Match 32.1%; Score 764.5; DB 1; Length 367;
Best Local Similarity 44.6%; Pred. No. 1.4e-49;
Matches 169; Conservative 50; Mismatches 105; Indels 55; Gaps 10;

Qy 11 LSP-EVQHIWDFLEQICSVQPIDLNFVDPSEGDGATNKIEISMDCIQMQDSDLSDPMW 69
Db 9 LEPTVEFMDLWSMLPY---SMQQL-----PLPETHSNWQELS-----PLEPSDPPPPPP 54
Qy 70 PQYTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDLSPSPAIPSN 129
Db 55 PPPLPL-----AAAAPPPLNPP--TPPRAAPSPVVPST 85
Qy 130 TDYGPHSFVSFOOSSTAKSATWTYSTELKKLYCIAKTCPIQIKVMTPPQGAIVRAM 189
Db 86 EDYGGDFDFRVGFEAGTAKSVCTCTSPVLNKNVYCRLAQPCPVQVRGVAPPGGSSLRV 145
Qy 190 PVYKKAHVTEVVKRCPNHELSEFNEQGIAPPSSHLIRVEGNSHAQYVEDPTTGROSLVP 249
Db 146 AVYKKEHVTEVVKRCPNHELSEFNEQGIAPPSSHLIRVEGNSHAQYVEDPTTGROSLVP 204
Qy 250 PYEPQVGTFTVLYNFMCMSCVGGMNRRLPILITVLETRDGOVLGRRCFEARIACAP 309
Db 205 PYEPVGSDDCTVLYNFMCMSCVGGMNRRLPILITVLETRDGOVLGRRCFEARIACAP 264
Qy 310 GRDKADEDSIRKQOVSDSTNGDGTG--TKRFRONTHGHIOMTSIKKRRSPDDELLYLVP 367
Db 265 GRDKADEDSIRKQOVSDSTNGDGTG--TKRFRONTHGHIOMTSIKKRRSPDDELLYLVP 316
Qy 368 GRETYEMLLKIKESLEMLQ 386
Db 317 GRRRYEMLLKIKESLEMLQ 335

RESULT 12
P53_CANFA
ID P53_CANFA STANDARD; PRT; 381 AA.
AC Q29537; Q9TV78;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (tumor suppressor p53).
GN TP53 OR P53.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=98178696; PubMed=9519881;
RA Veldhoen N., Milner J.;
RT "Isolation of canine p53 cDNA and detailed characterization of the
  full length canine p53 protein."
RL Oncogene 16:1077-1084(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
  Watarai T., Hasagawa A., Tsujimoto H.;
RT "Aberrations of p53 tumor suppressor gene in various spontaneous
  tumors in the dog."

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DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.
FT DOMAIN 1 48
FT DNA_BIND 307 273
FT DOMAIN 302 331
FT DOMAIN 332 350
FT DOMAIN 334 350
FT DOMAIN 283 295
FT MOD_RES 351 351
FT VARIANT 91 91
FT CONFLICT 22 22
SQ SEQUENCE 352 AA; 39753 MW; 196868A66351BFF5 CRC64;

Query Match 31.3%; Score 746.5; DB 1; Length 352;
Best Local Similarity 43.1%; Pred. No. 3e-48;
Matches 163; Conservative 54; Mismatches 92; Indels 69; Gaps 10;

Qy 16 FQHWDFLEQICVQPIDNFVDEPSEDGATNKIEISDMCIRMQSDLSDPMPQVYTNL 75
Db ||||| : : : : : ||| : : : |||
14 FQELWETVSYSP--PLETISLPTVNEPTGSW-----VATGDMFLDQDLS----- 55
Qy 76 GLLSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAQPSSFTDALSPTSAPTSNTDYPGP 135
Db : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
56 ---GTFDDKI-----FDIP-----IEPVPTNEVNPPTTVPVTDYPGS 91
Qy 136 HSFDVSFQOSSTAKSATWYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAMPVYKKA 195
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
92 YELELRQKSGTAKSVTSTYSETLNKLYCQIAKTSPIEVRSKPPGAILRAVAYKKT 151
Qy 196 EHVTVEVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLYPEPPQ 255
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
152 EHADVVRRCPPHQ-----NEDSVHRSHLIRVEGSLAQYFEDPYTKRQSVTVPEPPQ 206
Qy 256 VGTEFTVLYNFMNCSSCVGMNRRPILIVITETRGQVLCRCFEARICACGRORKA 315
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
207 PGSEMTTILSYMNCSCMGGMNRRPILITLTLET-EGVLGLRRCFEVRICACGRDRKT 265
Qy 316 DEDSIRKQOVSDDTKNGDGRKRPQNTGHQMTSIKRRRS-----PDDELLYLPVRG 368
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
266 EESRQKTPK-----KRKVTPTN-----SSSRKKSHSGEEDNREVTFHEVYG 311
Qy 369 RETYEMLLKTKESLELMQ 386
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
312 RERVEFLKKINDGLELLE 329

RESULT 14
P53_BOVIN
AC Q29628;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Bos taurus (Bovine), and
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913, 9915;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Bovine; TISSUE=Liver;
RX MEDLINE=95352829; PubMed=7626789;
RA Dequiedt F., Kettmann R., Burny A., Willems L.;
RT "Nucleotide sequence of the bovine p53 tumor-suppressor cDNA.";
RL DNA Seq. 5:261-264(1995).
RN [2]
RC SEQUENCE OF 13-386 FROM N.A.
RC SPECIES=Bovine; STRAIN=Holstein; TISSUE=Thymus;
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RX MEDLINE=96401400; PubMed=8807776;
RA Komori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida Y.;
RT "Predominant p53 mutations in enzootic bovine leukemic cell lines.";
RL Vet. Immunol. Immunopathol. 52:53-63(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B. indicus; STRAIN=Booran; TISSUE=Blood;
RA Bishop R.R.P., Gobright E.E.I.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation
CC as a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and BCL2 antigen expression, or by repression of Bcl-2
CC expression.
CC -|- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -|- SUBCELLULAR LOCATION: Nuclear.
CC -|- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -|- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC
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CC
CC EMBL; X81704; CAA57348.1; -
CC EMBL; D49825; BAA08629.1; -
CC EMBL; U74486; AAB51214.1; -
CC PIR; S51648; S51648.
CC HSSP; P04637; ITUP.
CC InterPro; IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PS00386; P53SUPPRESSR.
CC PRODOM; PD002681; P53; 1.
CC PROSITE; PS00348; P53; 1.
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
KW DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 94 285
FT DOMAIN 318 349 OLIGOMERIZATION.
FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
FT SIMILARITY).
FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 380 380 R -> T (IN REF. 2).
SQ SEQUENCE 386 AA; 43255 MW; 222473F28C549F31 CRC64;

Query Match 31.1%; Score 741.5; DB 1; Length 386;
Best Local Similarity 38.4%; Pred. No. 7.9e-48;
Matches 165; Conservative 68; Mismatches 126; Indels 71; Gaps 11;

Qy 11 LSPVEFQHIWDFLEQICVQPIDNFVDEPSEDGATNKIEISDMCIRMQSDLSDPMP 70
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
14 LSQETFSDLNLLPEN-----NLLSSELSAPVDD 42
Qy 71 QYTNGLLSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAQPSSFTDALSPTSAP 125
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
43 LLPYTDVATWLDECFNEAPQMEP-----SAPAAPPAT-----PAPATSWPL 85
Qy 126 ---IPSNNDYDGPCHSFDFVSFOQSSTAKSATWYSTELKLYCQIAKTCPIQIKVMT 182
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
86 SSFVPSQKTYPCNGYFRGLQSGTAKSVTCTYSPSLNKLFCQLAKCPVQLWVDSPPP 145
Qy 183 GAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPIT 242
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Db 146 GTRVRAMATYKLEHTEVRRCPHERSSDYG-LAPQHLIRVEGNLRAEYLDNRNT 204
QY 243 GRQSLVLPYEPQVGTFTTLYNMCNSSCVGGNRRPILLITVLETRDGOVLGRCPFE 302
Db 205 FRHSVVVPYEPSEIDESECTIHYNMCNSSCGMNRRLPILLITLEDSCGNLGRNSFE 264
QY 303 ARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIRKRRSP--DDEL 361
Db 265 VRVCACPGDRRTTEENLRKKGSCPEPPRSTKRALPTNT---SSSQPKKKPLDGEY 320
QY 362 LYLVRGRTYEMLLKIKESLELMQVLPQHTTETTRQOQQOQH-QHLLQKHLLS-ACFRN 419
Db 321 FTIQIRGFRYEMFRELNDALDEL-----KDALDREGESRAHSHLKSCKRPSCHRRK 375
QY 420 ELVEPRRETP 429
Db 376 PML--KREGP 383

RESULT 15
P53 MARMO
ID P53 MARMO STANDARD; PRT; 391 AA.
AC Q36006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97376996; PubMed=9233767;
RA Feitelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
RT Partial characterization of the woodchuck tumor suppressor, p53, and
RT its interaction with woodchuck hepatitis virus X antigen in
RT hepatocarcinogenesis.
RL Oncogene 15:327-336(1997).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -!- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AJ001022; CAA04478.1;
CC HSSP: P04637; 1TUP.
CC InterPro: IPR002117; P53.
CC Pfam: PF00870; P53; 1.
CC PRINTS: PR00386; P53SUPPRESSR.
CC ProDom: PD002681; P53; 1.
CC PROSITE: PS00348; P53; 1.
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```
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 100 290 BY SIMILARITY.
FT DOMAIN 323 334 OLIGOMERIZATION.
FT DOMAIN 336 385 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
FT SIMILARITY).
FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 391 AA; 43468 MW; E1D5D84BA40182 CRC64;

Query Match 30.9%; Score 736; DB 1; Length 391;
Best Local Similarity 38.0%; Pred. No. 2e-47;
Matches 164; Conservative 68; Mismatches 130; Indels 70; Gaps 9;

QY 11 LSPVFQHIWDFLEQPICSVQPIDLNFVDEPDESGATNKIEISMDICIRMQDSDLSQPMWP 70
Db 14 LSEQTFSDLNLLP-----ENNVLSPVLP 38
QY 71 QYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPA----- 125
Db 39 PMDDL-LLESDE--VENWFDK----GPDEALOMSAAPAKAPTAPASTLAAPSPATSWPL 91
QY 126 ----IPSTNDYPGPHGFDVFSQOSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQ 182
Db 92 SSSVPSQNTYPGVYGFRLGFLHSGTAKSVTCYSPSLNKLFCQLAKTCPVQLWVDSTPPP 151
QY 183 GAVIRAMPVYKKAHVTEVVKCPNHELRSNEGQIAPPSHLIRVEGNSHAQYVEDPIT 242
Db 152 GTRVRAMATYKKSQHMTEVRRCPHHE--RCSDSGLAPPQHLIRVEGNLRAEYLDNRNT 209
QY 243 GRQSLVLPYEPQVGTFTTLYNMCNSSCVGGNRRPILLITVLETRDGOVLGRCPFE 302
Db 210 FRHSVVVPYEPPEVGESECTIHYNYMCNSSCGMNRRLPILLITLEDSCGNLGRNSFE 269
QY 303 ARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIRKRRSP 357
Db 270 VRVCACPGDRRTTEENFRKR-----GEPCEPPPRSTKRALPNGTSSSQPKKKPL 321
QY 358 DDELLVLPVRGRTYEMLLKIKESLELMQVLPQHTTETTRQOQQOQHLLQKHLLSACF 417
Db 322 DGEYFTLKIRGRARFERFEMFQELNEALELKDQAQAEK-----EPGESRPHPSYLSKSKKQSTIS 376
QY 418 RNELVEPRRETP 429
Db 377 RHKKIIFKREGP 388

Search completed: August 7, 2003, 09:47:26
Job time : 9.94483 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:41:09 ; Search time 36.046 Seconds
(without alignments)
3207.225 Million cell updates/sec

Title: us-09-538-106-15

Perfect score: 2383

Sequence: 1 MSQSTQTNFLSEVFQHIW.....PKQSDVFFRHSKPPNRSVYP 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	2383	100.0	487	4 Q9H3D2	Q9h3d2 homo sapien
2	2335	98.0	470	11 Q99JEL	Q99jel rattus norv
3	2335	98.0	487	11 Q99JEO	Q99jeo rattus norv
4	2296	96.3	483	11 Q88897	Q88897 mus musculus
5	2185	91.7	471	4 Q9NPH7	Q9nph7 homo sapien
6	2185	91.7	516	4 Q9P1B7	Q9p1b7 homo sapien
7	2185	91.7	555	4 Q9H3D3	Q9h3d3 homo sapien
8	2185	91.7	641	4 Q75195	Q75195 homo sapien
9	2185	91.7	680	4 Q9H3D4	Q9h3d4 homo sapien
10	2185	91.7	680	4 Q9UE10	Q9ue10 homo sapien
11	2169	91.0	538	11 Q99JD7	Q99jd7 rattus norv
12	2169	91.0	555	11 Q99JD8	Q99jd8 rattus norv
13	2169	91.0	555	11 Q9QWZ0	Q9q wz0 mus musculus
14	2169	91.0	663	11 Q99JF3	Q99jef3 rattus norv
15	2169	91.0	680	11 Q99JP6	Q99jp6 rattus norv
16	2169	91.0	680	11 Q88898	Q88898 mus musculus

17	2011	84.4	393	4	075922	075922 homo sapien
18	1973	82.8	393	11	Q99JD9	Q99jd9 rattus norv
19	1938	81.3	389	11	Q88899	Q88899 mus musculus
20	1813	76.1	416	4	Q9P1B6	Q9p1b6 homo sapien
21	1813	76.1	461	4	Q9P1B5	Q9p1b5 homo sapien
22	1813	76.1	461	4	Q9UP26	Q9up26 homo sapien
23	1813	76.1	586	4	Q9UBV9	Q9ubv9 homo sapien
24	1813	76.1	586	4	Q9P1B4	Q9p1b4 homo sapien
25	1811	76.0	461	11	Q9QWY9	Q9qw y9 mus musculus
26	1811	76.0	586	11	Q89097	Q89097 mus musculus
27	1807	75.8	461	11	Q99JD6	Q99jd6 rattus norv
28	1807	75.8	586	11	Q99JF2	Q99jef2 rattus norv
29	1796	75.4	356	4	Q9UP74	Q9up74 homo sapien
30	1796	75.4	586	4	075080	075080 homo sapien
31	1744	73.2	582	13	Q9DEC7	Q9dec7 gallus gall
32	1659	69.6	365	13	Q98SW0	Q98sw0 xenopus lae
33	1544.5	64.8	457	13	Q8JHZ5	Q8jhz5 brachydanio
34	1504.5	63.1	576	13	Q8JFE3	Q8jfe3 brachydanio
35	1504.5	63.1	588	13	Q8JHZ6	Q8jhz6 brachydanio
36	1418	59.5	284	11	Q8C826	Q8c826 mus musculus
37	1363	57.2	501	4	Q9H3P8	Q9h3p8 homo sapien
38	1326.5	55.7	641	13	Q9W664	Q9w664 barbus barb
39	1304	54.7	631	11	Q99JP2	Q99jp2 mus musculus
40	1271.5	53.4	590	11	Q99JP1	Q99jp1 mus musculus
41	1251.5	52.5	426	4	Q8NH99	Q8nhw9 homo sapien
42	1248.5	52.4	450	4	Q8TDY5	Q8tdy5 homo sapien
43	1248.5	52.4	587	4	Q8TDY6	Q8tdy6 homo sapien
44	1217	51.1	232	4	Q96KR0	Q96kr0 homo sapien
45	1085.5	45.6	514	11	Q9CU77	Q9cu77 mus musculus

ALIGNMENTS

RESULT 1

Q9H3D2	PRELIMINARY;	PRT;	487 AA.
ID	Q9H3D2	PRELIMINARY;	PRT;
AC	Q9H3D2; 076078;		
DC	01-MAR-2001 (Tremblrel. 16, Created)		
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)		
DT	01-OCR-2002 (Tremblrel. 22, Last annotation update)		
DE	TA p63 gamma (P51 isoform TAP63GAMMA).		
GN	P63.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98448095; PubMed=9774969;		
RA	Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,		
RA	Andrews N.C. Caput D., McKeon F.;		
RT	"p63, a p53 homolog at 3q27-29, encodes multiple products with		
RT	transactivating, death-inducing, and dominant-negative activities.";		
RL	Mol. Cell 2:305-316(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Hagiwara K., McMenamin M.G., Harris C.C.;		
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.		
[3]			
RP	SEQUENCE OF 40-487 FROM N.A.		
RN	TISSUP-Skeletal muscle;		
RC	MEDLINE=98324755; PubMed=9662378;		
RA	Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Kato I.,		
RA	Ikawa Y., Nimura Y., Nakagawara A., Obinata M., Ikawa S.;		
RT	"Cloning and functional analysis of human p51, which structurally and		
RT	functionally resembles p53.";		
RL	Nat. Med. 4:839-843(1998).		
RN	[4]		
RP	SEQUENCE OF 40-487 FROM N.A.		
RX	MEDLINE=20388515; PubMed=10935472;		
RA	Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,		
RA	Yokota J.;		

"Mutation and expression of the p51 gene in human lung cancer.";

Neoplasia 1,71-79(1999).

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL; AF124540; AAG45609.1; -.

DR EMBL; AF124528; AAG45609.1; JOINED.

DR EMBL; AF124529; AAG45609.1; JOINED.

DR EMBL; AF124531; AAG45609.1; JOINED.

DR EMBL; AF124532; AAG45609.1; JOINED.

DR EMBL; AF124533; AAG45609.1; JOINED.

DR EMBL; AF124534; AAG45609.1; JOINED.

DR EMBL; AF124535; AAG45609.1; JOINED.

DR EMBL; AF075428; AAC62633.1; -.

DR EMBL; AB016072; BAA32592.1; -.

DR EMBL; AF116770; AAF43486.1; JOINED.

DR EMBL; AF116756; AAF43486.1; JOINED.

DR EMBL; AF116757; AAF43486.1; JOINED.

DR EMBL; AF116759; AAF43486.1; JOINED.

DR EMBL; AF116760; AAF43486.1; JOINED.

DR EMBL; AF116761; AAF43486.1; JOINED.

DR EMBL; AF116762; AAF43486.1; JOINED.

DR EMBL; AF116763; AAF43486.1; JOINED.

DR EMBL; AF116764; AAF43486.1; JOINED.

DR EMBL; AF116765; AAF43486.1; JOINED.

DR HSP; P04637; IYCS.

DR InterPro; IPR002117; P53.

DR Pfam; PF00870; P53; 1.

DR PRINTS; PR00386; P53SUPPRESSR.

DR PRODOM; PD002681; P53; 1.

DR PROSITE; PS00348; P53; 1.

DR Nuclear protein.

SW SEQUENCE 487 AA; 55687 MW; 86CC865BDF2643DD CRC64;

Query Match	100.0%;	Score	2383;	DB	4;	Length	487;
Best Local Similarity	100.0%;	Prod. No.	2.5e-202;				
Matches	448;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MSOSTONEFLSPVFOHIWDFLEQPTCSQVPIDLNFVDEPSEDGATNKIEISMDCLRQ	60				
Db	40	MSOSTONEFLSPVFOHIWDFLEQPTCSQVPIDLNFVDEPSEDGATNKIEISMDCLRQ	99				
Qy	61	DSLDSDPMWPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL	120				
Db	100	DSLDSDPMWPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL	159				
Qy	121	SPSPAIPSNNDYPCGPHSFSDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP	180				
Db	160	SPSPAIPSNNDYPCGPHSFSDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP	219				
Qy	181	PGQAVIRAMPYKKAETHVTEVWRKCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP	240				
Db	220	PGQAVIRAMPYKKAETHVTEVWRKCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP	279				
Qy	241	ITGRQSVLVPYEPQVGTETFTVLYNPMCNSSCVGGMNRRPILIIIVLETREDQGVIGRR	300				
Db	280	ITGRQSVLVPYEPQVGTETFTVLYNPMCNSSCVGGMNRRPILIIIVLETREDQGVIGRR	339				
Qy	301	FEARICACGRDKADESTRKQOVSDSTKNGDGTKRPFQNTHGCIQMTSTIKKRRSPDDE	360				
Db	340	FEARICACGRDKADESTRKQOVSDSTKNGDGTKRPFQNTHGCIQMTSTIKKRRSPDDE	399				
Qy	361	LLYLPVGRGTEYEMLLIKESLELMQYLPOHTIETYRQOQOQOQHLLQKHLLSACFRNE	420				
Db	400	LLYLPVGRGTEYEMLLIKESLELMQYLPOHTIETYRQOQOQOQHLLQKHLLSACFRNE	459				
Qy	421	LVPERRTPKQSDVFFRHSPPPNRSVTP	448				
Db	460	LVPERRTPKQSDVFFRHSPPPNRSVTP	487				

RESULT 2
Q99JE1
ID Q99JE1
PRELIMINARY;
PRT; 470 AA.

Q99JEL;	
01-JUN-2001	(TREMBLrel. 17, Created)
01-JUN-2001	(TREMBLrel. 17, Last sequence update)
01-OCT-2002	(TREMBLrel. 22, Last annotation update)
Tal KET gamma protein.	
P63.	
Rattus norvegicus (Rat).	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
NCBI_TaxID=10116;	
[1]	
SEQUENCE FROM N.A.	
STRAIN-Wistar; TISSUE-Tongue;	
MEDLINE=21363378; PubMed=11470269;	
Bamberger C., Schmalle H.;	
"Identification and tissue distribution of novel KET/p63 splice	
variants";	
FEBS Lett. 501:121-126(2001)).	
-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).	
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.	
EMBL; AJ277448; CAC37100.1; -.	
HSP; P04637; 1YCS.	
InterPro: IPR002117; P53.	
Pfam: PF00870; P53; 1.	
PRINTS; PR00386; P53SUPPRESSR.	
ProDom; PD002681; P53; 1.	
PROSITE; PS00348; P53; 1.	
Nuclear protein.	
SEQUENCE. 470 AA; 53399 MW; 96B7ED2FB30DD394 CRC64;	

Query Match	98.0%	Score 2335;	DB 11;	Length 470;
Best Local Similarity	98.0%;	Pred. No. 4.2e-198;		
Matches 439;	Conservative 2;	Mismatches 7;	Indels 0;	Gaps 0;
Qy	1	MSOSTQNFELSPVFOHIWDFLEQPTCSVQPIDLNFVDEPSEDGATNKIEISMDCI	RMQ	60
Db	23	MSQSTQISELSPVFOHIWDFLEQPTCSVQPIDLNFVDEPSENGATNKIEISMDCI	RMQ	82
Qy	61	DSLSDDPWQYNYNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSTFDAL	120	
Db	83	DSLSDDPWQYNYNLGLLNGMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSTFDAL	142	
Qy	121	SPSPAIPSNTDYPCPHSFDVSFQOSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP	180	
Db	143	SPSPAIPSNTDYPCPHSFDVSFQOSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP	202	
Qy	181	POGAVIRAMPVYKKAHVTEVWRKCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP	240	
Db	203	POGAVIRAMPVYKKAHVTEVWRKCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP	262	
Qy	241	ITGRQSVLVPYEPPOVGTETFTVLYNPMCMNSCVGGMNRRPILIIVLETRDQGVLGRR	300	
Db	263	ITGRQSVLVPYEPPOVGTETFTVLYNPMCMNSCVGGMNRRPILIIVLETRDQGVLGRR	322	
Qy	301	FEARICACGRDKRADEDSIRKQOVSDSTKNGDGTKRPFQNTHTGIMQTSIKKRRSPDDE	360	
Db	323	FEARICACGRDKRADEDSIRKQOVSDSAKNGDGTKRPFQNTHTGIMQTSIKKRRSPDDE	382	
Qy	361	LLYLPVREGRETYEMLLIKESLELMQVLPQHTTETVYRQOOQOOHQLLOKHLLSACFRNE	420	
Db	383	LLYLPVREGRETYEMLLIKESLELMQVLPQHTTETVYRQOOQOOHQLLOKHLLSACFRNE	442	
Qy	421	LVPEPRRETPKQSDVFFRHSKPPNRSVYP	448	
Db	443	LVESRRREAPQSDVFFRHSNPPNHSVYP	470	

RESULT 3	
Q99JE0	
ID Q99JE0	PRELIMINARY; PRT; 487 AA.
AC Q99JE0	
DT 01-JUN-2001	(TREMBlrel. 17, Created)
DT 01-JUN-2001	(TREMBlrel. 17, Last sequence update)

01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
TA2 KET gamma protein.
P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
RT variants.";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AJ277449; CAC37101.1; -.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 487 AA; 55499 MW; A688F392F32B3039 CRC64;

Query Match 98.08; Score 2335; DB 11; Length 487;
Best Local Similarity 98.08; Pred. No. 4.4e-198;
Matches 439; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 60
DB 1 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 60
QY 40 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 99
DB 40 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 99
QY 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
DB 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
QY 100 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 159
DB 100 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 159
QY 121 SPSPAIPTNDYPGPHSFDVSFQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPTNDYPGPHSFDVSFQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 160 SPSPAIPTNDYPGPHSFDVSFQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 219
DB 160 SPSPAIPTNDYPGPHSFDVSFQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 219
QY 181 PGQAVIRAMPYVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
DB 181 PGQAVIRAMPYVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
QY 220 PGQAVIRAMPYVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSSLIRVEGNSHAQYVEDP 279
DB 220 PGQAVIRAMPYVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSSLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLVPEYPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRRC 300
DB 241 ITGRQSVLVPEYPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRRC 300
QY 280 ITGRQSVLVPEYPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRRC 339
DB 280 ITGRQSVLVPEYPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRRC 339
QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDCTKRPFRONTHTGHIQMTSIIKKRSPDDE 360
DB 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDCTKRPFRONTHTGHIQMTSIIKKRSPDDE 360
QY 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDCTKRPFRONTHTGHIQMTSIIKKRSPDDE 399
DB 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDCTKRPFRONTHTGHIQMTSIIKKRSPDDE 399
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLKHLKLLSACFRNE 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLKHLKLLSACFRNE 420
QY 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLKHLKLLSACFRNE 459
DB 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLKHLKLLSACFRNE 459
QY 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448
DB 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448
QY 460 LVESRRRTPKQSDVFFRHSKPPNRSVYP 487
DB 460 LVESRRRTPKQSDVFFRHSKPPNRSVYP 487

RESULT 4
O88897 PRELIMINARY; PRT; 483 AA.
ID O88897
AC O88897
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TA*P63 gamma.
GN TRP63.

Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF075434; AAC62639.1; -.
DR HSSP; P04637; 1YCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 483 AA; 54969 MW; A90ED0C110C50EAD CRC64;

Query Match 96.38; Score 2296; DB 11; Length 483;
Best Local Similarity 96.98; Pred. No. 1.2e-194;
Matches 434; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 1 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 60
DB 1 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 60
QY 40 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 99
DB 40 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 99
QY 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
DB 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
QY 100 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 159
DB 100 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 159
QY 121 SPSPAIPTNDYPGPHSFDVSFQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPTNDYPGPHSFDVSFQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 160 SPSPAIPTNDYPGPHSFDVSFQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 219
DB 160 SPSPAIPTNDYPGPHSFDVSFQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 219
QY 181 PGQAVIRAMPYVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
DB 181 PGQAVIRAMPYVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
QY 220 PGQAVIRAMPYVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSSLIRVEGNSHAQYVEDP 279
DB 220 PGQAVIRAMPYVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSSLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLVPEYPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRRC 300
DB 241 ITGRQSVLVPEYPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRRC 300
QY 280 ITGRQSVLVPEYPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRRC 339
DB 280 ITGRQSVLVPEYPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRRC 339
QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDCTKRPFRONTHTGHIQMTSIIKKRSPDDE 360
DB 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDCTKRPFRONTHTGHIQMTSIIKKRSPDDE 360
QY 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDCTKRPFRONTHTGHIQMTSIIKKRSPDDE 395
DB 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDCTKRPFRONTHTGHIQMTSIIKKRSPDDE 395
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLKHLKLLSACFRNE 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLKHLKLLSACFRNE 420
QY 396 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLKHLKLLSACFRNE 455
DB 396 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLKHLKLLSACFRNE 455
QY 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448
DB 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448
QY 456 LVEPRRTPKQSDVFFRHSKPPNRSVYP 483
DB 456 LVEPRRTPKQSDVFFRHSKPPNRSVYP 483

RESULT 5
Q9NPH7 PRELIMINARY; PRT; 471 AA.
ID Q9NPH7
AC Q9NPH7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 isoform TAP63delta (P51 delta protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL NCB1_TaxID=9606;
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF116771; AAF61624.1; -;
DR EMBL; AF116769; AAF43489.1; JOINED.
DR EMBL; AF116756; AAF43488.1; JOINED.
DR EMBL; AF116757; AAF43489.1; JOINED.
DR EMBL; AF116759; AAF43489.1; JOINED.
DR EMBL; AF116761; AAF43489.1; JOINED.
DR EMBL; AF116762; AAF43489.1; JOINED.
DR EMBL; AF116763; AAF43489.1; JOINED.
DR EMBL; AF116764; AAF43489.1; JOINED.
DR EMBL; AF116765; AAF43489.1; JOINED.
DR EMBL; AF116766; AAF43489.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 471 AA; 52882 MW; 32EB39798FC1CE69 CRC64;

Query Match          91.7%; Score 2185; DB 4; Length 471;
Best Local Similarity 94.1%; Pred. No. 8e-185;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTNFLSPEVQHWDLEQPCISVQPIDLNFVDEPSEDGATNKEISMDCIRMQ 60
DB 1 MSQSTQTNFLSPEVQHWDLEQPCISVQPIDLNFVDEPSEDGATNKEISMDCIRMQ 60
QY 61 DSDLDSPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLDSPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIPSTNDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQKVTMP 180
DB 121 SPSPAIPSTNDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQKVTMP 180
QY 181 PGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQVDEP 240
DB 181 PGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQVDEP 240
QY 241 ITGROSLVYPYPPQVGTFTVLYNFMCSNCSVGMNRRPILIIIVTLTRDQVGLGRRC 300
DB 241 ITGROSLVYPYPPQVGTFTVLYNFMCSNCSVGMNRRPILIIIVTLTRDQVGLGRRC 300
QY 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHIQMTSIKKRSPDDE 360
DB 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHIQMTSIKKRSPDDE 360
QY 361 LLYLPVRGRETYYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLKLLSACFRNE 420
DB 361 LLYLPVRGRETYYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLKLLSACFRNE 420
QY 421 LVEPRETPKQSDVFFRHSKPP 442
DB 421 LVEPRETPKQSDVFFRHSKPP 442
QY 411 -----QTSIQSPSSYGNSSPP 426
DB 411 -----QTSIQSPSSYGNSSPP 426

RESULT 6
Q9P1B7 PRELIMINARY; PRT; 516 AA.
AC Q9P1B7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)

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DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE P51 isoform TAP63beta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL NCB1_TaxID=9606;
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF116769; AAF43488.1; JOINED.
DR EMBL; AF116756; AAF43488.1; JOINED.
DR EMBL; AF116757; AAF43488.1; JOINED.
DR EMBL; AF116759; AAF43488.1; JOINED.
DR EMBL; AF116760; AAF43488.1; JOINED.
DR EMBL; AF116761; AAF43488.1; JOINED.
DR EMBL; AF116762; AAF43488.1; JOINED.
DR EMBL; AF116763; AAF43488.1; JOINED.
DR EMBL; AF116764; AAF43488.1; JOINED.
DR EMBL; AF116765; AAF43488.1; JOINED.
DR EMBL; AF116766; AAF43488.1; JOINED.
DR EMBL; AF116767; AAF43488.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 516 AA; 57598 MW; 0755378110373881 CRC64;

Query Match          91.7%; Score 2185; DB 4; Length 516;
Best Local Similarity 94.1%; Pred. No. 9.1e-185;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTNFLSPEVQHWDLEQPCISVQPIDLNFVDEPSEDGATNKEISMDCIRMQ 60
DB 1 MSQSTQTNFLSPEVQHWDLEQPCISVQPIDLNFVDEPSEDGATNKEISMDCIRMQ 60
QY 61 DSDLDSPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLDSPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIPSTNDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQKVTMP 180
DB 121 SPSPAIPSTNDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQKVTMP 180
QY 181 PGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQVDEP 240
DB 181 PGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQVDEP 240
QY 241 ITGROSLVYPYPPQVGTFTVLYNFMCSNCSVGMNRRPILIIIVTLTRDQVGLGRRC 300
DB 241 ITGROSLVYPYPPQVGTFTVLYNFMCSNCSVGMNRRPILIIIVTLTRDQVGLGRRC 300
QY 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHIQMTSIKKRSPDDE 360
DB 301 FEARICACGRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHIQMTSIKKRSPDDE 360
QY 361 LLYLPVRGRETYYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLKLLSACFRNE 420
DB 361 LLYLPVRGRETYYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLKLLSACFRNE 420
QY 421 LVEPRETPKQSDVFFRHSKPP 442
DB 421 LVEPRETPKQSDVFFRHSKPP 442
QY 411 -----QTSIQSPSSYGNSSPP 426
DB 411 -----QTSIQSPSSYGNSSPP 426

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RESULT 7
Q9H3D3 ID Q9H3D3 PRELIMINARY; PRT; 555 AA.
AC Q9H3D3; Q9UP27;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TA p63 beta.
GN p63.
GE
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF124539; AAG45608.1; JOINED.
DR EMBL; AF124528; AAG45608.1; JOINED.
DR EMBL; AF124529; AAG45608.1; JOINED.
DR EMBL; AF124531; AAG45608.1; JOINED.
DR EMBL; AF124532; AAG45608.1; JOINED.
DR EMBL; AF124533; AAG45608.1; JOINED.
DR EMBL; AF124534; AAG45608.1; JOINED.
DR EMBL; AF124535; AAG45608.1; JOINED.
DR EMBL; AF124536; AAG45608.1; JOINED.
DR EMBL; AF124537; AAG45608.1; JOINED.
DR EMBL; AF075432; AAG62637.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR NUCLEAR protein.
SQ SEQUENCE 555 AA; 62433 MW; E22874BE7DBACBE CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 555;
Best Local Similarity 94.1%; Pred. No. 1e-184;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSQSTQNEFLSPVFOHINWDFLEQPCISQVQIDNLFVDFSEDPGATNKIEISMDICRMQ 60
Dy 40 MSQSTQNEFLSPVFOHINWDFLEQPCISQVQIDNLFVDFSEDPGATNKIEISMDICRMQ 99
Qy 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTATSPYAQPSSTFDAL 120
Dy 100 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTATSPYAQPSSTFDAL 159
Qy 121 SPSPAIPTNDYPCGHSFDFVSFQSSSTAKSATWTSTELKLYCQIAKTCPIQIKVMTTP 180
Dy 160 SPSPAIPTNDYPCGHSFDFVSFQSSSTAKSATWTSTELKLYCQIAKTCPIQIKVMTTP 219
Qy 181 PQGAVIRAMPYKAEHVEVVKRCPNHELRSRENEGOIAPPSHLIRVEGNSHAQYVEDP 240
Dy 220 PQGAVIRAMPYKAEHVEVVKRCPNHELRSRENEGOIAPPSHLIRVEGNSHAQYVEDP 279
Qy 241 ITGRQSLVLPYPPQVGTFTTLYNFMCMNSCVGGMNRRLPILLIVLTETRDGOVLGRRC 300
Dy 280 ITGRQSLVLPYPPQVGTFTTLYNFMCMNSCVGGMNRRLPILLIVLTETRDGOVLGRRC 339
Qy 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIRKRRSPDDE 360

us-09-538-106-15.rspt

RESULT 8
Q9H3D3 ID Q9H3D3 PRELIMINARY; PRT; 641 AA.
AC Q9H3D3; Q9UP27;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 isoform TAP63ALPHA (P51B protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98324755; PubMed=9662378;
RA Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I.,
RA Ikawa Y., Nimura Y., Nakagawara A., Obinata M.;
RT "Cloning and functional analysis of human p51, which structurally and
RT functionally resembles p53.";
RL Nat. Med. 4:839-844(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AB016073; BAA32593.1; JOINED.
DR EMBL; AF116769; AAF43487.1; JOINED.
DR EMBL; AF116756; AAF43487.1; JOINED.
DR EMBL; AF116757; AAF43487.1; JOINED.
DR EMBL; AF116759; AAF43487.1; JOINED.
DR EMBL; AF116760; AAF43487.1; JOINED.
DR EMBL; AF116761; AAF43487.1; JOINED.
DR EMBL; AF116762; AAF43487.1; JOINED.
DR EMBL; AF116763; AAF43487.1; JOINED.
DR EMBL; AF116764; AAF43487.1; JOINED.
DR EMBL; AF116765; AAF43487.1; JOINED.
DR EMBL; AF116766; AAF43487.1; JOINED.
DR EMBL; AF116767; AAF43487.1; JOINED.
DR EMBL; AF116768; AAF43487.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
DR NUCLEAR protein.
SQ SEQUENCE 641 AA; 72019 MW; 97AE61F66E63F618 CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 641;
Best Local Similarity 94.1%; Pred. No. 1.2e-184;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSQSTQNEFLSPVFOHINWDFLEQPCISQVQIDNLFVDFSEDPGATNKIEISMDICRMQ 60
Dy 1 MSQSTQNEFLSPVFOHINWDFLEQPCISQVQIDNLFVDFSEDPGATNKIEISMDICRMQ 60
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-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.

CC EMBL; Y16961; CA76562.1; -
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76776 MW; 6548A6F2187D852E CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 680;
Best Local Similarity 94.1%; Pred. No. 1.3e-184;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTNELSPVFOHINWDFLEQPCISVQPIDLNFVDFSESGATNKIEISMDCIRMQ 60
DB 1 MSQSTQTNELSPVFOHINWDFLEQPCISVQPIDLNFVDFSESGATNKIEISMDCIRMQ 99
QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 100 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPAIPSNIDYPGPHSFDVSFQOSTAKSATWTSTELKLYCOIAKTCPIQIKVMTTP 180
DB 160 SPSPAIPSNIDYPGPHSFDVSFQOSTAKSATWTSTELKLYCOIAKTCPIQIKVMTTP 219
QY 181 PQGAVIRAMPVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDP 240
DB 220 PQGAVIRAMPVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLVPEYEPQVGTETTVLYNFMCSNCCVGGMNRRLIIVITLETGQVLGRR 300
DB 280 ITGRQSVLVPEYEPQVGTETTVLYNFMCSNCCVGGMNRRLIIVITLETGQVLGRR 339
QY 301 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
DB 340 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 399
QY 361 LLVLPVGRGTYEMLLKIKESLELMQYLPOHTIETRYQOQQOQHLLQKHLISACFRNE 420
DB 400 LLVLPVGRGTYEMLLKIKESLELMQYLPOHTIETRYQOQQOQHLLQKHLISACFRNE 449
QY 421 LVEPRRETQKQSDVFFRHSKPP 442
DB 450 -----QTSQSPSSYGNSSPP 465

RESULT 11
Q99JD7 PRELIMINARY; PRT; 538 AA.
ID Q99JD7
AC Q99JD7
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TAI KET beta protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Wistar; Tissue=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C.; Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice variants";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y16961; CA76562.1; -

-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.

CC EMBL; AJ277452; CAC37104.1; -
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 538 AA; 60326 MW; 66D0CA19786BF21B CRC64;

Query Match 91.0%; Score 2169; DB 11; Length 538;
Best Local Similarity 93.2%; Pred. No. 2.5e-183;
Matches 412; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MSQSTQTNELSPVFOHINWDFLEQPCISVQPIDLNFVDFSESGATNKIEISMDCIRMQ 60
DB 23 MSQSTQTNELSPVFOHINWDFLEQPCISVQPIDLNFVDFSESGATNKIEISMDCIRMQ 82
QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 83 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 142
QY 121 SPSPAIPSNIDYPGPHSFDVSFQOSTAKSATWTSTELKLYCOIAKTCPIQIKVMTTP 180
DB 143 SPSPAIPSNIDYPGPHSFDVSFQOSTAKSATWTSTELKLYCOIAKTCPIQIKVMTTP 202
QY 181 PQGAVIRAMPVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDP 240
DB 203 PQGAVIRAMPVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDP 262
QY 241 ITGRQSVLVPEYEPQVGTETTVLYNFMCSNCCVGGMNRRLIIVITLETGQVLGRR 300
DB 263 ITGRQSVLVPEYEPQVGTETTVLYNFMCSNCCVGGMNRRLIIVITLETGQVLGRR 322
QY 301 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
DB 323 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 382
QY 361 LLVLPVGRGTYEMLLKIKESLELMQYLPOHTIETRYQOQQOQHLLQKHLISACFRNE 420
DB 383 LLVLPVGRGTYEMLLKIKESLELMQYLPOHTIETRYQOQQOQHLLQKHLISACFRNE 432
QY 421 LVEPRRETQKQSDVFFRHSKPP 442
DB 433 -----QTSQSPSSYGNSSPP 448

RESULT 12
Q99JD8 PRELIMINARY; PRT; 555 AA.
ID Q99JD8
AC Q99JD8
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TAI KET beta protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Wistar; Tissue=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C.; Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice variants";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AJ277451; CAC37103.1; -


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DR SMART, SM00454; SAM, 1.
DR PROSITE, PS00348; P53; 1.
DR Nucleic protein.
KW Nucleic protein.
SQ SEQUENCE 663 AA; 74660 MW; C953BBAC389D5B70 CRC64;

Query Match          91.08; Score 2169; DB 11; Length 663;
Best Local Similarity 93.28; Pred. No. 3.4e-183;
Matches 412; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MSOSTQTNFELSPVEVQHINWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 60
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Db 23 MSOSTQTNFELSPVEVQHINWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 82
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Db 83 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 142
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 SPSPATPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 143 SPSPATPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 202
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 PQGAVIRAMPVYKAEHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 203 PQGAVIRAMPVYKAEHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 262
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 ITGRQSVLVPEYPPQVGTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 263 ITGRQSVLVPEYPPQVGTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 322
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QY 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPFRTNTHGIOMTSIKKRRSPDDE 360
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 323 FEARICACPGDRKADSDSIRKQVSDSANKDGTKRPFRTNTHGIOMTSIKKRRSPDDE 382
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 LLYLPVGRGRTYEMLLKIKESLELMQYLPQHTIETIRYQQOQQOQHLLQKHLLSACFRNE 420
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 383 LLYLPVGRGRTYEMLLKIKESLELMQYLPQHTIETIRYQQOQQOQHLLQKHLLSACFRNE 442
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QY 421 LVEPRRETQKSDVFFRHSKPP 442
   :| || :| ||
Db 433 -----QTSMQSQSSSYGNSSPP 448

RESULT 15
Q9JJJ6 PRELIMINARY; PRT; 680 AA.
AC Q9JJJ6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TA2 KET alpha.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lingual epithelium;
RX MEDLINE=97460723; PubMed=9315105;
RA Schmale H., Bamberger C.;
RT "A novel protein with strong homology to the tumor suppressor p53.";
RL Oncogene 15:1363-1367(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lingual epithelium;
RA Schmale H.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; Y10258; CAB88216.1; -.
DR HSSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
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DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nucleic protein.
SQ SEQUENCE 680 AA; 76760 MW; AC45DABB88F61400 CRC64;

Query Match          91.08; Score 2169; DB 11; Length 680;
Best Local Similarity 93.28; Pred. No. 3.5e-183;
Matches 412; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MSOSTQTNFELSPVEVQHINWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 60
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Db 40 MSOSTQTNFELSPVEVQHINWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 99
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QY 61 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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Db 100 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 SPSPATPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 160 SPSPATPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 219
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 PQGAVIRAMPVYKAEHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 220 PQGAVIRAMPVYKAEHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 ITGRQSVLVPEYPPQVGTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 280 ITGRQSVLVPEYPPQVGTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 339
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPFRTNTHGIOMTSIKKRRSPDDE 360
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 340 FEARICACPGDRKADSDSIRKQVSDSANKDGTKRPFRTNTHGIOMTSIKKRRSPDDE 399
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 LLYLPVGRGRTYEMLLKIKESLELMQYLPQHTIETIRYQQOQQOQHLLQKHLLSACFRNE 420
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 400 LLYLPVGRGRTYEMLLKIKESLELMQYLPQHTIETIRYQQOQQOQHLLQKHLLSACFRNE 449
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 LVEPRRETQKSDVFFRHSKPP 442
   :| || :| ||
Db 450 -----QTSMQSQSSSYGNSSPP 465

Search completed: August 7, 2003, 09:51:40
Job time : 38.046 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:31:28 ; Search time 40.4138 seconds
(without alignments)
2301.535 Million cell updates/sec

Title: US-09-538-106-16

Perfect score: 3104

Sequence: 1 MLYLENNAAQTFSEPOYTNL.....FNFDMDARRNKQRIKEEGE 586

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3104	100.0	586	20	AA05956 Human cell regulat
2	3104	100.0	586	23	ABG95140 Human oncogene p63
3	3100	99.9	586	23	ABG95132 Human oncogene p51
4	3087	99.5	586	21	AAB11357 Human p63 protein
5	3087	99.5	586	23	ABP61909 Human lung cancer
6	3087	99.5	586	23	ABP74989 Human p53 homology
7	3080	99.2	586	20	AA041032 Human lung tumor a
8	3080	99.2	586	21	AAB11317 Human lung cancer-
9	3080	99.2	586	23	ABP61869 Human lung cancer

10	3080	99.2	586	23	ABB74949	Human lung tumour
11	3066	98.8	586	20	AA05962	Mouse cell regulat
12	3033	97.7	641	20	AA05247	Human p51 protein
13	3033	97.7	641	20	AA05953	Human cell regulat
14	3033	97.7	641	22	AAB82129	Human protein #2 u
15	3033	97.7	641	23	ABG95142	Human oncogene p63
16	3029	97.6	641	21	AAB11358	Human p63 protein
17	3029	97.6	641	23	ABG95128	Human oncogene p5B
18	3029	97.6	641	23	ABG95136	Human oncogene p51
19	3029	97.6	641	23	ABP61910	Human lung cancer
20	3029	97.6	641	23	ABP74990	Human p53 homology
21	3025	97.5	680	21	AAB11361	Human p63 protein
22	3025	97.5	680	21	AA050997	Human KET protein.
23	3025	97.5	680	23	ABP61913	Human lung cancer
24	3025	97.5	680	23	ABP74993	Human p53 homology
25	2995	96.5	680	20	AA05958	Human cell regulat
26	2991	96.4	680	21	AA050998	Rat KET protein.
27	2421	78.0	461	21	AAB11362	Human p63 protein
28	2421	78.0	461	23	ABG95131	Human oncogene p51
29	2421	78.0	461	23	ABG95138	Human oncogene p63
30	2421	78.0	461	23	ABP61914	Human lung cancer
31	2421	78.0	461	23	ABP74994	Human p53 homology
32	2398	77.3	461	20	AA05963	Mouse cell regulat
33	2350	75.7	516	20	AA05954	Human cell regulat
34	2350	75.7	516	21	AAB11363	Human p63 protein
35	2350	75.7	516	23	ABG95135	Human oncogene p51
36	2350	75.7	516	23	ABG95141	Human oncogene p63
37	2350	75.7	516	23	ABP61915	Human lung cancer
38	2350	75.7	516	23	ABP74995	Human p53 homology
39	2148	69.2	416	23	ABG95130	Human oncogene p51
40	2077	66.9	471	23	ABG95129	Human oncogene p51
41	2077	66.9	471	23	ABG95134	Human oncogene p51
42	1884	60.7	393	20	AA05957	Human cell regulat
43	1884	60.7	393	23	ABG95133	Human oncogene p51
44	1884	60.7	393	23	ABG95139	Human oncogene p63
45	1872	60.3	356	20	AA043135	Human p40 protein

ALIGNMENTS

RESULT 1
AA05956
ID AA05956 standard; Protein: 586 AA.
XX
AC AA05956;
XX
DT 16-AUG-1999 (first entry)
XX Human cell regulatory protein p63, isoform deltaNp63 alpha.
XX
DE Cell regulatory protein; p63; hu-deltaNp63 alpha; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy.
XX
OS Homo sapiens.
XX
PN WO9919357-A2.
XX
PD 22-APR-1999.
XX
PF 02-OCT-1998; 98WO-US21992.
XX
PR 29-MAY-1998; 98US-0087216.
PR 15-OCT-1997; 97US-0062076.
XX
PA (HARD) HARVARD COLLEGE.
PI McKeon F, Yang A;
XX
XX WPI; 1999-277595/23.
DR N-PSDB; AAX58575.
XX

PT New isolated p63 cell regulatory protein for, e.g. treatment of
 XX tumours
 PS
 XX
 PS Claim 23; Fig 12; 161pp; English.
 XX
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. It has been observed that the
 CC intron-exon organisation is conserved between p73 and p53, and from
 CC known exon and intron sizes for these 2 genes, it was possible to
 CC identify new members of this gene family using a PCR-based strategy
 CC of amplifying 2 exons in a conserved domain and their intervening
 CC intron. The human p53 gene was localised to chromosomal position
 CC 3q27-29. At least 6 different isoforms exist. Splice variants
 CC differing at the C-terminus have been designated as alpha, beta and
 CC gamma forms, while p63 members differing in the N-terminus are
 CC designated as delta and epsilon forms, where the delta form lacks the
 CC transactivation domain. The present sequence represents human
 CC p63 isoform hu-delta-p63 alpha. p63 was detected in a variety
 CC of human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05933-64), polynucleotides (see
 CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 XX
 XX Sequence 586 AA;
 SQ

Query Match 100.0%; Score 3104; DB 20; Length 586;
 Best Local Similarity 100.0%; Pred. No. 9.8e-244;
 Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLENNAQTQSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAPSS 60
 DB 1 MYLENNAQTQSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAPSS 60
 QY 61 TFDALSPSPAIPTNDYDGHFSDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
 DB 61 TFDALSPSPAIPTNDYDGHFSDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
 QY 121 VMTPPPGQAVIRAMPYKAEHVTYVKKRCPNHELSEFNEQGIAPPSSHLIRVEGNSHAQ 180
 DB 121 VMTPPPGQAVIRAMPYKAEHVTYVKKRCPNHELSEFNEQGIAPPSSHLIRVEGNSHAQ 180
 QY 181 YVEDPTTGROSLVLPYEPQVQTEFTVLYNFMNSCVCVGMNRRPILLIVLETRDGOV 240
 DB 181 YVEDPTTGROSLVLPYEPQVQTEFTVLYNFMNSCVCVGMNRRPILLIVLETRDGOV 240
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 DB 241 LGRRCFEARICACGRDRKADEDSIRKQVSDSTKNGDGTGKFRFRQNTHGQIOMTSIKRR 300
 QY 301 SPDELLYLVPVGRRETYEMLLIKESLEMLQYLPQHTIETVYQQQQQHQHLLQKQTSIQ 360
 DB 301 SPDELLYLVPVGRRETYEMLLIKESLEMLQYLPQHTIETVYQQQQQHQHLLQKQTSIQ 360
 QY 361 SPSSVGNSSPPLKNNMKNKLPVSVQLINPQORNALTPPTIPDGMANIPMGMTHMPMAG 420
 DB 361 SPSSVGNSSPPLKNNMKNKLPVSVQLINPQORNALTPPTIPDGMANIPMGMTHMPMAG 420
 QY 421 DMNGLSPTQALPPLPPLSPMSTSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIY 480
 DB 421 DMNGLSPTQALPPLPPLSPMSTSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIY 480
 QY 481 QIEHYSMDLALSLKIPEQFRHAIWKILDRHQLHEFSSPSHLIRTPSSASTVSGSSETR 540

DB 481 QIEHYSMDLALSLKIPEQFRHAIWKILDRHQLHEFSSPSHLIRTPSSASTVSGSSETR 540
 QY 541 GERVIDAVRFTLRQISFPPEWDFNFDMDARRNKQRIKEEGE 586
 DB 541 GERVIDAVRFTLRQISFPPEWDFNFDMDARRNKQRIKEEGE 586
 RESULT 2
 ABG95140
 ID ABG95140 standard; Protein; 586 AA.
 XX
 AC ABG95140;
 DT 04-DEC-2002 (first entry)
 XX
 DE Human oncogene p63 isoform deltaN p63 alpha.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 OS Homo sapiens.
 XX
 PN WO200269900-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 01-MAR-2002; 2002WO-US06518.
 XX
 PR 01-MAR-2001; 2001US-272751P.
 PA (CONF-) CONFORMA THERAPEUTICS CORP.
 XX
 PI Fritz LC, Burrows FJ;
 XX
 DR WPI; 2002-698710/75.
 DR N-PSDB; ABS73332.
 XX
 PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90
 PT
 PS Disclosure; Page 346-348; 389pp; English.
 XX
 CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock
 CC protein (HSP)-90, or selectively treating cells expressing (II)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.
 XX
 SQ Sequence 586 AA;

Query Match 100.0%; Score 3104; DB 23; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.8e-244;
Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYLNNNAQTFSEPOQYTNGLNSMDQIQONGSSSTSPYNTDHAQNSVTPAPSYAQPSS 60
DB 1 MLYLNNNAQTFSEPOQYTNGLNSMDQIQONGSSSTSPYNTDHAQNSVTPAPSYAQPSS 60

QY 61 TFDALSPSPAIPNDYDGPVPHSDVFSQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPAIPNDYDGPVPHSDVFSQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIK 120

QY 121 VMTPPGAVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180

QY 181 YVEDPITGRQSVLVPYEPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQV 240
DB 181 YVEDPITGRQSVLVPYEPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQV 240

QY 241 LGRRCFEARICACPGDRKKADESIKQVSDSTKNGDGTKRFRQNTGHIQMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKKADESIKQVSDSTKNGDGTKRFRQNTGHIQMTSIKRR 300

QY 301 SPDELLYLPVGRREYEMLLKIKESLELMOYLPOHTIETYROQOQOQHLLQKQTSIQ 360
DB 301 SPDELLYLPVGRREYEMLLKIKESLELMOYLPOHTIETYROQOQOQHLLQKQTSIQ 360

QY 361 SPSSYGNSSPPLKNMKNMKNLPSVSQLINPQORNALPTTIPDGMGANIPMGTMPMAG 420
DB 361 SPSSYGNSSPPLKNMKNMKNLPSVSQLINPQORNALPTTIPDGMGANIPMGTMPMAG 420

QY 421 DMNGLSPTQALPPPLSMPSSTHCTPPPPYPTDCSIVSFLARLGCSSCLDFTTQGLTIY 480
DB 421 DMNGLSPTQALPPPLSMPSSTHCTPPPPYPTDCSIVSFLARLGCSSCLDFTTQGLTIY 480

RESULT 3

ID ABG95132 standard; Protein; 586 AA.

AC ABG95132;

DT 04-DEC-2002 (first entry)

DE Human oncogene p51 isoform delNalpha.

KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW Hsp-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.

OS Homo sapiens.

XX WO200269900-A2.

XX 12-SEP-2002.

XX 01-MAR-2002; 2002WO-US06518.

PF

PR 01-MAR-2001; 2001US-272751P.

PA (CONF-) CONFORMA THERAPEUTICS CORP.

PI Fritz LC, Burrows FJ;

XX WPI; 2002-698710/75.

XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90

XX Disclosure; Page 331-333; 389pp; English.

XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock
XX protein (HSP)-90, or selectively treating cells expressing (II)
XX involving administering HSP90-inhibitor. The method is useful for
XX treating genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This is the amino acid sequence of a human oncogenic protein.

SQ Sequence 586 AA;

Query Match 99.9%; Score 3100; DB 23; Length 586;
Best Local Similarity 99.8%; Pred. No. 2.1e-243;
Matches 586; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLYLNNNAQTFSEPOQYTNGLNSMDQIQONGSSSTSPYNTDHAQNSVTPAPSYAQPSS 60
DB 1 MLYLNNNAQTFSEPOQYTNGLNSMDQIQONGSSSTSPYNTDHAQNSVTPAPSYAQPSS 60

QY 61 TFDALSPSPAIPNDYDGPVPHSDVFSQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPAIPNDYDGPVPHSDVFSQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIK 120

QY 121 VMTPPGAVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180

QY 181 YVEDPITGRQSVLVPYEPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQV 240
DB 181 YVEDPITGRQSVLVPYEPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQV 240

QY 241 LGRRCFEARICACPGDRKKADESIKQVSDSTKNGDGTKRFRQNTGHIQMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKKADESIKQVSDSTKNGDGTKRFRQNTGHIQMTSIKRR 300

QY 301 SPDELLYLPVGRREYEMLLKIKESLELMOYLPOHTIETYROQOQOQHLLQKQTSIQ 360
DB 301 SPDELLYLPVGRREYEMLLKIKESLELMOYLPOHTIETYROQOQOQHLLQKQTSIQ 360

QY 361 SPSSYGNSSPPLKNMKNMKNLPSVSQLINPQORNALPTTIPDGMGANIPMGTMPMAG 420
DB 361 SPSSYGNSSPPLKNMKNMKNLPSVSQLINPQORNALPTTIPDGMGANIPMGTMPMAG 420

QY 421 DMNGLSPTQALPPPLSMPSSTHCTPPPPYPTDCSIVSFLARLGCSSCLDFTTQGLTIY 480
DB 421 DMNGLSPTQALPPPLSMPSSTHCTPPPPYPTDCSIVSFLARLGCSSCLDFTTQGLTIY 480

QY 481 QIEHYSDMLASLKIPEQFRHAIWKGIILDRHQLHEFFSPSHLLRTPSSASTVSVGSSETR 540
|||||
Db 481 QIEHYSDMLASLKIPEQFRHAIWKGIILDRHQLHEFFSPSHLLRTPSSASTVSVGSSETR 540
QY 541 GERVIDAVRFTLRQTISFPFPRDEWDFNFDMDARNKQORKEEKE 586
|||||
Db 541 GERVIDAVRFTLRQTISFPFPRDEWDFNFDMDARNKQORKEEKE 586

RESULT 4

AAB11357
ID AAB11357 standard; Protein; 586 AA.
AC AAB11357;
XX
XX
DT 21-FEB-2001 (first entry)
DE Human p63 protein isoform #1.
DE Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW vaccine; detection.
XX
XX
OS Homo sapiens.
PN WO200061612-A2.
PD 19-OCT-2000.
PF 03-APR-2000; 2000WO-US08896.
XX 02-APR-1999; 99US-0285479.
PR 17-DEC-1999; 99US-0466396.
PR 30-DEC-1999; 99US-0476496.
PR 10-JAN-2000; 2000US-0480884.
PR 22-FEB-2000; 2000US-0510376.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Fan L;
PI WPI: 2000-628399/60.
DR N-PSDB; AAC66027.

XX
PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -
XX

PS Disclosure: Page 243-245; 261pp; English.

XX This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2, and then administered to the patient to inhibit
CC development of cancer.
XX

SQ Sequence 586 AA;

Query Match 99.5%; Score 3087; DB 21; Length 586;
Best Local Similarity 99.5%; Pred. No. 2.4e-242;
Matches 583; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYLENNAQTOFSEPYTNLGLNSMDQIQNGSSSTSPYNTDRAQNSVTAPSPYAQPSS 60
|||||
Db 1 MLYLENNAQTOFSEPYTNLGLNSMDQIQNGSSSTSPYNTDRAQNSVTAPSPYAQPSP 60
|||||
QY 61 TFDALSPSPAIPSNTPDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120

Db 61 TFDALSPSPAIPSNTPDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
|||||
QY 121 VMTPEPQAVIRAMPVYKKAEBHTVVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
|||||
Db 121 VMTPEPQAVIRAMPVYKKAEBHTVVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPVPEPPQVGTETFTVLYNFMCSNCSVGGMNRPRPILIIIVLETFRDGOV 240
|||||
Db 181 YVEDPITGRQSVLPVPEPPQVGTETFTVLYNFMCSNCSVGGMNRPRPILIIIVLETFRDGOV 240
QY 241 LGRRCFEARICACPGDRDRKKADEDSIRKQOVSDSTKNGDGTKRPFQNTHTGIOMTSIKKRR 300
|||||
Db 241 LGRRCFEARICACPGDRDRKKADEDSIRKQOVSDSTKNGDGTKRPFQNTHTGIOMTSIKKRR 300
QY 301 SPDDDELLYLPVGRGRTYEMLLKIKESLELMQYLPQHTTETRYRQOQOQOHOHLQKOTSIQ 360
|||||
Db 301 SPDDDELLYLPVGRGRTYEMLLKIKESLELMQYLPQHTTETRYRQOQOQOHOHLQKOTSIQ 360
QY 361 SPSSYGNSSPPLNKMNSMKNLPSVSQILNPOORNALTPTTIPDGMGANIPMGTHMPWAG 420
|||||
Db 361 SPSSYGNSSPPLNKMNSMKNLPSVSQILNPOORNALTPTTIPDGMGANIPMGTHMPWAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIIY 480
|||||
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIIY 480
QY 481 QIEHYSDMLASLKIPEQFRHAIWKGIILDRHQLHEFFSPSHLLRTPSSASTVSVGSSETR 540
|||||
Db 481 QIEHYSDMLASLKIPEQFRHAIWKGIILDRHQLHEFFSPSHLLRTPSSASTVSVGSSETR 540
QY 541 GERVIDAVRFTLRQTISFPFPRDEWDFNFDMDARNKQORKEEKE 586
|||||
Db 541 GERVIDAVRFTLRQTISFPFPRDEWDFNFDMDARNKQORKEEKE 586

RESULT 5

AABP61909
ID AABP61909 standard; Protein; 586 AA.
XX
AC AABP61909;
XX
DT 07-OCT-2002 (first entry)
DE Human lung cancer associated protein sequence SEQ ID NO:338.
KW Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200247534-A2.
PD 20-JUN-2002.
XX 30-NOV-2001; 2001WO-US47576.
PF 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
PR 28-JUN-2001; 2001US-0897778.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
XX
DR WPI: 2002-583465/62.
DR N-PSDB; ABQ92432.
XX
XX Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT by the polynucleotides, useful in pharmaceutical compositions such as
PT vaccines and as markers to indicate the presence of lung cancer
XX

Db 301 SPDDLLVLPVGRREYEMLLKIKESLELMQYLPQHTTETRYQQQQQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLNKMNSMKNLPSVSQLINPOORNALPTTTPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLNKMNSMKNLPSVSQLINPOORNALPTTTPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSLMSPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
Db 421 DMNGLSPTQALPPPLSLMSPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
QY 481 QIEHYSMDLALSLKIPEQFRHAIWKIGILDHRLQHEFSSPSSHLRTPSSASTVSVGSSETR 540
Db 481 QIEHYSMDLALSLKIPEQFRHAIWKIGILDHRLQHEFSSPSSHLRTPSSASTVSVGSSETR 540
QY 541 GERVIDAVRFTLRQTISFPFRDEWDFNDFMDARRNKQORKEGE 586
Db 541 GERVIDAVRFTLRQTISFPFRDEWDFNDFMDARRNKQORKEGE 586

RESULT 7
AAV41032
ID AAY41032 standard; protein; 586 AA.

AC AAY41032;
DT 07-DEC-1999 (first entry)
DE Human lung tumor antigen L503S.
XX Human; lung tumor; lung cancer; T cell stimulation.

OS Homo sapiens.
XX WO9947674-A2.
PN 23-SEP-1999.
XX 17-MAR-1999; 99WO-US05798.
PR 18-MAR-1998; 98US-0040802.
PR 18-MAR-1998; 98US-0040984.
PR 27-JUL-1998; 98US-0123912.
PR 27-JUL-1998; 98US-0123933.

XX (CORI-) CORIXA CORP.
XX Reed SG, Wang T;
XX WPI; 1999-571839/48.
DR N-PSDB; AAZ24648.

XX New isolated lung tumor polynucleotides, used to develop products for
the treatment, prevention and monitoring the progression of lung cancer

Example 2; Page 130-131; 148pp; English.

XX The invention provides isolated human lung tumor nucleic acids and
polypeptides. The polypeptides can be used for the treatment of lung
cancer. The polypeptides and polynucleotides can be used to stimulate T
cells or antigen presenting cells for use in the treatment of lung
cancer. The polypeptides and monoclonal antibodies specific for the
polypeptides can also be used to inhibit the development of lung cancer.
XX Agents which bind the polypeptides can be used for detecting lung cancer
and for monitoring the progression of lung cancer.

XX Sequence 586 AA;

Query Match 99.2%; Score 3080; DB 20; Length 586;
Best Local Similarity 99.3%; Pred. No. 8.8e-242;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYLNNNAQTOFSEPPQYTNLGLNMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
Db 1 MLYLNNNAQTOFSEPPQYTNLGLNMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPQCAVRAMPVYKKAHVTEVVKRCNPHLSRENEGQIAPPSSHLIRVEGNSHAQ 180
Db 121 VMTPPQCAVRAMPVYKKAHVTEVVKRCNPHLSRENEGQIAPPSSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPVPEPPQVGTETTVLYNFMCSNCCVGGMNRRLPILIIIVTLETRDQGV 240
Db 181 YVEDPITGRQSVLPVPEPPQVGTETTVLYNFMCSNCCVGGMNRRLPILIIIVTLETRDQGV 240
QY 241 LGRRCFEARICACGDRKKADEDSIRKQOVSDSTKNGDGTKRPFQNTHTGQMTSIIKRR 300
Db 241 LGRRCFEARICACGDRKKADEDSIRKQOVSDSTKNGDGTKRPFQNTHTGQMTSIIKRR 300
QY 301 SPDDLLVLPVGRREYEMLLKIKESLELMQYLPQHTTETRYQQQQQHLLQKQTSIQ 360
Db 301 SPDDLLVLPVGRREYEMLLKIKESLELMQYLPQHTTETRYQQQQQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLNKMNSMKNLPSVSQLINPOORNALPTTTPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLNKMNSMKNLPSVSQLINPOORNALPTTTPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSLMSPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
Db 421 DMNGLSPTQALPPPLSLMSPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
QY 481 QIEHYSMDLALSLKIPEQFRHAIWKIGILDHRLQHEFSSPSSHLRTPSSASTVSVGSSETR 540
Db 481 QIEHYSMDLALSLKIPEQFRHAIWKIGILDHRLQHEFSSPSSHLRTPSSASTVSVGSSETR 540
QY 541 GERVIDAVRFTLRQTISFPFRDEWDFNDFMDARRNKQORKEGE 586
Db 541 GERVIDAVRFTLRQTISFPFRDEWDFNDFMDARRNKQORKEGE 586

RESULT 8
AAB11317
ID AAB11317 standard; Protein; 586 AA.

AC AAB11317;
DT 21-FEB-2001 (first entry)
DE Human lung cancer-associated protein L530S.

XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW vaccine; detection.

XX Homo sapiens.

XX WO2000061612-A2.

XX 19-OCT-2000.

XX 03-APR-2000; 2000WO-US08896.

XX 02-APR-1999; 99US-0285479.

XX 17-DEC-1999; 99US-0466396.

XX 30-DEC-1999; 99US-0476496.

XX 10-JAN-2000; 2000US-0480884.

XX 22-FEB-2000; 2000US-0510376.

XX (CORI-) CORIXA CORP.

XX Wang T, Fan L;

XX WPI; 2000-628399/60.

DR N-PSDB; AAC65887.
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -
XX
XX
PS Claim 3; Page 163-164; 261pp; English.
XX
XX This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
XX
SQ Sequence 586 AA;
Query Match 99.2%; Score 3080; DB 21; Length 586;
Best Local Similarity 99.3%; Pred. No. 8.8e-242;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MYLENNATQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
Db 1 MYLENNATQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPSTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGROSVLVPEYPPQVGTFTVLYNFCNSSCVGMNRRPILIIIVTLETDRGOV 240
Db 181 YVEDPITGROSVLVPEYPPQVGTFTVLYNFCNSSCVGMNRRPILIIIVTLETDRGOV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIKKRR 300
Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIKKRR 300
QY 301 SPDELLYLVRGRETVEMLLKESLELMQYLPHQHTIETRYRQOQQOQHLLQKQTSIQ 360
Db 301 SPDELLYLVRGRETVEMLLKESLELMQYLPHQHTIETRYRQOQQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLNKMNSMKNLPSVQLINPQORNALTPTTIPDGMGANTPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLNKMNSMKNLPSVQLINPQORNALTPTTIPDGMGANTPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSPSTSHCTPPPPYPTDCSIVSFRLARLGCSSCLDYFTTQGLTTIY 480
Db 421 DMNGLSPTQALPPLSPSTSHCTPPPPYPTDCSIVSFRLARLGCSSCLDYFTTQGLTTIY 480
QY 481 QIEHYSMDDLASLKIPEQRHATWKGLDHRQLHEFSSPSHLIRTSSASTSVSGSETR 540
Db 481 QIEHYSMDDLASLKIPEQRHATWKGLDHRQLHEFSSPSHLIRTSSASTSVSGSETR 540
QY 541 GERVIDAVRTLTQTSIFSPRDEWDFNFDMDARRNKQORIKKEGE 586
Db 541 GERVIDAVRTLTQTSIFSPRDEWDFNFDMDARRNKQORIKKEGE 586
RESULT 9
ID ABP61869
XX ABP61869 standard; Protein; 586 AA.
AC ABP61869;
XX

DT 07-OCT-2002 (first entry)
XX
DE Human lung cancer associated protein sequence SEQ ID NO:152.
XX
KW Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200247534-A2.
XX
PD 20-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-0547576.
XX
PR 12-DEC-2000; 2000US-0735705.
XX
PR 07-MAY-2001; 2001US-0850716.
XX
PR 28-JUN-2001; 2001US-0897778.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD; Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
XX
DR WPI; 2002-583465/62.
DR N-PSDB; ABQ92292.
XX
XX Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT by the polynucleotides, useful in pharmaceutical compositions such as
PT vaccines and as markers to indicate the presence of lung cancer -
XX
PS Example 2; Page 253-254; 381pp; English.
XX
CC The present invention describes isolated human lung carcinoma
CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC activity, and can be used in gene therapy and in vaccines. Compositions
CC comprising (I) or (II) can be used for stimulating an immune response in
CC a patient and for treating lung cancer in a patient. Oligonucleotides of
CC (I) can be used for detecting the presence of a cancer in a patient, by
CC obtaining a biological sample from the patient, contacting the
CC biological sample with the oligonucleotide, detecting in the sample, an
CC amount of polynucleotide that hybridises to the oligonucleotide and
CC comparing the amount of polynucleotide that hybridises to the
CC oligonucleotide to a predetermined cut-off value, and determining the
CC presence of a cancer in the patient. (I) and (II) are useful in
CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
CC indicate the presence or absence of a cancer such as lung cancer.
CC ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 586 AA;
Query Match 99.2%; Score 3080; DB 23; Length 586;
Best Local Similarity 99.3%; Pred. No. 8.8e-242;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MYLENNATQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
Db 1 MYLENNATQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPSTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGROSVLVPEYPPQVGTFTVLYNFCNSSCVGMNRRPILIIIVTLETDRGOV 240
Db 181 YVEDPITGROSVLVPEYPPQVGTFTVLYNFCNSSCVGMNRRPILIIIVTLETDRGOV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIKKRR 300

DB 241 LGRRCFEARICACPRDRKADEDSIRKQVSDSTKNGDTRKPRFRQNTGHIQMTSIKRR 300
 QY 301 SPDELLYLPVGRRETYEMLKIKESLELMOYLPHQHTIETRYQQOQHLLQKQTSIQ 360
 DB 301 SPDELLYLPVGRRETYEMLKIKESLELMOYLPHQHTIETRYQQOQHLLQKQTSIQ 360
 QY 361 SPSSYGNSPPLNKMNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMMGTHMPMAG 420
 DB 361 SPSSYGNSPPLNKMNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMMGTHMPMAG 420
 QY 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
 DB 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
 QY 481 QIEHYSMDLALSLKIPQFRHAIWKGLDHRQLHEFSFSSPSHLLRTPSSASTVSGSSETR 540
 DB 481 QIEHYSMDLALSLKIPQFRHAIWKGLDHRQLHEFSFSSPSHLLRTPSSASTVSGSSETR 540
 QY 541 GERVIDAVRFTLRQTSISFPDRDEWDFNFDMDARRNKQORKEGE 586
 DB 541 GERVIDAVRFTLRQTSISFPDRDEWDFNFDMDARRNKQORKEGE 586

RESULT 10

ABB74949
 ID ABB74949 standard; Protein; 586 AA.
 AC ABB74949;
 DT 01-MAY-2002 (first entry)
 XX Human lung tumour L530S protein sequence SEQ ID NO:152.
 DE Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 KW immune response.
 KW Homo sapiens.
 OS
 XX WO200200174-A2.
 PN
 XX 03-JAN-2002.
 PD
 XX 28-JUN-2001; 2001WO-US21065.
 PF
 XX 28-JUN-2000; 2000US-0606421.
 PR 02-AUG-2000; 2000US-0630940.
 PR 21-AUG-2000; 2000US-0643597.
 PR 15-SEP-2000; 2000US-0662786.
 PR 09-OCT-2000; 2000US-0685696.
 PR 12-DEC-2000; 2000US-0735705.
 PR 07-MAY-2001; 2001US-0850716.

(CORI-) CORIXA CORP.

XX Wang T, Wang A, Shekly YAW, Li SX, Kalos MD, Henderson RA;
 PI McNeill PD, Fanger N, Retter MW, Warnerakis M, Fanger GR;
 PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
 XX
 DR WPI: 2002-090513/12.
 DR N-PSDB; ABL49106.
 XX
 PT Polynucleotides encoding lung,tumor polypeptides, useful for treating
 PT lung cancer or stimulating an immune response -
 XX
 PS Example 2; Page 246-247; 374pp; English.

XX The present invention describes human lung tumour proteins. Human lung
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumour proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumour proteins are useful for treating lung cancer or

CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
 CC ABB75070 represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 586 AA;
 Query Match 99.2%; Score 3080; DB 23; Length 586;
 Best Local Similarity 99.3%; Pred. No. 8.8e-242;
 Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MLYLNNAAQTQSFSPQYTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 DB 1 MLYLNNAAQTQSFSPQYTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 QY 61 TFDALSPSPATPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 DB 61 TFDALSPSPATPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 QY 121 VMTPPPGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPPPGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLPYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIIVTLETRDQGV 240
 DB 181 YVEDPITGRQSVLPYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIIVTLETRDQGV 240
 QY 241 LGRRCFEARICACPRDRKADEDSIRKQVSDSTKNGDTRKPRFRQNTGHIQMTSIKRR 300
 DB 241 LGRRCFEARICACPRDRKADEDSIRKQVSDSTKNGDTRKPRFRQNTGHIQMTSIKRR 300
 QY 301 SPDELLYLPVGRRETYEMLKIKESLELMOYLPHQHTIETRYQQOQHLLQKQTSIQ 360
 DB 301 SPDELLYLPVGRRETYEMLKIKESLELMOYLPHQHTIETRYQQOQHLLQKQTSIQ 360
 QY 361 SPSSYGNSPPLNKMNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMMGTHMPMAG 420
 DB 361 SPSSYGNSPPLNKMNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMMGTHMPMAG 420
 QY 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
 DB 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
 QY 481 QIEHYSMDLALSLKIPQFRHAIWKGLDHRQLHEFSFSSPSHLLRTPSSASTVSGSSETR 540
 DB 481 QIEHYSMDLALSLKIPQFRHAIWKGLDHRQLHEFSFSSPSHLLRTPSSASTVSGSSETR 540
 QY 541 GERVIDAVRFTLRQTSISFPDRDEWDFNFDMDARRNKQORKEGE 586
 DB 541 GERVIDAVRFTLRQTSISFPDRDEWDFNFDMDARRNKQORKEGE 586

RESULT 11

AA05962
 ID AA05962 standard; Protein; 586 AA.
 XX
 AC AA05962;
 XX
 DT 16-AUG-1999 (first entry)
 XX
 DE Mouse cell regulatory protein p63, isoform deltaNp63 alpha.
 XX
 KW Cell regulatory protein; p63; mu-deltaNp63 alpha; mouse;
 KW cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; therapy.
 OS Mus sp.
 XX
 PN WO9919357-A2.
 XX
 PD 22-APR-1999.
 XX
 PF 02-OCT-1998; 98WO-US21992.
 XX

PR 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 XX (HARD) HARVARD COLLEGE.
 PA McKeon F, Yang A;
 PI WPI; 1999-277595/23.
 XX N-PSDB; AAX58581.
 DR New isolated p63 cell. regulatory protein for, e.g. treatment of
 XX tumours
 PT
 XX
 PS Claim 23; Fig 18; 161pp; English.
 XX
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
 CC RACE. Sequencing of the amplification product indicated that the
 CC amplified cDNA possessed a truncated N-terminus, i.e. the
 CC transactivation domain was absent. Additional splice variants were
 CC identified by screening a cDNA library with a probe corresponding
 CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
 CC variants differing at the C-terminus are designated as alpha, beta
 CC and gamma forms, while p63 members differing in the N-terminus are
 CC designated as deltaN and TA forms, where the deltaN form lacks the
 CC transactivation domain. The present sequence represents mouse p63
 CC isotype mu-deltaNp63 alpha. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 XX
 SQ Sequence 586 AA;

Query Match 98.8%; Score 3066; DB 20; Length 586;
 Best Local Similarity 98.5%; Pred. No. 1.2e-240;
 Matches 577; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLYENNAQTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
 DB 1 MLYENNAQTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
 QY 61 TDALSPSPAIPNTDYPGPHSPDVQFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
 DB 61 TDALSPSPAIPNTDYPGPHSPDVQFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
 QY 121 VMTPPQGAIVIRAMPYKKAHEVTVVKKPCPNHLSRENEGQIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPPQGAIVIRAMPYKKAHEVTVVKKPCPNHLSRENEGQIAPPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFCNNSCVGMNRRPILIIIVTLETRDGV 240
 DB 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFCNNSCVGMNRRPILIIIVTLETRDGV 240
 QY 241 LGRRCFEARICACGRDRKADESIKQVQSDSTKNGDGTKRPFQNTGHIQMTSIKKRR 300
 DB 241 LGRRCFEARICACGRDRKADESIKQVQSDSTKNGDGTKRPFQNTGHIQMTSIKKRR 300
 QY 301 SPDELLYLPVGRGRETYYEMLLKIKESLELMQYLPOHTIETIYRQOOQOOHLLQKQTSIQ 360
 DB 301 SPDELLYLPVGRGRETYYEMLLKIKESLELMQYLPOHTIETIYRQOOQOOHLLQKQTSIQ 360

QY 361 SPSSYGNSSPPLNKMNSMKNLPSVSQLINPQORNALPTPTTIDCGMAGNIPMGTHMPMAG 420
 DB 361 SSSYGNSSPPLNKMNSMKNLPSVSQLINPQORNALPTTTPMPEGMAGNIPMGTHMPMAG 420
 QY 421 DMNGLSPTQALPPPLSMPSTSHCTPPPTDCTSIVSFLARLGCSSCLDYFTTQGLTIY 480
 DB 421 DMNGLSPTQALPPPLSMPSTSHCTPPPTDCTSIVSFLARLGCSSCLDYFTTQGLTIY 480
 QY 481 QIEHYSMDLALSLKIPQFRHAIWKGLDHRQLHRESSPSHLLRTPSSASTVSVGSSETR 540
 DB 481 QIEHYSMDLALSLKIPQFRHAIWKGLDHRQLHRESSPSHLLRTPSGASTVSVGSSETR 540
 QY 541 GERVIDAVRFTLQRTISFFPRDEWDFNDFMDARRNKQQRKEE 586
 DB 541 GERVIDAVRFTLQRTISFFPRDEWDFNDFMDARRNKQQRKEE 586

RESULT 12

AAY45247
 ID AAY45247 standard; Protein; 641 AA.
 XX
 AC AAY45247;
 XX
 DT 07-JAN-2000 (first entry)
 XX
 DE Human p51 protein B.
 XX
 KW Human; p51; p53 related gene; cell proliferation; regulation; cancer;
 KW tumour suppression; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..59 /label= transactivation_domain
 FT Domain 142..321 /label= DNA_binding_domain
 FT Domain 353..397 /label= oligomerisation_domain
 XX
 PN WO9950412-A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-JP01512.
 XX
 PR 27-MAR-1998; 98JP-0100467.
 XX
 PA (SAKA) OTSUKA PHARM CO LTD.
 PA (IKAW/) IKAWA Y.
 XX
 PI Ikawa Y, Ikawa S, Obinata M;
 XX
 DR WPI; 1999-591318/50.
 DR N-PSDB; AAZ25771.
 XX
 PT New p53 related human gene p51, useful for diagnosis, investigation and
 PT treatment of cancers and screening for potential cell proliferation
 PT agents -
 XX
 PS Example 1; Page 152-154; 163pp; Japanese.
 XX
 CC The present sequence represents a human p51 protein, which is related to
 CC p53 and has cell proliferation regulation and tumour suppression
 CC activity. The p51 gene can be used in the investigation, diagnosis and
 CC treatment of diseases such as cancer, with which the p53 family cell
 CC proliferation regulation is associated. The p51 protein may be used for
 CC screening potential agonists and antagonists of its regulatory function,
 CC for use as drugs,
 XX
 SQ Sequence 641 AA;

Query Match

97.7%; Score 3033; DB 20; Length 641;

Best Local Similarity	100.0%;	Pred. No. 6.6e-238;			
Matches	572;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	15	PQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDALSPSPAI	PSN	74	
DB	70	PQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDALSPSPAI	PSN	129	
QY	75	TDYPGHSFDVYFQOQSSTAKSATWYTYTELKLYCQIAKTCPIQIKVMTPPQGA	IVRAM	134	
DB	130	TDYPGHSFDVYFQOQSSTAKSATWYTYTELKLYCQIAKTCPIQIKVMTPPQGA	IVRAM	189	
QY	135	PVYKKAEBHTEVVKRCNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGR	QSVLV	194	
DB	190	PVYKKAEBHTEVVKRCNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGR	QSVLV	249	
QY	195	PYPQPGVGTFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETRDQGVILGRRCFE	ARICACP	254	
DB	250	PYPQPGVGTFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETRDQGVILGRRCFE	ARICACP	309	
QY	255	GRDKADEDSIRKQOVS DSTKNGDGTKRPFQNTHG IOMTSI KKRSPDDELL	LYPVGR	314	
DB	310	GRDKADEDSIRKQOVS DSTKNGDGTKRPFQNTHG IOMTSI KKRSPDDELL	LYPVGR	369	
QY	315	ETYEMLLKIESLELMQYLPOHTIETVROQQOQHLLKQTSIQSPSSYGNSSPP	LUNK	374	
DB	370	ETYEMLLKIESLELMQYLPOHTIETVROQQOQHLLKQTSIQSPSSYGNSSPP	LUNK	429	
QY	375	MNSMNLKPSVSQLINPOORNALPTTTIPDGMGANIPMGMTHMPAGDMNGLSPTQ	ALPPP	434	
DB	430	MNSMNLKPSVSQLINPOORNALPTTTIPDGMGANIPMGMTHMPAGDMNGLSPTQ	ALPPP	489	
QY	435	LSPSTSHCTPPPPYPDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHYSMDD	LASLK	494	
DB	490	LSPSTSHCTPPPPYPDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHYSMDD	LASLK	549	
QY	495	IPQGFRAHWKGI LDHROLHEFFSPSHLLRTPSSASIVSVGSSSTRGERVDAV	RETLRQ	554	
DB	550	IPQGFRAHWKGI LDHROLHEFFSPSHLLRTPSSASIVSVGSSSTRGERVDAV	RETLRQ	609	
QY	555	TISFPPRDEWDFNFDMDARRNKQORIKERGE	586		
DB	610	TISFPPRDEWDFNFDMDARRNKQORIKERGE	641		

RESULT 13	
AAAY05953	
ID	AAAY05953 standard; protein; 641 AA.
XX	
AC	AAAY05953;
XX	
DT	16-AUG-1999 (first entry)
XX	
DE	Human cell regulatory protein p63, isoform huTap63 alpha.
XX	
KW	Cell regulatory protein; p63; huTap63 alpha; Tap63 alpha; human;
KW	cancer; tumour suppressor; cell cycle control; apoptosis;
KW	cell proliferation; cell differentiation; therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO9919357-A2.
XX	
PD	22-APR-1999.
XX	
PF	02-OCT-1998; 98WO-US21992.
XX	
PR	29-MAY-1998; 98US-0087216.
PR	15-OCT-1997; 97US-0062076.
XX	
PA	(HARD) HARVARD COLLEGE.
XX	
PI	McKeon F, Yang A;
XX	

WPI; 1999-277595/23.
N-PSDB; AAX58572.

New isolated p63 cell regulatory protein for, e.g. treatment of tumours

Claim 23; Fig 9; 16lpp; English.

The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isootypes exist. Splice variants differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as delta1 and TA forms, where the delta1 form lacks the transactivation domain. The present sequence represents human p63 isootype TA-p63 alpha. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. Delta1 isoforms of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAX05953-64), polynucleotides (see AAX58572-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.

Sequence 641 AA;

		97.7%;	Score 3033;	DB 20;	Length 641;
Query Match		Best Local Similarity	100.0%;	Pred. No. 6.6e-238;	
Matches	572;	Conservative	0;	Mismatches	0;
				Indels	0; Gaps
QY	15	PQYTNGLLNSMDQIQNGSSSTSPYNTHDAQNSTAPSPAQSSTFDALSPSPAISN	74		
Db	70	PQYTNGLLNSMDQIQNGSSSTSPYNTHDAQNSTAPSPAQSSTFDALSPSPAISN	129		
QY	75	TDPGPHSFDFVQSOSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAVIRAM	134		
Db	130	TDPGPHSFDFVQSOSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAVIRAM	189		
QY	135	PVKKAHEHTVEVKRCPNHLSREFNEGQIAPPSSHILIRVEGNSHAQYVEDPITGRQSVLV	194		
Db	190	PVKKAHEHTVEVKRCPNHLSREFNEGQIAPPSSHILIRVEGNSHAQYVEDPITGRQSVLV	249		
QY	195	PIEPPQVGTEFTVLNYFMNCSSCVCGMNRRLIIIVTLFTRDGOVLGRRCFEARICACP	254		
Db	250	PIEPPQVGTEFTVLNYFMNCSSCVCGMNRRLIIIVTLFTRDGOVLGRRCFEARICACP	309		
QY	255	GRDKADEDSIRKQOVSdstkngdgtkrppfnthgIQMTSikKRSPDDbELLyPVrGR	314		
Db	310	GRDKADEDSIRKQOVSdstkngdgtkrppfnthgIQMTSikKRSPDDbELLyPVrGR	369		
QY	315	ETYMllLKIESLElMQYLPOHTIETYRQOOQQOHLLQKOTSIQSPSSYGNSPPLNK	374		
Db	370	ETYMllLKIESLElMQYLPOHTIETYRQOOQQOHLLQKOTSIQSPSSYGNSPPLNK	429		
QY	375	MNSMNLKPSVSQLINPQORNALPTTTPDGMGANIPMWGTHMPAGDMNGLSPTQALPPP	434		
Db	430	MNSMNLKPSVSQLINPQORNALPTTTPDGMGANIPMWGTHMPAGDMNGLSPTQALPPP	489		
QY	435	LSPMSTSHCNPPPPYPPTDCSIVSFARLGCSCLDYFTTOGLTIYQIETHYSMDDLASLK	494		

Db	490	LSMPTSHCTPPPPYPTDCSIVSFLARLGCSCCLDYFTTQGLTTIYQIEHYGMDLALSLK	549
QY	495	IPEQFRHAIWKGLDHRQLHEFSSPSHLLRTPTSSASTVSVGSSETRGERVIDAVRFTLRQ	554
Db	550	IPEQFRHAIWKGLDHRQLHEFSSPSHLLRTPTSSASTVSVGSSETRGERVIDAVRFTLRQ	609
QY	555	TISFPFPRDEWDFNFDMDARRNKQRIKEEGE	586
Db	610	TISFPFPRDEWDFNFDMDARRNKQRIKEEGE	641
RESULT 14			
AA82129	ID	AA82129 standard; protein; 641 AA.	
XX	AC	AA82129;	
XX	DT	03-AUG-2001 (first entry)	
XX	DE	Human protein #2 used to produce a chimeric p53 protein.	
XX	KW	Human; cytostatic; gene therapy; p53; human tumour.	
XX	OS	Homo sapiens.	
FH	Key	Location/Qualifiers	
FT	Domain	1..59	
FT	Domain	/label= Transactivation_domain	
FT	Domain	142..321	
FT	Domain	/label= DNA_binding_domain	
FT	Domain	353..397	
FT	Domain	/label= Oligomerisation_domain	
XX	PN	JP2000354488-A.	
XX	XX		
PD	26-DEC-2000.		
XX	PF	09-APR-1999; 99JP-0139034.	
XX	PR	09-APR-1999; 99JP-0139034.	
XX	PA	(IKAW/) IKAWA H.	
XX	PA	(SAKA) OTSUKA PHARM CO LTD.	
XX	DR	WPI; 2001-268293/28.	
XX	DR	N-PSDB; AAF86589.	
XX	PT	Chimera gene of the p53 family, useful for gene therapy, and treatment	
XX	PT	of cancer, comprises a transcription activating region and a DNA	
XX	PS	binding region -	
XX	PS	Example 1; Page 37-40; 57pp; Japanese.	
CC	CC	The present invention relates to a chimera gene of p53 family encoding a	
CC	CC	transcription activating region, a DNA binding region, and an oligomer	
CC	CC	formation region of different p53 family proteins. The chimeric gene can	
CC	CC	be used for gene therapy of p53 variant human tumours, and analysis of	
CC	CC	the function of the p53 family gene. The present sequence was used in the	
XX	XX	present invention.	
XX	SQ	Sequence 641 AA;	
Query Match			
Best Local Similarity 97.7%; Score 3033; DB 22; Length 641;			
Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	15	PQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN	74
Db	70	PQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN	129
QY	75	TDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPPGAVIRAM	134
Db	130	TDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPPGAVIRAM	189

QY	135	PYKKAHVTEVVKCPNHELHREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGROSLV	194
Db	190	PYKKAHVTEVVKCPNHELHREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGROSLV	249
QY	195	PYEPQVGTFTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDQVGLGRCCFEARICACP	254
Db	250	PYEPQVGTFTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDQVGLGRCCFEARICACP	309
QY	255	GRDKADEDSIRKQVSDSTKNGDGTFRPFRONTGHIQMTSIIKKRSPPDELLYLPRGR	314
Db	310	GRDKADEDSIRKQVSDSTKNGDGTFRPFRONTGHIQMTSIIKKRSPPDELLYLPRGR	369
QY	315	ETYEMLLKIKESLELMQYLPQHTIETIROQQOQHQHLLQKQTSIQSPSSYGNSSPPLNK	374
Db	370	ETYEMLLKIKESLELMQYLPQHTIETIROQQOQHQHLLQKQTSIQSPSSYGNSSPPLNK	429
QY	375	MNSMKNLPSVSQLINPQQRNALTPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP	434
Db	430	MNSMKNLPSVSQLINPQQRNALTPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP	489
QY	435	LSMPTSHCTPPPPYPTDCSIVSFLARLGCSCCLDYFTTQGLTTIYQIEHYGMDLALSLK	494
Db	490	LSMPTSHCTPPPPYPTDCSIVSFLARLGCSCCLDYFTTQGLTTIYQIEHYGMDLALSLK	549
QY	495	IPEQFRHAIWKGLDHRQLHEFSSPSHLLRTPTSSASTVSVGSSETRGERVIDAVRFTLRQ	554
Db	550	IPEQFRHAIWKGLDHRQLHEFSSPSHLLRTPTSSASTVSVGSSETRGERVIDAVRFTLRQ	609
QY	555	TISFPFPRDEWDFNFDMDARRNKQRIKEEGE	586
Db	610	TISFPFPRDEWDFNFDMDARRNKQRIKEEGE	641
RESULT 15			
ABG95142	ID	ABG95142 standard; Protein; 641 AA.	
XX	AC	ABG95142;	
XX	DT	04-DEC-2002 (first entry)	
XX	DE	Human oncogene p63 isoform TA p63 alpha.	
XX	KW	Chromosome aberration; oncogenic fusion protein; cancer; oncogene;	
XX	KW	proliferative disease; cellular protein isoform; heat shock protein 90;	
XX	KW	HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;	
XX	KW	T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;	
XX	KW	acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;	
XX	KW	acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;	
XX	KW	papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;	
XX	KW	rhabdomyosarcoma; synovial sarcoma; viral infection.	
OS	OS	Homo sapiens.	
XX	PN	WO200269900-A2.	
XX	XX		
XX	PD	12-SEP-2002.	
XX	PF	01-MAR-2002; 2002WO-US06518.	
XX	PR	01-MAR-2001; 2001US-272751P.	
XX	PA	(CONF-) CONFORMA THERAPEUTICS CORP.	
XX	PI	Fritz LC, Burrows FJ;	
XX	DR	WPI; 2002-698710/75.	
XX	DR	N-PSDB; ABS73334.	
PT	PT	Treating genetically-defined disease associated with chromosomal	
PT	PT	aberrations yielding oncogenic fusion proteins, e.g. cell proliferative	
PT	PT	diseases, involves administering an inhibitor of heat shock protein 90	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:54 ; Search time 16.1655 seconds
(without alignments)
1533.769 Million cell updates/sec

Title: US-09-538-106-16

Perfect score: 3104

Sequence: 1 MLYENNAQTQFSEPOYTNL.....FNFDMDARRNKQRIEEGE 586

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3087	99.5	586	4	US-09-643-597-338
2	3087	99.5	586	4	US-09-542-615A-338
3	3087	99.5	586	4	US-09-606-421B-338
4	3080	99.2	586	4	US-09-643-597-152
5	3080	99.2	586	4	US-09-480-884A-152
6	3080	99.2	586	4	US-09-542-615A-152
7	3080	99.2	586	4	US-09-606-421B-152
8	3029	97.6	641	4	US-09-643-597-339
9	3029	97.6	641	4	US-09-542-615A-339
10	3029	97.6	641	4	US-09-606-421B-339
11	3025	97.5	680	4	US-09-643-597-342
12	3025	97.5	680	4	US-09-542-615A-342
13	3025	97.5	680	4	US-09-606-421B-342
14	2421	78.0	461	4	US-09-643-597-343
15	2421	78.0	461	4	US-09-542-615A-343
16	2421	78.0	461	4	US-09-606-421B-343
17	2350	75.7	516	4	US-09-643-597-344
18	2350	75.7	516	4	US-09-542-615A-344
19	2350	75.7	516	4	US-09-606-421B-344
20	1893	61.0	426	4	US-09-277-196-19
21	1872	60.3	356	4	US-09-643-597-341
22	1872	60.3	356	4	US-09-277-196-2
23	1872	60.3	356	4	US-09-542-615A-341
24	1872	60.3	356	4	US-09-606-421B-341
25	1813	58.4	448	4	US-09-643-597-340
26	1813	58.4	448	4	US-09-542-615A-340
27	1813	58.4	448	4	US-09-606-421B-340

Sequence 3, Appli
Sequence 20, Appli
Sequence 2, Appli
Sequence 27, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 25, Appli
Sequence 26, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 32, Appli
Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-643-597-338
; Sequence 338, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-338

Query Match	99.5%	Score 3087;	DB 4;	Length 586;
Best Local Similarity	99.5%	Pred. No. 2.8e-278;		
Matches 583;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	MLYENNAQTQFSEPOYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS	60	
Db	1	MLYENNAQTQFSEPOYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSP	60	
Qy	61	TFDALSPSPAIPTNDYPGPHSFQSSSTAKSATWTYSTELKLYCQIAKTCPTQIK	120	
Db	61	TFDALSPSPAIPTNDYPGPHSFQSSSTAKSATWTYSTELKLYCQIAKTCPTQIK	120	
Qy	121	VMTPPGAVIRAMPVYKKAHVTEVYKRCNHELSEFNEGQIAPSHLLIRVGNSHAQ	180	
Db	121	VMTPPGAVIRAMPVYKKAHVTEVYKRCNHELSEFNEGQIAPSHLLIRVGNSHAQ	180	
Qy	181	YVEDPITGRQSVLYPEPPQVGTFTTLYNFMNCSSCGVMNRRLIIVTLETRDQGV	240	
Db	181	YVEDPITGRQSVLYPEPPQVGTFTTLYNFMNCSSCGVMNRRLIIVTLETRDQGV	240	
Qy	241	LGRRCFEARICACPGDRKKADEDSIRKQOVSDSTKNGDGRKPRFRQNTGHQMTSIKKRR	300	

Db 301 SPDDLLYLPVGRGTYEMLVKIKESLELMQYLPQHTIETRYQQQQQHQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLNKMNSMKNKLPVSQSLNPOORNALTPPTIPDGMGANIPMMGTHMPWAG 420
Db 361 SPSSYGNSSPPLNKMNSMKNKLPVSQSLNPOORNALTPPTIPDGMGANIPMMGTHMPWAG 420
QY 421 DMNGLSPPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIY 480
Db 421 DMNGLSPPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIY 480
QY 481 QIEHYSMDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLIRTPSSASTVSGSSETR 540
Db 481 QIEHYSMDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLIRTPSSASTVSGSSETR 540
QY 541 GERVIDAVRFTLROTISPPRDEWDFNDFMDARRNKOORKEGE 586
Db 541 GERVIDAVRFTLROTISPPRDEWDFNDFMDARRNKOORKEGE 586

RESULT 4

US-09-643-597-152

; Sequence 152, Application US/09643597

; Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skelky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643.597

; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 152

; LENGTH: 586

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-643-597-152

Query Match 99.2%; Score 3080; DB 4; Length 586;

Best Local Similarity 99.3%; Pred. No. 1.3e-277;

Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYLNNATQFSEPYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
Db 1 MLYLNNATQFSEPYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDFVSFOQSSSTAKSATWTYSELKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNTDYPGPHSFDFVSFOQSSSTAKSATWTYSELKLYCQIAKTCPIQIK 120
QY 121 VMTPPQCAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQCAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPVPEPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDQGV 240
Db 181 YVEDPITGRQSVLPVPEPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLETRDQGV 240
QY 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGTFRPFQNTHTGQMTSIKRR 300
Db 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGTFRPFQNTHTGQMTSIKRR 300
QY 301 SPDDLLYLPVGRGTYEMLVKIKESLELMQYLPQHTIETRYQQQQQHQHLLQKQTSIQ 360
Db 301 SPDDLLYLPVGRGTYEMLVKIKESLELMQYLPQHTIETRYQQQQQHQHLLQKQTSIQ 360

Db 361 SPSSYGNSSPPLKMNKMNKLPVSQINPQORNALTPPTIPDGMGANIPMMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
QY 481 QIEHYSMDDLASLIKPEQFRHAIWKGLDHRQLHEFSSPSHLLRTPSSASTVSGSSETR 540
Db 481 QIEHYSMDDLASLIKPEQFRHAIWKGLDHRQLHEFSSPSHLLRTPSSASTVSGSSETR 540
QY 541 GERVIDAVRFTLRQTISFFPRDEWDFNFDMDARRNKQORIKEE 586
Db 541 GERVIDAVRFTLRQTISFFPRDEWDFNFDMDARRNKQORIKEE 586
RESULT 6
US-09-542-615A-152
; Sequence 152, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, TongTong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy R.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542, 615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-542-615A-152

Query Match 99.2%; Score 3080; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 1.3e-277;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLYLNNNAQTQSEPOYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
Db 1 MLYLNNNAQTQSEPOYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPPGAVIRAMPYKKAHVTEVVKRCPNHELRSREFNEGOIAPPSSHLIRVEGNSHAQ 180
Db 121 VMTPPPGAVIRAMPYKKAHVTEVVKRCPNHELRSREFNEGOIAPPSSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVPYEPQVGTFTTLYNFMCMNSCVGGMNRRPILIIIVTLETRDGV 240
Db 181 YVEDPITGRQSVLVPYEPQVGTFTTLYNFMCMNSCVGGMNRRPILIIIVTLETRDGV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFRRONTGHIOMTSIKKRR 300
Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFRRONTGHIOMTSIKKRR 300
QY 301 SPDDLLYLPVGRRETYEMLLIKESLELMQVLPQHTIETRYQOQOQOHHLLQKOTSQ 360
Db 301 SPDDLLYLPVGRRETYEMLLIKESLELMQVLPQHTIETRYQOQOQOHHLLQKOTSQ 360
QY 361 SPSSYGNSSPPLKMNKMNKLPVSQINPQORNALTPPTIPDGMGANIPMMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKMNKMNKLPVSQINPQORNALTPPTIPDGMGANIPMMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480

Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
QY 481 QIEHYSMDDLASLIKPEQFRHAIWKGLDHRQLHEFSSPSHLLRTPSSASTVSGSSETR 540
Db 481 QIEHYSMDDLASLIKPEQFRHAIWKGLDHRQLHEFSSPSHLLRTPSSASTVSGSSETR 540
QY 541 GERVIDAVRFTLRQTISFFPRDEWDFNFDMDARRNKQORIKEE 586
Db 541 GERVIDAVRFTLRQTISFFPRDEWDFNFDMDARRNKQORIKEE 586
RESULT 7
US-09-606-421B-152
; Sequence 152, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, TongTong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606, 421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-606-421B-152

Query Match 99.2%; Score 3080; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 1.3e-277;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLYLNNNAQTQSEPOYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
Db 1 MLYLNNNAQTQSEPOYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSNNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPPGAVIRAMPYKKAHVTEVVKRCPNHELRSREFNEGOIAPPSSHLIRVEGNSHAQ 180
Db 121 VMTPPPGAVIRAMPYKKAHVTEVVKRCPNHELRSREFNEGOIAPPSSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVPYEPQVGTFTTLYNFMCMNSCVGGMNRRPILIIIVTLETRDGV 240
Db 181 YVEDPITGRQSVLVPYEPQVGTFTTLYNFMCMNSCVGGMNRRPILIIIVTLETRDGV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFRRONTGHIOMTSIKKRR 300
Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFRRONTGHIOMTSIKKRR 300
QY 301 SPDDLLYLPVGRRETYEMLLIKESLELMQVLPQHTIETRYQOQOQOHHLLQKOTSQ 360
Db 301 SPDDLLYLPVGRRETYEMLLIKESLELMQVLPQHTIETRYQOQOQOHHLLQKOTSQ 360
QY 361 SPSSYGNSSPPLKMNKMNKLPVSQINPQORNALTPPTIPDGMGANIPMMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKMNKMNKLPVSQINPQORNALTPPTIPDGMGANIPMMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480

OY 481 OIEHYSMDLASIKPEOFRAHFKGILDRHOLFHESSSHLLRTPSSASTVSGSSSTR 540
DB 481 OIEHYSMDLASIKPEOFRAHFKGILDRHOLFHESSSHLLRTPSSASTVSGSSSTR 540
OY 541 GERVIDAVFTLRQTISFPPEDEMDNFMDARRNKQORIKEEGE 586
DB 541 GERVIDAVFTLRQTISFPPEDEMDNFMDARRNKQORIKEEGE 586

RESULT 8

US-09-643-597-339
; Sequence 339, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-339

Query Match 97.6%; Score 3029; DB 4; Length 641;

Best Local Similarity 99.8%; Pred. No. 8e-273;

Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 15 POYTNIGLINSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYQPSSTFDALSPSPAIPSN 74
DB 70 POYTNIGLINSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYQPSSTFDALSPSPAIPSN 129
OY 75 TDYPRHSDVYFQOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMPPPQGAIVIRAM 134
DB 130 TDYPRHSDVYFQOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMPPPQGAIVIRAM 189
OY 135 PYKKAHEVTEVVKCPNHELRENEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 194
DB 190 PYKKAHEVTEVVKCPNHELRENEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 249
OY 195 PEPPOVGTEFTTVLYNFCNSSCVGMMRRPILIIIVLETRDGOVLGRCEARICACP 254
DB 250 PEPPOVGTEFTTVLYNFCNSSCVGMMRRPILIIIVLETRDGOVLGRCEARICACP 309
OY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDELTYLPVGR 314
DB 310 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDELTYLPVGR 369
OY 315 EYEMILIKESLELMQYLPQHTIETYROQOQOQHLLQKOTSIQSPSSYGNSSPPLNK 374
DB 370 EYEMILIKESLELMQYLPQHTIETYROQOQOQHLLQKOTSIQSPSSYGNSSPPLNK 429
OY 375 MNSMNLKDSVSOILNPOORNALPTTIPDGMCANIPMGTHMPMAGDMNGLSPTQALPPP 434
DB 430 MNSMNLKDSVSOILNPOORNALPTTIPDGMCANIPMGTHMPMAGDMNGLSPTQALPPP 489
OY 435 LSPSTSHCTPPPPYPTDCSIVGFARLGCSSCLDYFTTQGLTTIYOIEHYSMDLASIK 494
DB 435 LSPSTSHCTPPPPYPTDCSIVGFARLGCSSCLDYFTTQGLTTIYOIEHYSMDLASIK 494

DB 490 LSPSTSHCTPPPPYPTDCSIVGFARLGCSSCLDYFTTQGLTTIYOIEHYSMDLASIK 549
OY 495 IPEOFRAHFKGILDRHOLFHESSSHLLRTPSSASTVSGSSSTRGERVIDAVFTLRQ 554
DB 550 IPEOFRAHFKGILDRHOLFHESSSHLLRTPSSASTVSGSSSTRGERVIDAVFTLRQ 609
OY 555 TISFPPEDEMDNFMDARRNKQORIKEEGE 586
DB 610 TISFPPEDEMDNFMDARRNKQORIKEEGE 641

RESULT 9

US-09-542-615A-339
; Sequence 339, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-339

Query Match 97.6%; Score 3029; DB 4; Length 641;

Best Local Similarity 99.8%; Pred. No. 8e-273;

Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 15 POYTNIGLINSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYQPSSTFDALSPSPAIPSN 74
DB 70 POYTNIGLINSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYQPSSTFDALSPSPAIPSN 129
OY 75 TDYPRHSDVYFQOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMPPPQGAIVIRAM 134
DB 130 TDYPRHSDVYFQOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMPPPQGAIVIRAM 189
OY 135 PYKKAHEVTEVVKCPNHELRENEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 194
DB 190 PYKKAHEVTEVVKCPNHELRENEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 249
OY 195 PEPPOVGTEFTTVLYNFCNSSCVGMMRRPILIIIVLETRDGOVLGRCEARICACP 254
DB 250 PEPPOVGTEFTTVLYNFCNSSCVGMMRRPILIIIVLETRDGOVLGRCEARICACP 309
OY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDELTYLPVGR 314
DB 310 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDELTYLPVGR 369
OY 315 EYEMILIKESLELMQYLPQHTIETYROQOQOQHLLQKOTSIQSPSSYGNSSPPLNK 374
DB 370 EYEMILIKESLELMQYLPQHTIETYROQOQOQHLLQKOTSIQSPSSYGNSSPPLNK 429
OY 375 MNSMNLKDSVSOILNPOORNALPTTIPDGMCANIPMGTHMPMAGDMNGLSPTQALPPP 434
DB 430 MNSMNLKDSVSOILNPOORNALPTTIPDGMCANIPMGTHMPMAGDMNGLSPTQALPPP 489
OY 435 LSPSTSHCTPPPPYPTDCSIVGFARLGCSSCLDYFTTQGLTTIYOIEHYSMDLASIK 494
DB 435 LSPSTSHCTPPPPYPTDCSIVGFARLGCSSCLDYFTTQGLTTIYOIEHYSMDLASIK 494

Db 550 IPEOFRAIKGILDRHQLHEPSSPSHLTPSSASTVSIGSSETGERVIDAVFTLRQ 609
QY 555 TISPPREDEWNEFMDARRNKQOIRKEGE 586
| | | | |
Db 610 TISPPREDEWNEFMDARRNKQOIRKEGE 641

RESULT 10
US-09-606-421B-339
; Sequence 339, Application US/09606421B
; Patent No. 653135
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-339

Query Match 97.6%; Score 3029; DB 4; Length 641;
Best Local Similarity 99.8%; Pred. No. 8e-273;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PQTNTGLNLMDOQIONGSSSTSPYNTDHAQNSVTAAPSPYAPSSFTDALSPSPALPSN 74
| | | | |
Db 70 PQTNTGLNLMDOQIONGSSSTSPYNTDHAQNSVTAAPSPYAPSSFTDALSPSPALPSN 129
| | | | |
QY 75 TDYPGHSPFVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIKWTPPGCAVIRAM 134
| | | | |
Db 130 TDYPGHSPFVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIKWTPPGCAVIRAM 189
| | | | |
QY 135 PYVKAHEHTVEVYKRCNHLSREFNQGLAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
| | | | |
Db 190 PYVKAHEHTVEVYKRCNHLSREFNQGLAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
| | | | |
QY 195 PYEPPOVGTFTTVLYNFMCNSSCVGGMNRPILIIYVLTETRDGOVLGRRCFEARICACP 254
| | | | |
Db 250 PYEPPOVGTFTTVLYNFMCNSSCVGGMNRPILIIYVLTETRDGOVLGRRCFEARICACP 309
| | | | |
QY 255 GRPKRADEDSIRKQOVSSTKNGDGTFRPRONTGHIOMTSIKRRSPDDELLYLPVGR 314
| | | | |
Db 310 GRPKRADEDSIRKQOVSSTKNGDGTFRPRONTGHIOMTSIKRRSPDDELLYLPVGR 369
| | | | |
QY 315 EYEMMLKIKESLEIMQYLPOHTIETRYRQOQOHOHLQKOTSIOSSPSYGSSPPLNK 374
| | | | |
Db 370 EYEMMLKIKESLEIMQYLPOHTIETRYRQOQOHOHLQKOTSIOSSPSYGSSPPLNK 429
| | | | |
QY 375 MNSMNLKPSVSQILNPOQRNALPPTIIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 434
| | | | |
Db 430 MNSMNLKPSVSQILNPOQRNALPPTIIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 489
| | | | |
QY 435 LSNPSTSHCTPPPPYPTDCSIVSFARLGSSCLDFTTQGLTTIYQIEHYSMDLASLK 494
| | | | |
Db 490 LSNPSTSHCTPPPPYPTDCSIVSFARLGSSCLDFTTQGLTTIYQIEHYSMDLASLK 549
| | | | |
QY 495 IPEOFRAIKGILDRHQLHEPSSPSHLTPSSASTVSIGSSETGERVIDAVFTLRQ 554
| | | | |
Db 550 IPEOFRAIKGILDRHQLHEPSSPSHLTPSSASTVSIGSSETGERVIDAVFTLRQ 609
| | | | |

QY 555 TISPPREDEWNEFMDARRNKQOIRKEGE 586
| | | | |
Db 610 TISPPREDEWNEFMDARRNKQOIRKEGE 641

RESULT 11
US-09-643-597-342
; Sequence 342, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-342

Query Match 97.5%; Score 3025; DB 4; Length 680;
Best Local Similarity 99.8%; Pred. No. 2.1e-272;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PQTNTGLNLMDOQIONGSSSTSPYNTDHAQNSVTAAPSPYAPSSFTDALSPSPALPSN 74
| | | | |
Db 109 PQTNTGLNLMDOQIONGSSSTSPYNTDHAQNSVTAAPSPYAPSSFTDALSPSPALPSN 168
| | | | |
QY 75 TDYPGHSPFVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIKWTPPGCAVIRAM 134
| | | | |
Db 169 TDYPGHSPFVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIKWTPPGCAVIRAM 228
| | | | |
QY 135 PYVKAHEHTVEVYKRCNHLSREFNQGLAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
| | | | |
Db 229 PYVKAHEHTVEVYKRCNHLSREFNQGLAPPSHLIRVGNSHAQYVEDPITGRQSVLV 288
| | | | |
QY 195 PYEPPOVGTFTTVLYNFMCNSSCVGGMNRPILIIYVLTETRDGOVLGRRCFEARICACP 254
| | | | |
Db 289 PYEPPOVGTFTTVLYNFMCNSSCVGGMNRPILIIYVLTETRDGOVLGRRCFEARICACP 348
| | | | |
QY 255 GRPKRADEDSIRKQOVSSTKNGDGTFRPRONTGHIOMTSIKRRSPDDELLYLPVGR 314
| | | | |
Db 349 GRPKRADEDSIRKQOVSSTKNGDGTFRPRONTGHIOMTSIKRRSPDDELLYLPVGR 408
| | | | |
QY 315 EYEMMLKIKESLEIMQYLPOHTIETRYRQOQOHOHLQKOTSIOSSPSYGSSPPLNK 374
| | | | |
Db 409 EYEMMLKIKESLEIMQYLPOHTIETRYRQOQOHOHLQKOTSIOSSPSYGSSPPLNK 468
| | | | |
QY 375 MNSMNLKPSVSQILNPOQRNALPPTIIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 434
| | | | |
Db 469 MNSMNLKPSVSQILNPOQRNALPPTIIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 528
| | | | |
QY 435 LSNPSTSHCTPPPPYPTDCSIVSFARLGSSCLDFTTQGLTTIYQIEHYSMDLASLK 494
| | | | |
Db 529 LSNPSTSHCTPPPPYPTDCSIVSFARLGSSCLDFTTQGLTTIYQIEHYSMDLASLK 588
| | | | |
QY 495 IPEOFRAIKGILDRHQLHEPSSPSHLTPSSASTVSIGSSETGERVIDAVFTLRQ 554
| | | | |
Db 550 IPEOFRAIKGILDRHQLHEPSSPSHLTPSSASTVSIGSSETGERVIDAVFTLRQ 609
| | | | |

Db 589 IPEQFHAIMKGIILDRHQLHEFSSPSHLRTSPSSASTVSGSSETRGERVIDAVRFTLRQ 648
QY 555 TISPPRDEMDNFMDARRNKQORIKEGE 586
Db 649 TISPPRDEMDNFMDARRNKQORIKEGE 680

RESULT 12
US-09-542-615A-342
Sequence 342, Application US/09542615A
Patent No. 6518256
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
TYPE: PRT
ORGANISM: Homo sapiens
US-09-542-615A-342

Query Match 97.5%; Score 3025; DB 4; Length 680;
Best local Similarity 99.8%; Pred. No. 2,1e-272;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 POYTNGLINSMDOQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSTFDALSPSPAIPSN 74
Db 109 POYTNGLINSMDOQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSTFDALSPSPAIPSN 168
QY 75 TDYPGHSPDVSFOOSTSTAKSATWTYSTELKLYCOIATCPLOIKVMPPOGAVIRAM 134
Db 169 TDYPGHSPDVSFOOSTSTAKSATWTYSTELKLYCOIATCPLOIKVMPPOGAVIRAM 228
QY 135 PUYKKAHEYTEVVKRCPNHELREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 194
Db 229 PUYKKAHEYTEVVKRCPNHELREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 288
QY 195 PYEPPOVGTEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLAGRCEARICACP 254
Db 289 PYEPPOVGTEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLAGRCEARICACP 348
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHOIOMTSIKKRSPPDELLYLPVRGR 314
Db 349 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHOIOMTSIKKRSPPDELLYLPVRGR 408
QY 315 EYTEMILKIKESLELMQYLPQHTIETYYRQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
Db 409 EYTEMILKIKESLELMQYLPQHTIETYYRQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 468
QY 375 MNSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALP 434
Db 469 MNSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALP 528
QY 435 LSMPSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTTTIOIHYSMDDLASLK 494
Db 529 LSMPSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTTTIOIHYSMDDLASLK 588
QY 495 IPEQFHAIMKGIILDRHQLHEFSSPSHLRTSPSSASTVSGSSETRGERVIDAVRFTLRQ 554
Db 589 IPEQFHAIMKGIILDRHQLHEFSSPSHLRTSPSSASTVSGSSETRGERVIDAVRFTLRQ 648
QY 555 TISPPRDEMDNFMDARRNKQORIKEGE 586
Db 649 TISPPRDEMDNFMDARRNKQORIKEGE 680

Db 649 TISPPRDEMDNFMDARRNKQORIKEGE 680

RESULT 13
US-09-606-421B-342
Sequence 342, Application US/09606421B
Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
TYPE: PRT
ORGANISM: Homo sapiens
US-09-606-421B-342

Query Match 97.5%; Score 3025; DB 4; Length 680;
Best local Similarity 99.8%; Pred. No. 2,1e-272;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 POYTNGLINSMDOQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSTFDALSPSPAIPSN 74
Db 109 POYTNGLINSMDOQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSTFDALSPSPAIPSN 168
QY 75 TDYPGHSPDVSFOOSTSTAKSATWTYSTELKLYCOIATCPLOIKVMPPOGAVIRAM 134
Db 169 TDYPGHSPDVSFOOSTSTAKSATWTYSTELKLYCOIATCPLOIKVMPPOGAVIRAM 228
QY 135 PUYKKAHEYTEVVKRCPNHELREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 194
Db 229 PUYKKAHEYTEVVKRCPNHELREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 288
QY 195 PYEPPOVGTEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLAGRCEARICACP 254
Db 289 PYEPPOVGTEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLAGRCEARICACP 348
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHOIOMTSIKKRSPPDELLYLPVRGR 314
Db 349 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHOIOMTSIKKRSPPDELLYLPVRGR 408
QY 315 EYTEMILKIKESLELMQYLPQHTIETYYRQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
Db 409 EYTEMILKIKESLELMQYLPQHTIETYYRQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 468
QY 375 MNSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALP 434
Db 469 MNSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALP 528
QY 435 LSMPSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTTTIOIHYSMDDLASLK 494
Db 529 LSMPSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTTTIOIHYSMDDLASLK 588
QY 495 IPEQFHAIMKGIILDRHQLHEFSSPSHLRTSPSSASTVSGSSETRGERVIDAVRFTLRQ 554
Db 589 IPEQFHAIMKGIILDRHQLHEFSSPSHLRTSPSSASTVSGSSETRGERVIDAVRFTLRQ 648
QY 555 TISPPRDEMDNFMDARRNKQORIKEGE 586
Db 649 TISPPRDEMDNFMDARRNKQORIKEGE 680

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RESULT 14
US-09-643--597-343
; Sequence 343, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-643-597-343

Query Match      78.0%; Score 2421; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.6e-216;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYLNNAAQOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYLNNAAQOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSTNDPGRHSDVDFQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSTNDPGRHSDVDFQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
QY 121 VMPPPGAVIRAMPYKKAHVTEVVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMPPPGAVIRAMPYKKAHVTEVVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYPPEPVGTEFTVLYNFMCNSSCVGMMNRPLIIVTLETBDGOV 240
DB 181 YVEDPITGRQSVLYPPEPVGTEFTVLYNFMCNSSCVGMMNRPLIIVTLETBDGOV 240
QY 241 LGRRCFEARICACPGDRKADSDSIRKQVSDSTKNGDGTFRFRONTGHIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKADSDSIRKQVSDSTKNGDGTFRFRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPRGRRETEYEMLLIKESIELMOYLPOHTIETRYROOQOOHOLLQKQTSIQ 360
DB 301 SPDELLYLPRGRRETEYEMLLIKESIELMOYLPOHTIETRYROOQOOHOLLQKQTSIQ 360
QY 361 SPSSYGSSPPLKKNMSMNLPSVSQILNPOORNALPTTIIPDGMGANTPMGTHMPMAG 420
DB 361 SPSSYGSSPPLKKNMSMNLPSVSQILNPOORNALPTTIIPDGMGANTPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456

RESULT 15
US-09-542-615A-343
; Sequence 343, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
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; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-542-615A-343
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Query Match      78.0%; Score 2421; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.6e-216;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLYLNNAAQOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYLNNAAQOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSTNDPGRHSDVDFQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSTNDPGRHSDVDFQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
QY 121 VMPPPGAVIRAMPYKKAHVTEVVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMPPPGAVIRAMPYKKAHVTEVVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYPPEPVGTEFTVLYNFMCNSSCVGMMNRPLIIVTLETBDGOV 240
DB 181 YVEDPITGRQSVLYPPEPVGTEFTVLYNFMCNSSCVGMMNRPLIIVTLETBDGOV 240
QY 241 LGRRCFEARICACPGDRKADSDSIRKQVSDSTKNGDGTFRFRONTGHIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKADSDSIRKQVSDSTKNGDGTFRFRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPRGRRETEYEMLLIKESIELMOYLPOHTIETRYROOQOOHOLLQKQTSIQ 360
DB 301 SPDELLYLPRGRRETEYEMLLIKESIELMOYLPOHTIETRYROOQOOHOLLQKQTSIQ 360
QY 361 SPSSYGSSPPLKKNMSMNLPSVSQILNPOORNALPTTIIPDGMGANTPMGTHMPMAG 420
DB 361 SPSSYGSSPPLKKNMSMNLPSVSQILNPOORNALPTTIIPDGMGANTPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456
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Job time: 18.1655 secs
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:46:34 ; Search time 25.0181 Seconds

(without alignments) 2781.719 Million cell updates/sec

Title: US-09-538-106-16

Perfect score: 3104
Sequence: 1 MLYENNAQTQFSEQYTNL.....FNFMARRNRKQRIKGE 586

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3087	99.5	586	9 US-09-735-705-338	Sequence 338, App
2	3087	99.5	586	10 US-09-850-716A-338	Sequence 338, App
3	3087	99.5	586	10 US-09-897-778-338	Sequence 338, App
4	3080	99.2	586	9 US-09-735-705-152	Sequence 152, App
5	3080	99.2	586	10 US-09-850-716A-152	Sequence 152, App
6	3080	99.2	586	10 US-09-897-778-152	Sequence 152, App
7	3080	99.2	586	11 US-09-466-396A-152	Sequence 152, App
8	3029	97.6	641	9 US-09-735-705-339	Sequence 339, App
9	3029	97.6	641	10 US-09-850-716A-339	Sequence 339, App
10	3029	97.6	641	10 US-09-897-778-339	Sequence 339, App
11	3025	97.5	680	9 US-09-735-705-342	Sequence 342, App
12	3025	97.5	680	10 US-09-850-716A-342	Sequence 342, App
13	3025	97.5	680	10 US-09-897-778-342	Sequence 342, App
14	2421	78.0	461	9 US-09-735-705-343	Sequence 343, App
15	2421	78.0	461	10 US-09-850-716A-343	Sequence 343, App

16	2421	78.0	461	10 US-09-897-778-343	Sequence 343, App
17	2350	75.7	516	9 US-09-735-705-344	Sequence 344, App
18	2350	75.7	516	10 US-09-850-716A-344	Sequence 344, App
19	2350	75.7	516	10 US-09-897-778-344	Sequence 344, App
20	1893	61.0	426	15 US-10-274-874-19	Sequence 19, Appl
21	1872	60.3	356	9 US-09-735-705-341	Sequence 341, Appl
22	1872	60.3	356	10 US-09-850-716A-341	Sequence 341, App
23	1872	60.3	356	10 US-09-897-778-341	Sequence 341, App
24	1872	60.3	356	15 US-10-274-874-2	Sequence 2, Appl
25	1813	58.4	448	9 US-09-735-705-340	Sequence 340, App
26	1813	58.4	448	10 US-09-850-716A-340	Sequence 340, App
27	1813	58.4	448	10 US-09-897-778-340	Sequence 340, App
28	1741.5	56.1	635	14 US-10-155-059-3	Sequence 3, Appl
29	1741	56.1	636	10 US-09-732-884-10	Sequence 10, Appl
30	1279.5	41.2	420	15 US-10-274-874-20	Sequence 20, Appl
31	707.5	22.8	393	9 US-09-776-695-32	Sequence 32, Appl
32	707.5	22.8	393	10 US-09-732-384-3	Sequence 3, Appl
33	707.5	22.8	393	10 US-09-860-211-9	Sequence 9, Appl
34	707.5	22.8	393	11 US-09-029-377-4	Sequence 4, Appl
35	707.5	22.8	393	11 US-09-860-286-9	Sequence 9, Appl
36	707.5	22.8	393	15 US-10-274-874-4	Sequence 4, Appl
37	707.5	22.8	393	15 US-10-160-290-2	Sequence 2, Appl
38	707.5	22.8	428	15 US-10-076-691-2	Sequence 2, Appl
39	703.5	22.7	401	10 US-09-968-851-34	Sequence 34, Appl
40	701	22.6	390	15 US-10-038-010-6	Sequence 6, Appl
41	700.5	22.6	353	15 US-10-146-473-78	Sequence 78, Appl
42	698	22.5	390	15 US-10-160-280-3	Sequence 3, Appl
43	694	22.4	394	14 US-10-155-059-4	Sequence 4, Appl
44	692	22.3	381	10 US-09-968-851-36	Sequence 36, Appl
45	679.5	21.9	374	10 US-09-968-851-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-735-705-338
Sequence 338, Application US/09735705
Patent No. US2002052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Lidun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-705-338

Query Match 99.5% Score 3087; DB 9; Length 586;
Best Local Similarity 99.5%; Pred No. 7.9e+248;
Matches 583; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLYENNAQTQFSEQYTNLGLNMDQIQNGSSSTSPYNTDHAQNSVTAPSPAPSS 60
|||||
1 MLYENNAQTQFSEQYTNLGLNMDQIQNGSSSTSPYNTDHAQNSVTAPSPAPSS 60
Db

QY		61	TEDALSPBALPISNTDYGPHSPFDVSPFOOSSSTAKSATMTYSLELKKLYOIAKTCPIOTK	120
Dd		61	TEDALSPBALPISNTDYGPHSPSDVSFPOOSTAKSATMTYSTELKKLYOIAKTCPIOTK	120
QY		121	VMPDPGCAVIRAMPVYKKAHVTEVKRCPNHELSEREFNEGOIAPPSHLIRVEGNSHAQ	180
Dd		121	VMPDPGCAVIRAMPVYKKAHVTEVVKRCPNHELSRENEGOIAPPSHLIRVEGNSSHAQ	180
QY		181	YVEDPITGRSVLVLPYEPPOVGTEFTTYLVYNMCKMSCCVGGNNRRILITVLETBDOGV	240
Dd		181	YVEDPITGRSVLVLPYEPPOVGTEFTTYLVYNMCKMSCSCVGGNNRRILITVLETBDOGV	240
QY		241	LGRRCFEARICACPGDRKADEDISRKOQVSDSTKNGDGTAKPRFRONTHTGIOMTSIKRRR	300
Dd		241	LGRRCFEARICACPGDRKADEDISRKOQVSDSTKNNGDTKRPFQRNTHGIOMTSIKRRR	300
QY		301	SPDEBELLYPVRGRTTYYMLLKIKESLELMOYLPHOTTETTYQOOQQOQHLLQOKOTSIO	360
Dd		301	SPDEBELLYPVRGRTTYYEMLLKIKESLELMOYLPHOTTETTYROOQQOQHLLQOKOTSIO	360
QY		361	SPSSYGNSSPPLNKMSNMNKLIPYSQOLINPOORNALLPTTPDGMGANIPMMGTHPMAG	420
Dd		361	SPSSYGNSSPPLNKMSNMNKLIPYSQOLINPOORNALLPTTPDGMGANIPMMGTHPMAG	420
QY		421	DMNLGLSPTQALPPPLSMBSTSHCTPPPEPYPTDCSIVSFRLARGCSCCLDYFTTGGLTTY	480
Dd		421	DMNLGLSPTQALPPPLSMBSTSHCTPPPEPYPTDCSIVSFRLARGCSCCLDYFTTGGLTTY	480
QY		481	OIEHYSMODLASIKRPEOFRAAIWKGIIIDHRQLHFESSSHLLRPSSASTYSVGSSETR	540
Dd		481	OIEHYSMODLASIKRPEOFRAAIWKGIIIDHRQLHFESSSHLLRPSSASTYSVGSSETR	540
QY		541	GERYIDAVERTLRQTISFPDPDENWFNDMDARRNKQORIKEEGE	586
Dd		541	GERYIDAVERTLRQTISFPDPDENWFNDMDARRNKQORIKEEGE	586
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	US-09-850-716A-338			
	? Sequence 338, Application US/09850716A			
	? Patent No. US2002011539A1			
	? GENERAL INFORMATION:			
	? APPLICANT: Kalos, Michael D.			
	? APPLICANT: McNeill, Patricia D.			
	? APPLICANT: Retter, Marc W.			
	? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
	? FILE REFERENCE: 210121.455C15			
	? CURRENT APPLICATION NUMBER: US/09/850,716A			
	? CURRENT FILING DATE: 2001-05-07			
	? NUMBER OF SEQ ID NOS: 440			
	? SOFTWARE: FastSeq for Windows Version 3.0			
	? SEQ ID NO 338			
	? LENGTH: 586			
	? TYPE: PRF			
	? ORGANISM: Homo sapiens			
	? US-09-850-716A-338			

	Query Match	99.5%	Score 3087;	DB 10;	Length 586;
	Best Local Similarity	99.5%;	Pred. No. 7.9e+248;		
	Matches 583;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	MLYLENNAQOTFESEPOYTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS	60		
Db	1	MLYLENNAQOTFSEPOYTNIGLINSMDQIRNGSSSTSPYNTDHAQNSVTAPSPYAQPS	60		
QY	61	TFDALSPSPATPSTNDYDGPSPFVSPFOGSSPAKATWTYSTELKKLCOIAKTCPIQIX	120		
Db	61	TFDALSPSPATPSTNDYDGPSPSDVSPFOGSSPAKATWTYSTELKKLCOIAKTCPIQIX	120		
QY	121	VMTPPGCAVIRAPPVYKKAHVEVYRCNPHELSREFNegoIAPPSHLIVENGSNAQ	180		
Db	121	VMTPPGCAVIRAPPVYKKAHVEVYRCNPHELSREFNegoIAPPSHLIVENGSNAQ	180		

QY	181	YVBDPLTGOSVLYVPEPQVGTETETVLYNPMCNSSCVGGMNRPLIIVTLETRGOV	240
Db	181	YVBDPLTGOSVLYVPEPQVGTETETVLYNPMCNSSCVGGMNRPLIIVTLETRGOV	240
QY	241	IGRRCPEARICACPGHRRKDAEDSIRKQOVSDBTKNGDGTAKPRPONTHTGIOMTSIKRR	300
Db	241	IGRRCPEARICACPGHRRKDAEDSIRKQOVSDBTKNGDGTAKPRPONTHTGIOMTSIKRR	300
QY	301	SPDDELLIYLVYKGREYEMILKIKSLSLMOYLPHQHTETRYRQOOOQOHHLLQKQTSIO	360
Db	301	SPDDELLIYLVYKGREYEMILKIKSLSLMOYLPHQHTETRYRQOOOQOHHLLQKQTSIO	360
QY	361	SPSSYGNSSPPLNKKNMKNKLPSVSQLINPOORNALPFTTIPDGMGANIPMGCTHMPMAG	420
Db	361	SPSSYGNSSPPLNKKNMKNKLPSVSQLINPOORNALPFTTIPDGMGANIPMGCTHMPMAG	420
QY	421	DMNGSLPTQALPPLPSMPTSHCTPPEPYPTDCSIVSFSLAGCSSCIDLFTTQGLTTIY	480
Db	421	DMNGSLPTQALPPLPSMPTSHCTPPEPYPTDCSIVSFSLAGCSSCIDLFTTQGLTTIY	480
QY	481	QIEHYSMDDLASIKIPEQFRRAIMKGLIDHRQLEHFESSPMLTPSSASTVSYGSETR	540
Db	481	QIEHYSMDDLASIKIPEQFRRAIMKGLIDHRQLEHFESSPMLTPSSASTVSYGSETR	540
QY	541	GEYVIDAVRFTLQRTISPPRPDENMDFNMDADARNKQRIKKEGE	586
Db	541	GEYVIDAVRFTLQRTISPPRPDENMDFNMDADARNKQRIKKEGE	586

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RESULT 3
US-09-897-778-338
Sequence 338. Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Marnetrakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455016
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-338

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Query Match	99.5%	Score 3087	DB 10	Length 586
Best Local Similarity	99.5%	Pred. No. 7.9e-248		
Matches	583	Conservative	1	Mismatches 2
			Indels	0
			Gaps	0
QY	1	MLYLENNAQOTFSEPOYTNLGLNSMDQIONGSSSTSPYNTDHAQNSVTAPSPYAQDSS	60	
Db	1	MLYLENNAQOTFSEQOTNLGLNSMDQIINGSSSTSPYNTDHAQNSVTAPSPAQAQSP	60	
QY	61	TFDALSPSPALPSNTDYPGPHSEFDVSPQOQSTAKSATWYSTEKLKLYLCQIAKTCPIQIK	120	
Db	61	TFDALSPSPALPSNTDYPGPHSSDVSPQOQSTAKSATWYSTEKLKLYLCQIAKTCPIQIK	120	
QY	121	VMTPPPGCAVIRAMPVYKKAHEHYEVYKRCNNHLSREFNQGQIAPSHLIRVEGNSHAQ	180	
Db	121	VMTPPPGCAVIRAMPVYKKAHEHYEVYKRCNNHLSREFNQGQIAPSHLIRVEGNSHAQ	180	

OY 181 YVEDITGRQSVLYVEPPQVGTETFTVLYNFMCMSSCGVGNRRPILIIYVLETRDQV 240
DB 181 YVEDITGRQSVLYVEPPQVGTETFTVLYNFMCMSSCGVGNRRPILIIYVLETRDQV 240
OY 241 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGGTRKPRFQNTHGIOMTSIKKRR 300
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DB 301 SPDDLLVLPVGRGRTYEMLKIKESLEIMOYLPOHTIETRYOQOQOHOHLQKOTSIQ 360
OY 361 SPSSYGNSSPPLNKNMKNKLPVSQILNPOORNALPTTIPDGANIPMGTHMPAG 420
DB 361 SPSSYGNSSPPLNKNMKNKLPVSQILNPOORNALPTTIPDGANIPMGTHMPAG 420
OY 421 DMNGSLPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIIY 480
DB 421 DMNGSLPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIIY 480
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DB 481 QIEHYSMDLASLKIPEQFRHAIWKIGILDHROLHEFSSPSHLLRTPSSASTVSGSSETR 540
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DB 541 GERVIDAVRFTLRQTIISFPPEDEWDFNFDMDARRNKQORIKEGE 586

RESULT 4
US-09-735-705-152
Sequence 152, Application US/09735705
Patent No. US20020052329A1

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-735-705-152

Query Match 99.2%, Score 3080; DB 9; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-247;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MLYLENNNAQTFSEQYTNLGLNSMDQOIONGSSSTSPYNDHAQNSVTAPSPYAQSS 60
DB 1 MLYLENNNAQTFSEQYTNLGLNSMDQOIONGSSSTSPYNDHAQNSVTAPSPYAQSS 60
OY 61 TFDALSPALPNSNDYDGPSPFVSFOOSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPALPNSNDYDGPSPFVSFOOSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
OY 121 VMTPPQGAIVIRAMPVYKKAHEVTEVKRCPNHELISREFNEGOIALPSPHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPVYKKAHEVTEVKRCPNHELISREFNEGOIALPSPHLIRVEGNSHAQ 180

DB 121 VMTPPQGAIVIRAMPVYKKAHEVTEVKRCPNHELISREFNEGOIALPSPHLIRVEGNSHAQ 180
OY 181 YVEDITGRQSVLYVEPPQVGTETFTVLYNFMCMSSCGVGNRRPILIIYVLETRDQV 240
DB 181 YVEDITGRQSVLYVEPPQVGTETFTVLYNFMCMSSCGVGNRRPILIIYVLETRDQV 240
OY 241 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGGTRKPRFQNTHGIOMTSIKKRR 300
DB 241 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGGTRKPRFQNTHGIOMTSIKKRR 300
OY 301 SPDDLLVLPVGRGRTYEMLKIKESLEIMOYLPOHTIETRYOQOQOHOHLQKOTSIQ 360
DB 301 SPDDLLVLPVGRGRTYEMLKIKESLEIMOYLPOHTIETRYOQOQOHOHLQKOTSIQ 360
OY 361 SPSSYGNSSPPLNKNMKNKLPVSQILNPOORNALPTTIPDGANIPMGTHMPAG 420
DB 361 SPSSYGNSSPPLNKNMKNKLPVSQILNPOORNALPTTIPDGANIPMGTHMPAG 420
OY 421 DMNGSLPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIIY 480
DB 421 DMNGSLPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIIY 480
OY 481 QIEHYSMDLASLKIPEQFRHAIWKIGILDHROLHEFSSPSHLLRTPSSASTVSGSSETR 540
DB 481 QIEHYSMDLASLKIPEQFRHAIWKIGILDHROLHEFSSPSHLLRTPSSASTVSGSSETR 540
OY 541 GERVIDAVRFTLRQTIISFPPEDEWDFNFDMDARRNKQORIKEGE 586
DB 541 GERVIDAVRFTLRQTIISFPPEDEWDFNFDMDARRNKQORIKEGE 586

RESULT 5
US-09-850-716A-152
Sequence 152, Application US/09850716A
Patent No. US20020115139A1

GENERAL INFORMATION:

APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-850-716A-152

Query Match 99.2%, Score 3080; DB 10; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-247;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MLYLENNNAQTFSEQYTNLGLNSMDQOIONGSSSTSPYNDHAQNSVTAPSPYAQSS 60
DB 1 MLYLENNNAQTFSEQYTNLGLNSMDQOIONGSSSTSPYNDHAQNSVTAPSPYAQSS 60
OY 61 TFDALSPALPNSNDYDGPSPFVSFOOSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPALPNSNDYDGPSPFVSFOOSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
OY 121 VMTPPQGAIVIRAMPVYKKAHEVTEVKRCPNHELISREFNEGOIALPSPHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPVYKKAHEVTEVKRCPNHELISREFNEGOIALPSPHLIRVEGNSHAQ 180
OY 181 YVEDITGRQSVLYVEPPQVGTETFTVLYNFMCMSSCGVGNRRPILIIYVLETRDQV 240
DB 181 YVEDITGRQSVLYVEPPQVGTETFTVLYNFMCMSSCGVGNRRPILIIYVLETRDQV 240
OY 241 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGGTRKPRFQNTHGIOMTSIKKRR 300
DB 241 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGGTRKPRFQNTHGIOMTSIKKRR 300


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Db 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFONTGIGIOMTSIKRR 300
QY 301 SPDELLYLTVRGRREYEMMLKIKESLELMQYLPORHTIETYROOOOHOHLQOKOTSIO 360
Db 301 SPDELLYLTVRGRREYEMMLKIKESLELMQYLPORHTIETYROOOOHOHLQOKOTSIO 360
QY 361 SPSSYGNSSPPLKMKMSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKMKMSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSFTQALPPLSPMSTSHCTPPPPYPTDCSIVSFLARLCCSCLDFTTQGLTTIY 480
Db 421 DMNGLSFTQALPPLSPMSTSHCTPPPPYPTDCSIVSFLARLCCSCLDFTTQGLTTIY 480
QY 481 QIEHYSMDDLASLKIPQGFHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSVSSETR 540
Db 481 QIEHYSMDDLASLKIPQGFHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSVSSETR 540
QY 541 GERVIDAVRFTLRQTISFPPEDEMDNFDMDARRNKQORIKEGE 586
Db 541 GERVIDAVRFTLRQTISFPPEDEMDNFDMDARRNKQORIKEGE 586
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RESULT 6
US-09-897-778-152
; Sequence 152, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marinakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-897-778-152
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Query Match 99.2%; Score 3080; DB 10; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-247;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNAOQFSEPOYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSS 60
Db 1 MYLENNAOQFSEPOYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSS 60
QY 61 TFDALSPSPAIPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
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QY 121 VMTPPQGAIVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVGNASHAQ 180
Db 121 VMTPPQGAIVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVGNASHAQ 180
QY 181 YVEDPITGROSIVLVEPPPOVTEFTTVLYNFMCNSSCVGAMNRRPLIIVTLETRDGOV 240
Db 181 YVEDPITGROSIVLVEPPPOVTEFTTVLYNFMCNSSCVGAMNRRPLIIVTLETRDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFONTGIGIOMTSIKRR 300
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Db 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFONTGIGIOMTSIKRR 300
QY 301 SPDELLYLTVRGRREYEMMLKIKESLELMQYLPORHTIETYROOOOHOHLQOKOTSIO 360
Db 301 SPDELLYLTVRGRREYEMMLKIKESLELMQYLPORHTIETYROOOOHOHLQOKOTSIO 360
QY 361 SPSSYGNSSPPLKMKMSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKMKMSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSFTQALPPLSPMSTSHCTPPPPYPTDCSIVSFLARLCCSCLDFTTQGLTTIY 480
Db 421 DMNGLSFTQALPPLSPMSTSHCTPPPPYPTDCSIVSFLARLCCSCLDFTTQGLTTIY 480
QY 481 QIEHYSMDDLASLKIPQGFHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSVSSETR 540
Db 481 QIEHYSMDDLASLKIPQGFHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSVSSETR 540
QY 541 GERVIDAVRFTLRQTISFPPEDEMDNFDMDARRNKQORIKEGE 586
Db 541 GERVIDAVRFTLRQTISFPPEDEMDNFDMDARRNKQORIKEGE 586
```

```
RESULT 7
US-09-466-396A-152
; Sequence 152, Application US/09466396A
; Publication No. US20030119763A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.455C4
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRF
; ORGANISM: Homo sapien
US-09-466-396A-152
```

```
Query Match 99.2%; Score 3080; DB 11; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-247;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNAOQFSEPOYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSS 60
Db 1 MYLENNAOQFSEPOYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSS 60
QY 61 TFDALSPSPAIPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVGNASHAQ 180
Db 121 VMTPPQGAIVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVGNASHAQ 180
QY 181 YVEDPITGROSIVLVEPPPOVTEFTTVLYNFMCNSSCVGAMNRRPLIIVTLETRDGOV 240
Db 181 YVEDPITGROSIVLVEPPPOVTEFTTVLYNFMCNSSCVGAMNRRPLIIVTLETRDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFONTGIGIOMTSIKRR 300
Db 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFONTGIGIOMTSIKRR 300
QY 301 SPDELLYLTVRGRREYEMMLKIKESLELMQYLPORHTIETYROOOOHOHLQOKOTSIO 360
Db 301 SPDELLYLTVRGRREYEMMLKIKESLELMQYLPORHTIETYROOOOHOHLQOKOTSIO 360
QY 361 SPSSYGNSSPPLKMKMSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKMKMSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
```


QY 421 DMNGISPTQALPPPLSMSTSHCTPPPYPTDCSIVSEFLARLGSCSSCLDYFTTQGLITTY 480
DB 421 DMNGISPTQALPPPLSMSTSHCTPPPYPTDCSIVSEFLARLGSCSSCLDYFTTQGLITTY 480
QY 481 QIEHYSMDLASLKIPEQFRHAIWKGLDHRQLEHSSPSHLRTPSSASTVSVGSSETR 540
DB 481 QIEHYSMDLASLKIPEQFRHAIWKGLDHRQLEHSSPSHLRTPSSASTVSVGSSETR 540
QY 541 GERVIDAVFTLRQITISFPFRDEMFNDMDARNRKQORIKEGE 586
DB 541 GERVIDAVFTLRQITISFPFRDEMFNDMDARNRKQORIKEGE 586

RESULT 8
US-09-735-705-339
; Sequence 339, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Jasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-339

Query Match 97.6%; Score 3029; DB 9; Length 641;
Best Local Similarity 99.8%; Pred. No. 5.9e-243;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PQTMLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYQAPSTFDALSPSPAIRSN 74
DB 70 PQTMLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYQAPSTFDALSPSPAIRSN 129
QY 75 TDYPCPHSFVDSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 134
DB 130 TDYPCPHSFVDSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 189
QY 135 PYKKAHEVTEVVKCPNHELRENEGQIAPPSHLIRVEGNSHAQYVEDPTTGQSVLY 194
DB 190 PYKKAHEVTEVVKCPNHELRENEGQIAPPSHLIRVEGNSHAQYVEDPTTGQSVLY 249
QY 195 PYEPQVGTETFTVLYNFMCNSSCGVGNRRRILITVLETRDQVGLRCEARICACP 254
DB 250 PYEPQVGTETFTVLYNFMCNSSCGVGNRRRILITVLETRDQVGLRCEARICACP 309
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIKRRSPDDELTYLPVGR 314
DB 310 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIKRRSPDDELTYLPVGR 369
QY 315 EYEMLLIKESLELMQYLPQHTTETIROQOQOQHLLQKOTSIOSSSVGNSSPPLNK 374
DB 370 EYEMLLIKESLELMQYLPQHTTETIROQOQOQHLLQKOTSIOSSSVGNSSPPLNK 429
QY 375 MNSMNLKPSVSQLINPQQRNALPTTIPDGMGANIPMGTHMPMAGDMNGISPTQALPPP 434

DB 430 MNSMNLKPSVSQLINPQQRNALPTTIPDGMGANIPMGTHMPMAGDMNGISPTQALPPP 489
QY 435 LSMSTSHCTPPPPPTDCSIVSEFLARLGSCSSCLDYFTTQGLITTYQIEHYSMDLASL 494
DB 490 LSMSTSHCTPPPPPTDCSIVSEFLARLGSCSSCLDYFTTQGLITTYQIEHYSMDLASL 549
QY 495 IPEQFRHAIWKGLDHRQLEHSSPSHLRTPSSASTVSVGSSETRGERVIDAVFTLRQ 554
DB 550 IPEQFRHAIWKGLDHRQLEHSSPSHLRTPSSASTVSVGSSETRGERVIDAVFTLRQ 609
QY 555 TISFPFRDEMFNDMDARNRKQORIKEGE 586
DB 610 TISFPFRDEMFNDMDARNRKQORIKEGE 641

RESULT 9
US-09-850-716A-339
; Sequence 339, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-339

Query Match 97.6%; Score 3029; DB 10; Length 641;
Best Local Similarity 99.8%; Pred. No. 5.9e-243;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PQTMLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYQAPSTFDALSPSPAIRSN 74
DB 70 PQTMLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYQAPSTFDALSPSPAIRSN 129
QY 75 TDYPCPHSFVDSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 134
DB 130 TDYPCPHSFVDSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 189
QY 135 PYKKAHEVTEVVKCPNHELRENEGQIAPPSHLIRVEGNSHAQYVEDPTTGQSVLY 194
DB 190 PYKKAHEVTEVVKCPNHELRENEGQIAPPSHLIRVEGNSHAQYVEDPTTGQSVLY 249
QY 195 PYEPQVGTETFTVLYNFMCNSSCGVGNRRRILITVLETRDQVGLRCEARICACP 254
DB 250 PYEPQVGTETFTVLYNFMCNSSCGVGNRRRILITVLETRDQVGLRCEARICACP 309
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIKRRSPDDELTYLPVGR 314
DB 310 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIKRRSPDDELTYLPVGR 369
QY 315 EYEMLLIKESLELMQYLPQHTTETIROQOQOQHLLQKOTSIOSSSVGNSSPPLNK 374
DB 370 EYEMLLIKESLELMQYLPQHTTETIROQOQOQHLLQKOTSIOSSSVGNSSPPLNK 429
QY 375 MNSMNLKPSVSQLINPQQRNALPTTIPDGMGANIPMGTHMPMAGDMNGISPTQALPPP 434
DB 430 MNSMNLKPSVSQLINPQQRNALPTTIPDGMGANIPMGTHMPMAGDMNGISPTQALPPP 489
QY 435 LSMSTSHCTPPPPPTDCSIVSEFLARLGSCSSCLDYFTTQGLITTYQIEHYSMDLASL 494
DB 490 LSMSTSHCTPPPPPTDCSIVSEFLARLGSCSSCLDYFTTQGLITTYQIEHYSMDLASL 549

QY 495 IPEOFRAIAIKGILDHQOLHEFSSPSHLRTPSSASTVSVGSSSETRGERVIDAVRFLRQ 554
| | | | |
Db 550 IPEOFRAIAIKGILDHQOLHEFSSPSHLRTPSSASTVSVGSSSETRGERVIDAVRFLRQ 609
| | | | |
QY 555 TISPPRDEWNDFNFDMDARRNKQOARIKEGE 586
| | | | |
Db 610 TISPPRDEWNDFNFDMDARRNKQOARIKEGE 641
| | | | |

RESULT 10

US-09-897-778-339
; Sequence 339, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-339

Query Match 97.6%; Score 3029; DB 10; Length 641;
Best Local Similarity 99.8%; Pred. No. 5.9e-243;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PÖYTNGLILMSMOQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPSPALPSN 74
| | | | |
Db 70 PÖYTNGLILMSMOQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPSPALPSN 129
| | | | |
QY 75 TDVPGHSPFVSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQGAIVRAM 134
| | | | |
Db 130 TDVPGHSPFVSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQGAIVRAM 189
| | | | |
QY 135 PYVKAHAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
| | | | |
Db 190 PYVKAHAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
| | | | |
QY 195 PYEPPOVGTETFTVLYNFMKNSSCVGGMNRPLIITYLTETRGQVILGRCFEARIACAP 254
| | | | |
Db 250 PYEPPOVGTETFTVLYNFMKNSSCVGGMNRPLIITYLTETRGQVILGRCFEARIACAP 309
| | | | |
QY 255 GDRKKADEDSIRKQOVSSTKNGDGTKRPRÖNTHGIÖMTSIRKRRSPDDELLYLPRGR 314
| | | | |
Db 310 GDRKKADEDSIRKQOVSSTKNGDGTKRPRÖNTHGIÖMTSIRKRRSPDDELLYLPRGR 369
| | | | |
QY 315 EYTEMILKIKESLELMQYLPOHTIETVYRQOQOQOHOHLQÖTSIQSPSSYGNSPPLNK 374
| | | | |
Db 370 EYTEMILKIKESLELMQYLPOHTIETVYRQOQOQOHOHLQÖTSIQSPSSYGNSPPLNK 429
| | | | |
QY 375 MNSMNLKIPSVÖSÖLINPÖQRNALPTPTIPDGMGANIPMGTHMPMAGDMNGLSPTÖALPP 434
| | | | |
Db 430 MNSMNLKIPSVÖSÖLINPÖQRNALPTPTIPDGMGANIPMGTHMPMAGDMNGLSPTÖALPP 489
| | | | |
QY 435 LSMPSHCTPPPPYPIDCSIVSFARLGGSSCLDFTTÖGLTTIYÖIEHYSMDDLASLK 494
| | | | |
Db 490 LSMPSHCTPPPPYPIDCSIVSFARLGGSSCLDFTTÖGLTTIYÖIEHYSMDDLASLK 549
| | | | |
QY 495 IPEOFRAIAIKGILDHQOLHEFSSPSHLRTPSSASTVSVGSSSETRGERVIDAVRFLRQ 554
| | | | |

Db 550 IPEOFRAIAIKGILDHQOLHEFSSPSHLRTPSSASTVSVGSSSETRGERVIDAVRFLRQ 609
| | | | |
QY 555 TISPPRDEWNDFNFDMDARRNKQOARIKEGE 586
| | | | |
Db 610 TISPPRDEWNDFNFDMDARRNKQOARIKEGE 641
| | | | |

RESULT 11

US-09-735-705-342
; Sequence 342, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Lijun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-342

Query Match 97.5%; Score 3025; DB 9; Length 680;
Best Local Similarity 99.8%; Pred. No. 1.4e-242;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PÖYTNGLILMSMOQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPSPALPSN 74
| | | | |
Db 109 PÖYTNGLILMSMOQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPSPALPSN 168
| | | | |
QY 75 TDVPGHSPFVSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQGAIVRAM 134
| | | | |
Db 169 TDVPGHSPFVSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQGAIVRAM 228
| | | | |
QY 135 PYVKAHAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
| | | | |
Db 229 PYVKAHAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 288
| | | | |
QY 195 PYEPPOVGTETFTVLYNFMKNSSCVGGMNRPLIITYLTETRGQVILGRCFEARIACAP 254
| | | | |
Db 289 PYEPPOVGTETFTVLYNFMKNSSCVGGMNRPLIITYLTETRGQVILGRCFEARIACAP 348
| | | | |
QY 255 GDRKKADEDSIRKQOVSSTKNGDGTKRPRÖNTHGIÖMTSIRKRRSPDDELLYLPRGR 314
| | | | |
Db 349 GDRKKADEDSIRKQOVSSTKNGDGTKRPRÖNTHGIÖMTSIRKRRSPDDELLYLPRGR 408
| | | | |
QY 315 EYTEMILKIKESLELMQYLPOHTIETVYRQOQOQOHOHLQÖTSIQSPSSYGNSPPLNK 374
| | | | |
Db 409 EYTEMILKIKESLELMQYLPOHTIETVYRQOQOQOHOHLQÖTSIQSPSSYGNSPPLNK 468
| | | | |
QY 375 MNSMNLKIPSVÖSÖLINPÖQRNALPTPTIPDGMGANIPMGTHMPMAGDMNGLSPTÖALPP 434
| | | | |
Db 469 MNSMNLKIPSVÖSÖLINPÖQRNALPTPTIPDGMGANIPMGTHMPMAGDMNGLSPTÖALPP 528
| | | | |
QY 435 LSMPSHCTPPPPYPIDCSIVSFARLGGSSCLDFTTÖGLTTIYÖIEHYSMDDLASLK 494
| | | | |
Db 529 LSMPSHCTPPPPYPIDCSIVSFARLGGSSCLDFTTÖGLTTIYÖIEHYSMDDLASLK 588
| | | | |

495 IPEQFRAHAIWKIGILDHROLHEFFSSPHLLRTPSSASTVSGSSETRGERVIDAVFTLRQ 554
|||||
589 IPEQFRAHAIWKIGILDHROLHEFFSSPHLLRTPSSASTVSGSSETRGERVIDAVFTLRQ 648
|||
555 TISFPPRDEWMDNFMDARRNKQORIKEGE 586
|||||
649 TISFPPRDEWMDNFMDARRNKQORIKEGE 680
|||

RESULT 12
US-09-850-716A-342
; Sequence 342, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Reiter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-342

Query Match 97.5%; Score 3025; DB 10; Length 680;
Best Local Similarity 99.8%; Pred No. 1.4e-242;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPALPSN 74
|||||
DB 109 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPALPSN 168
|||||
QY 75 TDYBGRPHSDVFSFOOSSTAKSATWTYSTEKLKLYCOIAKTCIOIKWTPPPQGAIVIRAM 134
|||||
DB 169 TDYBGRPHSDVFSFOOSSTAKSATWTYSTEKLKLYCOIAKTCIOIKWTPPPQGAIVIRAM 228
|||||
QY 135 PYKKAHEHTEYVKRCPNHELREPNEGQIAPPSHILIREGNSHQAQYEDPTTGQSVLV 194
|||||
DB 229 PYKKAHEHTEYVKRCPNHELREPNEGQIAPPSHILIREGNSHQAQYEDPTTGQSVLV 288
|||||
QY 195 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRLIIVTLETTRDGOVLGRCPPEARICACP 254
|||||
DB 289 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRLIIVTLETTRDGOVLGRCPPEARICACP 348
|||||
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGIGIOMTSIKKRRSPDDELLYLPVGR 314
|||||
DB 349 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGIGIOMTSIKKRRSPDDELLYLPVGR 408
|||||
QY 315 EYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSSPSYGNSSPPLNK 374
|||||
DB 409 EYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSSPSYGNSSPPLNK 468
|||||
QY 375 MNSMNLKPSVSOLINPQORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
|||||
DB 469 MNSMNLKPSVSOLINPQORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 528
|||||
QY 435 LSMPSHCTPPPPPTDCSIVSFLARIGCSSCLDYFTTQGLTTIYQIEHYSMDLASIK 494
|||||
DB 529 LSMPSHCTPPPPPTDCSIVSFLARIGCSSCLDYFTTQGLTTIYQIEHYSMDLASIK 588
|||||
QY 495 IPEQFRAHAIWKIGILDHROLHEFFSSPHLLRTPSSASTVSGSSETRGERVIDAVFTLRQ 554
|||||
DB 589 IPEQFRAHAIWKIGILDHROLHEFFSSPHLLRTPSSASTVSGSSETRGERVIDAVFTLRQ 648
|||||
QY 555 TISFPPRDEWMDNFMDARRNKQORIKEGE 586
|||||

DB 649 TISFPPRDEWMDNFMDARRNKQORIKEGE 680
|||

RESULT 13
US-09-897-778-342
; Sequence 342, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Mainerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-342

Query Match 97.5%; Score 3025; DB 10; Length 680;
Best Local Similarity 99.8%; Pred No. 1.4e-242;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPALPSN 74
|||||
DB 109 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPALPSN 168
|||||
QY 75 TDYBGRPHSDVFSFOOSSTAKSATWTYSTEKLKLYCOIAKTCIOIKWTPPPQGAIVIRAM 134
|||||
DB 169 TDYBGRPHSDVFSFOOSSTAKSATWTYSTEKLKLYCOIAKTCIOIKWTPPPQGAIVIRAM 228
|||||
QY 135 PYKKAHEHTEYVKRCPNHELREPNEGQIAPPSHILIREGNSHQAQYEDPTTGQSVLV 194
|||||
DB 229 PYKKAHEHTEYVKRCPNHELREPNEGQIAPPSHILIREGNSHQAQYEDPTTGQSVLV 288
|||||
QY 195 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRLIIVTLETTRDGOVLGRCPPEARICACP 254
|||||
DB 289 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRLIIVTLETTRDGOVLGRCPPEARICACP 348
|||||
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGIGIOMTSIKKRRSPDDELLYLPVGR 314
|||||
DB 349 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGIGIOMTSIKKRRSPDDELLYLPVGR 408
|||||
QY 315 EYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSSPSYGNSSPPLNK 374
|||||
DB 409 EYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSSPSYGNSSPPLNK 468
|||||
QY 375 MNSMNLKPSVSOLINPQORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
|||||
DB 469 MNSMNLKPSVSOLINPQORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 528
|||||
QY 435 LSMPSHCTPPPPPTDCSIVSFLARIGCSSCLDYFTTQGLTTIYQIEHYSMDLASIK 494
|||||
DB 529 LSMPSHCTPPPPPTDCSIVSFLARIGCSSCLDYFTTQGLTTIYQIEHYSMDLASIK 588
|||||
QY 495 IPEQFRAHAIWKIGILDHROLHEFFSSPHLLRTPSSASTVSGSSETRGERVIDAVFTLRQ 554
|||||
DB 589 IPEQFRAHAIWKIGILDHROLHEFFSSPHLLRTPSSASTVSGSSETRGERVIDAVFTLRQ 648
|||||
QY 555 TISFPPRDEWMDNFMDARRNKQORIKEGE 586
|||||
DB 649 TISFPPRDEWMDNFMDARRNKQORIKEGE 680
|||||

```

RESULT 14
US-09-735-705-343
; Sequence 343, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-343

```

```

Query Match      78.0%; Score 2421; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.1e-192;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQOFSEPOYTNTGLNSMDQOIONGSSSTPYNTDHAQNSVTAAPSPYAPSS 60
DB 1 MLYENNAQOFSEPOYTNTGLNSMDQOIONGSSSTPYNTDHAQNSVTAAPSPYAPSS 60
QY 61 TFDALSPSPAIPSNTDYPGPHSFDVSPFOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNTDYPGPHSFDVSPFOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPEPGAVIRAMPYKKAHEVTEYVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPEPGAVIRAMPYKKAHEVTEYVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILLIVTLETBDGY 240
DB 181 YVEDPITGRQSVLPYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILLIVTLETBDGY 240
QY 241 LGRRCFEARICACPGDRKADDEDSIRKQOYSDSTKNGDGTKRPFRONTGHIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKADDEDSIRKQOYSDSTKNGDGTKRPFRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPRGRREYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIO 360
DB 301 SPDELLYLPRGRREYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLKNKMSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLKNKMSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456

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RESULT 15
US-09-850-716A-343
; Sequence 343, Application US/09850716A
; Patent No. US20020115139A1

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; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-343

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```

Query Match      78.0%; Score 2421; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.1e-192;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQOFSEPOYTNTGLNSMDQOIONGSSSTPYNTDHAQNSVTAAPSPYAPSS 60
DB 1 MLYENNAQOFSEPOYTNTGLNSMDQOIONGSSSTPYNTDHAQNSVTAAPSPYAPSS 60
QY 61 TFDALSPSPAIPSNTDYPGPHSFDVSPFOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNTDYPGPHSFDVSPFOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPEPGAVIRAMPYKKAHEVTEYVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPEPGAVIRAMPYKKAHEVTEYVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILLIVTLETBDGY 240
DB 181 YVEDPITGRQSVLPYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILLIVTLETBDGY 240
QY 241 LGRRCFEARICACPGDRKADDEDSIRKQOYSDSTKNGDGTKRPFRONTGHIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKADDEDSIRKQOYSDSTKNGDGTKRPFRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPRGRREYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIO 360
DB 301 SPDELLYLPRGRREYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLKNKMSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLKNKMSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456

```

Search completed: August 7, 2003, 09:57:09
Job time : 26.0181 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:03 ; Search time 18.4749 Seconds
(without alignments)
3050.350 Million cell updates/sec

Title: US-09-538-106-16

Perfect score: 3104

Sequence: 1 MLYLENNAQGFSEPOYTNL.....FNFDMDARRNKQRIKERGE 586

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_76:*
2: pir1:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	839.5	27.0	396	1 JH0631	cellular tumor ant
2	762	24.5	363	1 A29376	cellular tumor ant
3	758.5	24.4	367	1 S02193	cellular tumor ant
4	744	24.0	386	1 S51648	cellular tumor ant
5	723	23.3	391	1 S02192	cellular tumor ant
6	712	22.9	396	1 JH0633	cellular tumor ant
7	707.5	22.8	393	1 DNH053	cellular tumor ant
8	703	22.6	393	1 S06594	cellular tumor ant
9	702	22.6	390	1 DNMS33	cellular tumor ant
10	700	22.6	391	1 J06193	tumor suppressor p
11	697.5	22.5	393	2 J06176	tumor suppressor p
12	688.5	22.2	381	2 S38824	cellular tumor ant
13	259.5	8.4	77	2 T19626	cellular tumor ant
14	152.5	4.9	925	2 T19361	hypothetical prote
15	134.5	4.3	901	2 J06093	dead finger nuclea
16	133	4.3	1081	2 S66736	transcription acti
17	133	4.3	1520	1 TVEFA	protein-tyrosine k
18	132.5	4.2	2578	2 A56922	transcription fact
19	130.5	4.2	2529	2 A56923	transcription fact
20	129	4.2	963	2 T40290	hypothetical prote
21	129	4.2	964	2 T41547	hypothetical prote
22	129	4.2	1051	2 G59436	KIAA1304 protein l
23	129	4.2	1621	2 T15264	hypothetical prote
24	128.5	4.1	628	2 S19150	hypothetical prote
25	126.5	4.1	628	2 J00110	hypothetical 69k p
26	126	4.1	2897	2 B48666	cell proliferation
27	126	4.1	3256	2 A48666	hypothetical prote
28	125.5	4.0	628	2 S01955	hypothetical prote
29	125	4.0	724	2 T47149	hypothetical prote

30	124.5	4.0	533	2 J50304	developmental cont
31	124.5	4.0	811	2 J07619	hypoxia-inducible
32	124.5	4.0	864	2 H85335	hypothetical prote
33	124.5	4.0	864	2 T04518	hypothetical prote
34	124.5	4.0	1572	2 S45251	SNF2alpha protein
35	124	4.0	590	2 A44068	cell pattern forma
36	124	4.0	826	2 I38972	hypoxia-inducible
37	123.5	4.0	862	2 B53689	homeotic protein C
38	123.5	4.0	921	2 A48184	transcription init
39	123.5	4.0	921	2 A45183	TBP-associated fac
40	123	4.0	969	2 T15446	hypothetical prote
41	123	4.0	1145	2 T18235	transcription acti
42	123	4.0	2232	2 T34434	hypothetical prote
43	123	4.0	3942	2 T42730	Bassoon protein -
44	122.5	3.9	1221	2 T23472	hypothetical prote
45	122.5	3.9	1366	2 B86292	FH2.12 protein -

ALIGNMENTS

RESULT 1

JH0631
cellular tumor antigen p53 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0631
R:de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A:Reference number: JH0631; MUID:92210006; PMID:1339362
A:Accession: JH0631
A:Molecule type: mRNA
A:Residues: 1-396 <DEF>
A:Cross-references: GB:M75145; NID:9213828; PIDN:AAA49605.1; PID:9213829
A:Experimental source: liver
A:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactiv
C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; nucleus; pho
F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match	27.0%	Score 839.5	DB 1	Length 396
Best Local Similarity	55.2%	Pred No. 8e-51		
Matches 169	Conservative 47	Mismatches 79	Indels 11	Gaps 6
QY	49	VTAPSPYAQPS-STFDALS-DSPAIPSNVDYGPSPVSVFOQSSSTAKSATWTYTELKK	106	
DB	61	VSATEPAPQPSISTLDTSPTSTVPTSDYFGALGFLRFQSSSTAKSVCTYSPDLNK	120	
QY	107	LYCOIAKTCPIQIKMTPPPGCAVIRAMPYKKAHYTEVVKRCPNHLSREFNQIAP	166	
DB	121	LECOIAKTCPIQIVVDHPPEGAVALAIKKISDVADVVRCHHSTSSNNNGP-AP	179	
QY	167	PSHLIRVSGNSHAQYEDPITGROSIVLVPYEPQVETFTVLVYFMKNSSCVGGMNRRP	226	
DB	180	RCHLVRVSGNRSSEMEDNGNLTNRHSLVLYPYEPQVGSCTIVLYFMKNSSCGMGNRRP	239	
QY	227	ILIVLTETRDGQVIGRCFARICACPGRRKADEDSIRKQO---VSDTKNGDGTTRP	283	
DB	240	ILITLTETRGQVILGRRCFARICACPGRRKADEDSIRKQOETTLTKRPAQGIKRA	299	
QY	284	FRQ-NTHGIQMTSIRKRS---PDDELLYLPVGRRETYEMLKKESELMOYLPQITI	338	
DB	300	MKEASLPAPQPGASKRKTKSSPAVSDELYTLQIRKEKEYEMLKFNDSLELSELPVADA	359	
QY	339	ETVROQ 344		
DB	360	DKYRQK 365		

RESULT 2

529376

RESULT 2

A29376


```

Db      239 NMRRRLIITLEDSCGNLGRNSEFEVRCACPGDRRTREENLRKKGSCEPPRSTK 298
      282 REFRRONTGICQMTSIKRRSP-DDELLLPVGRRETYEMLKIKESLEMLQIPIQTIIT 340
      299 RALPTNT-----SSSPQPKRPLDGEYFTLQINGFRKYEFRLELDALDEL-----KDALDG 349
Qy      341 YRQOQOQOQH-OHLQKOTSIQSSSYGNSSPPLNK 374
      350 REPGRSRAHSHSLKSK-----KRPSCHKKPKMLKR 380

RESULT 5
502192
cellular tumor antigen p53 - rat
N:Alternate names: gene p53 protein; nuclear oncoprotein p53
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02192; S41149
R:Sousai, T.; de Fromental, C.C.; Breugnot, C.; May, E.
Nucleic Acids Res. 16, 11384, 1988
A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A:Reference number: S02192; MUID:89083585; PMID:3060862
A:Accession: S02192
A:Molecule type: mRNA
A:Residues: 1-391 <SOU>
A:Cross-references: EMBL:X13058; NID:g56828; PIDN:CAA31457.1; PID:g56829
R:Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A:Title: Structure of the rat p53 tumor suppressor gene.
A:Reference number: S41149; MUID:93181268; PMID:8441680
A:Accession: S41149
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173, 'W', 175-391 <HUL>
A:Cross-references: EMBL:U07909
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:
A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho;
P:174,177,226,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match      23.3%; Score 723; DB 1; Length 391;
Best Local Similarity 41.1%; Pred. No. 9.8e-43;
Matches 158; Conservative 64; Mismatches 116; Indels 46; Gaps 9;

Qy      18 TNLGLNSMDQ-----QIONGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPS 68
      35 TATGSPNSMEDLFLPDVAELLEGPEALQVSAPAAQEPGTEAPAPVAPASATPWLSSS 94
      69 PAIPNTDYPGPHSDVFOQOSTAKSATWTYSTELKILYCOIATCPQIQTVMPPPOG 128
      95 --VPSQKTYQNGYGHFLQSGTAKSVCTYSISLNLKFLCOLACTCPVOLWVSTPPG 152
      129 AVIRAMPYKKAHEHYEVVRCQPNHELREFNEGQ-IPPSHLIRVEGSHAOYVEDPIT 187
      153 TVRRMAITYKKSQHMTVEVVRKCPNHE---KCSDGGLAPQHLIRVEGPAVEYIDDRQT 209
      188 GRSVLVPEPPQVGEFTTVLYNFMNCSSCGVGNRRPILITVLETRDGOVLGRGFE 247
      210 FRHSVYVPEPPVGSVDYTIHYKWCSSCGGNRRPILITVLEDSGGLGRDSFE 269
      248 ARICACPRDKRADDSIRKQVSDSTKNGDGTAKPFRONTNGIOMTSIKRRSP-DDEL 306
      270 VAVCACPRDRRTREENRKRKEHCPELPSPSAKALPTST-----SSSPQKKKPLDGEY 325
      307 LYLPRGSEYEMLKIKESLEMLQYLPHQTIETVYRQOQOQHLLQKQTSIOSPSSYG 366
      326 FTLKRGREEREMPELWALELK-----DARAAESGSDRA 362
      367 NSSPLINK--MNSMKLPSVSQ 387

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```

Db      363 HSSYPKTKGQSTSRHKKPMIKKY 386

RESULT 6
JH0633
cellular tumor antigen p53 - golden hamster
N:Alternate names: tumor-suppressor protein p53
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0633
R:Legros, Y.; McIntyre, P.; Sousai, T.
Gene 112, 247-250, 1992
A:Title: The cDNA cloning and immunological characterization of hamster p53.
A:Reference number: JH0633; MUID:92210007; PMID:1555773
A:Accession: JH0633
A:Molecule type: mRNA
A:Residues: 1-396 <LEG>
A:Cross-references: GB:M75144; NID:g191414; PIDN:AAA37085.1; PID:g191415
A:Experimental source: kidney, strain MP1
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
P:179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match      22.9%; Score 712; DB 1; Length 396;
Best Local Similarity 44.8%; Pred. No. 5.8e-42;
Matches 147; Conservative 53; Mismatches 110; Indels 18; Gaps 5;

Qy      2 IYLENNAQTFSEPDYTNLGLNSMDQOQNGSSSTSPYNTDHAQNSVTAPSPYAQPSST 61
      44 LFLSENV-----AGMLEDEGEALQSGAAAAPAAAEPPVATPAPVASAPRT 92
      62 FDALSPPAIPSNVDYPCGPHSDVFSFOOSTAKSATWTYSTELKILYCOIATCPQIQT 121
      93 PMPWLSSS--VPSYKTYQGDYGRFLGFLHSGTAKSVCTYSPSLNKLFCOLAKTCPVQLWV 150
      122 MPPPOGAVIRAMPYKKAHEHYEVVRCQPNHELREFNEGQIAPPSHLIRVEGSHAOY 181
      151 SSTPPGTVRRMAITYKILQYMTVEVVRCPNHERSE-GDG-LAPQHLIRVEGNMHAHY 208
      182 VEDPITGRSVLYPEPPQVGEFTTVLYNFMNCSSCGVGNRRPILITVLETRDGOVL 241
      209 LDDKQTFRHSVYVPEPPVGSDDCTTIHKNYCNSSCGGNRRPILITVLEDSGNL 268
      242 GRCEFEARICACPGDRKADSDSIRKQVSDSTKNGDGTAKPFRONTNGIOMTSIKRRS 301
      269 GRNSEFVRICACPGDRRTREKNFQKKGPCPELPKSAKRALPTNT---SSSPQPKRKT 325
      302 PDDELLLPVGRRETYEMLKIKESLEL 329
      326 LDGEYFTLKIRQERFKMFQELWALEL 353
      367 NSSPLINK--MNSMKLPSVSQ 387

RESULT 7
DNH053
cellular tumor antigen p53 [validated] - human
N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppr
C:Species: Homo sapiens (man)
C>Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C:Accession: A25224; A43073; J04036; S40773; S42669; A22837; A50600; A25397; B25397;
4905; I58354; I78850; I52681; S60153
R:Lamb, P.; Crawford, L.
Mol. Cell. Biol. 6, 1379-1385, 1986
A:Title: Characterization of the human p53 gene.
A:Reference number: A25224; MUID:87064416; PMID:2946935
A:Accession: A25224
A:Molecule type: DNA
A:Residues: 1-393 <LAM>
A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1;
R:Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.

```


Gene 70, 245-252, 1988
A:Title: A variation in the structure of the protein-coding region of the human p53 gene
A:Reference number: J0436; MUID:89108008; PMID:2905688
A:Accession: A43073
A:Molecule type: DNA
A:Residues: 1-393 <BUCl>
A:Cross-references: EMBL:M22898; NID:9189474
A:Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro allele
A:Accession: J0436
A:Molecule type: DNA
A:Residues: 1-71, 'P', 73-393 <BUc2>
A:Cross-references: EMBL:M22898; NID:9189474; PIDN:AAA59988.1; PID:9189476
A:Note: this 72-Pro allele was found in both normal and malignant cell lines
R:Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.
submitted to the EMBL Data Library, August 1990
A:Reference number: S40773
A:Accession: S40773
A:Molecule type: DNA
A:Residues: 1-393 <CHU>
A:Cross-references: EMBL:X54156; NID:935213; PIDN:CAA38095.1; PID:935214
R:Matlashewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, S.
EMBO J. 3, 3257-3262, 1984
A:Title: Isolation and characterization of a human p53 cDNA clone: expression of the human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.
A:Reference number: A22837; MUID:85230577; PMID:4006916
A:Accession: A22837
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-393 <ZAK>
A:Cross-references: EMBL:X02469; EMBL:M60950; NID:935209; PIDN:CAA26306.1; PID:935210
R:Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Biol. 5, 1601-1610, 1985
A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tumor antigen p53
A:Reference number: A55060; MUID:85267676; PMID:3894933
A:Accession: A55060
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-393 <HAP>
A:Cross-references: GB:K03199; NID:9189478; PIDN:AAA59989.1; PID:9189479
A:Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
R:Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arat, N.; Rotter, V.
Mol. Cell. Biol. 6, 4650-4656, 1986
A:Title: Molecular basis for heterogeneity of the human p53 protein.
A:Reference number: A93086; MUID:87089826; PMID:3025664
A:Accession: A25397
A:Molecule type: mRNA
A:Residues: 1-78, 'T', 80-393 <HAR1>
A:Cross-references: EMBL:M14694; NID:9339813; PIDN:AAA61211.1; PID:9339814
A:Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
A:Accession: B25397
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-78, 'T', 80-393 <HAR2>
A:Cross-references: EMBL:M14694; NID:9339815; PIDN:AAA61212.1; PID:9339816
A:Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
R:Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
Mol. Cell. Biol. 7, 961-963, 1987
A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.
A:Reference number: S42452; MUID:87144273; PMID:3547088
A:Accession: S42452
A:Molecule type: mRNA; DNA
A:Residues: 66-71, 'P', 73-79 <MKI2>
A:Experimental source: clone lambda C113
A:Note: 72-Cys was also found, and appears to represent a polymorphism
A:Accession: S42453
A:Molecule type: mRNA; DNA
A:Residues: 66-79 <MKI3>
A:Experimental source: clone J6K
R:Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vonsden, K.H.; Crook, T.

EMBO J. 10, 2879-2887, 1991
A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
A:Reference number: I38082; MUID:92007731; PMID:1915267
A:Accession: I38082
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189, 'LLSLSEKKEICVSMIMTETLFDIWMCPMSRLRLALV', 'VPSSTTTTCVTPAMAA' <F01>
A:Cross-references: EMBL:X60010; NID:9506432; PIDN:CAA42625.1; PID:9506433
A:Note: deletion of a C nucleotide causes a frameshift at position 566
A:Accession: I38083
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-192, 'R', 194-393 <F02>
A:Cross-references: EMBL:X60011; NID:9506434; PIDN:CAA42626.1; PID:9506435
A:Accession: I38084
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-393 <F03>
A:Cross-references: EMBL:X60012; NID:9506436; PIDN:CAA42627.1; PID:9506437
A:Accession: I38085
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-245, 'T', 247-393 <F04>
A:Cross-references: EMBL:X60013; NID:9506438; PIDN:CAA42628.1; PID:9506439
A:Accession: I38086
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F05>
A:Cross-references: EMBL:X60014; NID:9506440; PIDN:CAA42629.1; PID:9506441
A:Accession: I38087
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F06>
A:Cross-references: EMBL:X60015; NID:9506442; PIDN:CAA42630.1; PID:9506443
A:Accession: I38088
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
A:Cross-references: EMBL:X60016; NID:9506444; PIDN:CAA42631.1; PID:9506445
A:Accession: I38089
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F08>
A:Cross-references: EMBL:X60017; NID:9506446; PIDN:CAA42632.1; PID:9506447
A:Accession: I38090
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
A:Cross-references: EMBL:X60018; NID:9506448; PIDN:CAA42633.1; PID:9506449
A:Accession: I38091
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212, 'Q', 214-393 <F10>
A:Cross-references: EMBL:X60019; NID:9506450; PIDN:CAA42634.1; PID:9506451
A:Accession: I38092
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-253, 'D', 255-393 <F11>
A:Cross-references: EMBL:X60020; NID:9506452; PIDN:CAA42635.1; PID:9506453
A:Note: all sequences submitted to the EMBL/GenBank/DBJ databases June 1991
R:Putrel, P.A.; Barrett, J.C.; Wiseman, R.W.
Nucleic Acids Res. 19, 6977, 1991
A:Title: An Alu polymorphism intragenic to the TP53 gene.
A:Reference number: I38093; MUID:92107726; PMID:1762941
A:Accession: I38093
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-393 <FUT>
A:Cross-references: EMBL:X54156; NID:935213; PIDN:CAA38095.1; PID:935214
R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakata
Cancer Res. 51, 5800-5805, 1991
A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell lines
A:Reference number: A44905; MUID:92034678; PMID:1933850

[illegible]

Query Match 22.2%; Score 688.5; DB 2; Length 381;
Best Local Similarity 43.8%; Pred. No. 2.4e-40;
Matches 144; Conservative 56; Mismatches 94; Indels 35; Gaps 8;

OY 45 AONSVT-APSPYAOPSSFTDALSPSPA-----ISPMNDYPGPMSFDVFSFOOSSTAKS 95
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 69 AADVTELEPGVVA-----PAPTNPWLSFVSQKTYGNGNYGHGLGSLGTAKS 118
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 96 ATWTYTELLKKLYCOIAKTCEPIQIKVMTPRPGCAVIRAMPYYKKAENHTEVVKRCPNHEL 155
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 VMCTYSPLNKLFLPOLAKTCPCVOLMWASATPAGSGRVAMALYKKSKOHTETEVARRCPNHE- 177
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 156 SRENEGO-IAPRSHLIRVEGNSHAQVEDITRKOSLVIVYEPPDYGETPTTVLYLNPMC 214
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 --RCSDDGLPRQHILIRVEGNLTPEYLEDKOTRHSHVVYEPPEACSEYTIHKYMC 235
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 215 NSSCGVGNNRRPILIIVLETRDGVLCGRCCFEARICACPGDRKADSDSIKROOVSDST 274
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 236 NSSCGGMNRRLPILITILEDSSGNLGRDSFEVRVACPCPDRTREBENFRKKVELCPE 295
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 275 KNGGCKRPFFQNTHGIOMTSIKKRBSDDLVLPRNGRETTEMLKIKSLDELMOYLPR 334
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 296 LPPGSAKRALPTCT--SASPQRKKPKPDGGGYFTLKIRGRKFEMFRELNLEALKD-- 349
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 335 QHTIE-----TYRQQQQQHQHLLLOKOT 357
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 350 AHATEESGDSPRAHSLSLPRAFQALKEKS 378
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
I46226
cellular tumor antigen p53 - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-May-2000
C:Accession: I46226
R:Devilee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse,
Anticancer Res. 14, 2039-2046, 1994
A:title: The canine p53 gene is subject to somatic mutations in thyroid carcinoma.
A:Reference number: I46226; MUID:95150524; PMID:7847847
A:Accession: I46226
A>Status: Preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-77 <DEV>
A:Cross-references: GB:L27630; NID:g508454; PID:nAC37327.1; PID:g508455
C:Genetics:
A:Gene: p53
A:Introns: 24/1: 61/3
C:Superfamily: cellular tumor antigen p53

Query Match 8.4%; Score 259.5; DB 2; Length 77;
Best Local Similarity 60.3%; Pred. No. 1.7e-11;
Matches 47; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

OY 139 KAENHTEVVKRCPNHELISREFNEGQIAPRSHLIRVEGNSHAQVEDIPITGRQSYLVYPER 198
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 KSEPVTEVLRRCRNHERCSDSDG-IAPRQHILIRVEGNLRAKYLDRTTFRHSVVPYER 59
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 199 PQVGEPTTVLYNPMCN 216
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 PEVGFDTVTIHYNYMCMNS 77
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
I19361
hypothetical protein C17g1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: I19361
R:White, S.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19114
A:Accession: I19361

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:32:13 ; Search time 10.3921 Seconds

(without alignments)
2651.784 Million cell updates/sec

Title: US-09-538-106-16

Perfect score: 3104
Sequence: 1 MLYENNAQTQSEPOYTNL.....FNEDMARRNKQRIKEGE 586

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1741	56.1	636	1 P73_HUMAN	015350 homo sapien
2	1720.5	55.4	637	1 P73_CERAE	09xsk8 cercopithec
3	839.5	27.0	396	1 P53_ONCMY	P25035 oncorhynch
4	819.5	26.4	369	1 P53_BARBU	09w678 barbus barb
5	806.5	26.0	373	1 P53_BRARE	P79734 brachydact
6	795	25.6	376	1 P53_ICTPU	093379 ictalurus p
7	762	24.5	363	1 P53_XENLA	P07193 xenopus lae
8	761.5	24.4	386	1 P53_PIG	09tub2 sus scrofa
9	758.5	24.4	367	1 P53_CHICK	P10360 gallus gall
10	753.5	24.0	367	1 P53_CHICK	P41685 fellis silve
11	745	24.0	367	1 P53_TETMU	09w679 tetradon m
12	744	24.0	381	1 P53_CANFA	029537 canis famli
13	744	24.0	386	1 P53_BOVIN	029628 bos taurus
14	738.5	23.8	391	1 P53_MARMO	036006 marmota mon
15	737.5	23.8	352	1 P53_ORYLA	P79820 oryctolagus
16	727	23.4	382	1 P53_SHEEP	P51664 ovis aries
17	723	23.3	391	1 P53_RAT	P10361 rattus norv
18	721	23.2	391	1 P53_CAVPO	09wut6 cavia porce
19	719.5	23.2	393	1 P53_TUPGB	09tut1 tupia glis
20	717.5	23.1	366	1 P53_PLAPE	012946 platichthys
21	712	22.9	396	1 P53_MESAU	000362 mesocricetu
22	707.5	22.8	393	1 P53_HUMAN	P04637 homo sapien
23	703	22.6	314	1 P53_SPEBE	064662 speomophilu
24	703	22.6	383	1 P53_CERAE	P13461 cercopithec
25	703	22.6	393	1 P53_MACFA	P56423 macaca fasc
26	703	22.6	393	1 P53_MACFA	P56424 macaca mula
27	702.5	22.6	342	1 P53_XIPHE	057538 xiphophorus
28	702.5	22.6	342	1 P53_XIPHE	092143 xiphophorus
29	702	22.6	390	1 P53_MOUSE	P02340 mus musculu
30	701.5	22.6	393	1 P53_CRGR	009185 cricetus
31	700	22.6	391	1 P53_RABIT	095330 oryctolagus
32	689.5	22.2	280	1 P53_HORSE	P79892 equus cabal
33	591.5	19.1	207	1 P53_EQUAS	029480 equus asinu

34	134.5	4.3	1386	1 ZAP3_MOUSE	Q91017 mus musculu
35	133.5	4.3	5147	1 PCLO_HUMAN	Q9yev0 homo sapien
36	133	4.3	1081	1 GALY_YEAST	P19659 saccharomyc
37	133	4.3	1520	1 ABL_DROME	P00522 drosophila
38	129.5	4.2	701	1 CGL_HUMAN	Q13495 homo sapien
39	129.5	4.2	766	1 TLE4_MOUSE	Q62441 mus musculu
40	129	4.2	964	1 YOKA_SCHPO	074522 schizosacch
41	128.5	4.1	589	1 SPY_DROME	044783 drosophila
42	128.5	4.1	628	1 V70K_TMYVC	P28478 turnip yell
43	128.5	4.1	766	1 TLE4_HUMAN	Q04727 homo sapien
44	127.5	4.1	1344	1 TUSE_HUMAN	Q9nrf4 homo sapien
45	126.5	4.1	628	1 V70K_TYMYA	P20131 turnip yell

ALIGNMENTS

RESULT 1
ID P73_HUMAN STANDARD: PRT; 636 AA.
AC 015350; 015351; 09NTR8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor protein p73 (p53-like transcription factor) (p53-related protein).
GN TP73 OR P73.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RC TISSUE=Colon;
RX MEDLINE=97433090; PubMed=9288759;
RA Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A., Minty A., Chalton P., Lelias J.-M., Dumont X., Ferrara P., McKeon F., Caput D.;
RT "Monoclonally expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers.";
RL Cell 90:809-819(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC MEDLINE=99289209; PubMed=10362363;
RX MEDLINE=99289209; PubMed=10362363;
RA Yoshikawa H., Nagashima M., Khan M.A., Mckenamin M.G., Hagihara K., Harris C.C.;
RT "Mutational analysis of p73 and p53 in human cancer cell lines.";
RL Oncogene 18:3415-3421(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC MEDLINE=98389621; PubMed=9721206;
RX MEDLINE=98389621; PubMed=9721206;
RA Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B., Jenkins R., Smith D.I., Liu W.;
RT "Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions.";
RL Genomics 51:359-363(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).
RC TISSUE=Neuroblastoma;
RX MEDLINE=99021697; PubMed=9802988;
RA De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M., Amicchiariello-Petrucelli M., Leviero M., Mellino G.;
RT "Two new p73 splice variants, gamma and delta, with different transcriptional activity.";
RL J. Exp. Med. 188:1763-1768(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).
RC TISSUE=Breast cancer, Hepatoma, Lymphocytes, and SKIN;
RX MEDLINE=99310938; PubMed=10381648;
RA De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Mellino G., Costanzo A., Leviero M., Knight R.A.;
RT "Additional complexity in p73: induction by mitogens in lymphoid cells and identification of two new splicing variants epsilon and zeta.";

```

RL  Cell Death Differ. 6:389-390(1999).
RM  [6]
RP  SEQUENCE FROM N.A. (ISOFORM KAPPA).
RA  Thomas D.;
RL  Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN  [7]
RP  PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
RX  MEDLINE=99318135; Pubmed=10391251;
RA  Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
RA  Kharbanda S., Weichselbaum R., Kufe D.;
RT  "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
RT  to DNA damage.";
RL  Nature 399:814-817(1999).
RN  [8]
RP  ERRATUM.
RA  Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
RA  Kharbanda S., Weichselbaum R., Kufe D.;
RL  Nature 400:792-792(1999).
RN  [9]
RP  FUNCTION.
RX  MEDLINE=99217940; Pubmed=10203277;
RA  Kaelin W.G. Jr.;
RT  "The emerging p53 gene family.";
RL  J. Natl. Cancer Inst. 91:594-598(1999).
RN  [10]
RP  STRUCTURE BY NMR OF 439-506.
RX  MEDLINE=99380160; Pubmed=10449409;
RA  Chi S.W., Ayed A., Arrowsmith C.H.;
RT  "Structural structure of a conserved C-terminal domain of p73 with
RT  structural homology to the SAM domain.";
RL  EMBO J. 18:4438-4445(1999).
CC  -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
CC  WHEN OVEREXPRESSED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
CC  PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
CC  PROTEIN.
CC  -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
CC  TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
CC  AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
CC  INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
CC  INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
CC  -1- SUBCELLULAR LOCATION: Nuclear.
CC  -1- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=7;
CC  Name=Alpha;
CC  IsoId=O15350-1; Sequence=Displayed;
CC  Name=Beta;
CC  IsoId=O15350-2; Sequence=VSP_006539;
CC  Name=Gamma;
CC  IsoId=O15350-3; Sequence=VSP_006540, VSP_006541;
CC  Note=The splicing of exon 11 results in a frameshift from the
CC  original reading frame;
CC  Name=Delta;
CC  IsoId=O15350-4; Sequence=VSP_006542, VSP_006543;
CC  Name=Epsilon;
CC  IsoId=O15350-5; Sequence=VSP_006544, VSP_006545;
CC  Note=The splicing of exon 11 results in a frameshift from the
CC  original reading frame. The splicing of exon 13 reverts the
CC  reading frame to the sequence of isoform Alpha;
CC  Name=Zeta;
CC  IsoId=O15350-6; Sequence=VSP_006546;
CC  Name=Kappa;
CC  IsoId=O15350-7; Sequence=VSP_006538;
CC  -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
CC  SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
CC  -1- INDUCTION: NOT INDUCED BY DNA DAMAGE.
CC  -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
CC  BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
CC  TO THE ABL TYROSINE KINASE SH3 DOMAIN.
CC  -1- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE
CC  CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
CC  IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
CC  NEUROBLASTOMA AND OLIGODENDROGLIOMA.
CC  -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

```

[illegible]

DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 66 256 BY SIMILARITY.
 FT DOMAIN 298 329 OLIGOMERIZATION.
 FT DOMAIN 342 365 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 276 292 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 368 368 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 369 AA: 41233 MW: 0BE2CF2CEA74C304 CRC64;
 Query Match 26.4%; Score 819.5; DB 1; Length 369;
 Best Local Similarity 51.2%; Pred. No. 4.1e-49;
 Matches 167; Conservative 49; Mismatches 87; Indels 23; Gaps 8;
 QY 29 QIQQSSSTSPYNTDHAQNSVT-APSPYAQSPSTDALSPSPALDSNTDYPGPHSFVSF 87
 DB 26 ELINDEYLPSSFDPIFDVNLTEQOPQSTSP-----PTASVPATDYDPEHGKLG 77
 QY 88 QOOSTAKSATWTPTSTELKLYQIAKTCPIQIKVMTPPGAVIRAMPYKKAHEVTV 147
 DB 78 POSGTAKTSTCTYSSDLNKLFCQIAKTCVQWVAVPQGVIRATATYKKEHVAEVV 137
 QY 148 KRCPNHELSEFNEGOIAPPSHLIRVGNASHAQYEDPITGROSLVPEYEPQVGEFTT 207
 DB 138 RCRPHHERPD-GDG-LAPAAHLIVEGSRALYREDVDVNSHVSVPYEVQOLSEFTT 195
 QY 208 VLYNMCNSSCYGGMNRRPILITVLETRDGOVLGRCEPARIACPGDRKADSDSIRK 267
 DB 196 VLYNMCNSSCYGGMNRRPILITVLETRDGOVLGRCEPARIACPGDRKADSDSIRK 255
 QY 268 QOVSTKNGD---GTRKPF-RONTMGIQMTSIRKR----SPDELLLYLVGRGEETE 318
 DB 256 DQ---ETITLDIRPANKRSLTKDSTSYPRPESGKAKLSSDSEITVTLQGRKERVE 312
 QY 319 MLTKIKESLELMQYLPQHTIETRYROO 344
 DB 313 MLTKINDSELSDVVPSEMDRYROK 338
 RESULT 5
 P53_BRARE STANDARD; PRT; 373 AA.
 AC P79734; 090440:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR DRP53.
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 OX [1]
 RN RP MEDLINE-97344388; PubMed-9200835;
 RP MEDLINE-97344388; PubMed-9200835;
 RA Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
 RA Thongkum T., Barnes D.W., Hendricks J.D., Bailey G.S.,
 RA "Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
 RT expression during embryogenesis.";
 RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
 RN [2]
 RP SEQUENCE OF 140-212 FROM N.A.
 RA Winge P.;
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.

CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U60804; AAB40617.1; -;
 DR EMBL; U46693; AAB97408.1; -;
 DR HSSP; P04637; 1TUP.
 DR ZFIN; ZDB-GENE-990415-270; tp53.
 DR InterPro: IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PROSITE; PS00348; P53; 1.
 DR ProDom; PD002681; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 70 260 BY SIMILARITY.
 FT DOMAIN 301 332 OLIGOMERIZATION.
 FT DOMAIN 345 366 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 280 296 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 372 372 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 373 AA: 41899 MW: AC7AB724F6B61FF CRC64;
 Query Match 26.0%; Score 806.5; DB 1; Length 373;
 Best Local Similarity 48.0%; Pred. No. 3.2e-48;
 Matches 171; Conservative 55; Mismatches 97; Indels 33; Gaps 10;
 QY 5 ENNAQTOFSEPOYTN-----GLNSMDQIQNGSSSTSYNTDHAQNSTARS 53
 DB 3 QNDQO-EFAELWEKNLTIOPPGGSCWDIIN--DEEYLPQS---EDNFEEN-VLEQO 53
 QY 54 PYAQSSTFDALSPSPALPSNTDYPGPHSFVSFOOSTAKSATWTPTSTELKLYQIAK 113
 DB 54 P--QBST-----LPSTVETPESDYEDHGFRLRFPQSGTAKSTCTYSSDLNKLFCQIAK 107
 QY 114 TCIPIQIKVMTPPGAVIRAMPYKKAHEVTVKRCPNHELSEFNEGOIAPPSHLIRV 173
 DB 108 TCPVQGVVDVAPPQGVVAFATAYKKEHVAEVVRCRPHHE--RPDGDNLAPAGHLIRV 165
 QY 174 EGNASHAQYEDPITGROSLVPEYEPQVGEFTTYLYNMCNSSCYGGMNRRPILITVL 233
 DB 166 EGNORANRREDNITLHRSVFPVEAQAEMWTVLLANMCNSSCYGGMNRRPILITVL 225
 QY 234 ETRDGOVLGRCEPARIACPGDRKADSDSIRK-QQVDSSTKNGDGTTRPRONTGIG 292
 DB 226 ETQEGQLGRBFEYAVVACPGDRKTESNKKQDETMAKTGTGTRSLVKESSNAT 285
 QY 293 M---TSIKRRSPDELLLYLVGRGEYEMLKIKESLELMQYLPQHTIETRYROO 344
 DB 286 LPEGSKKAKGSSDSEIFTTLQVGRERYEILKLNDSELSDVVPASDAERYROK 341
 RESULT 6
 P53_ICTPU STANDARD; PRT; 376 AA.
 AC 093379;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Ictalurus punctatus (Channel catfish).

OY 155 LSREFNGIAPPRLIRVEGNSHAOYEDPITGROSVLYPEPPQVGTETTVLYLNFMC 214
 Db 173 RCPDSDG-LAPQHLIRVEGMLHAKYLDDBRTEFHSVVPPEPEVSDCTTHYNMC 231
 OY 215 NSSCGVMNRRLIYVLETRDGOVLGRCFEARIACPGDRKRADEDSIRKQVSDST 274
 Db 222 NSSCGVMNRRLIYVLETRDGOVLGRCFEARIACPGDRKRADEDSIRKQVSDST 291
 OY 275 KNGDGTAKRFRONTGICMTSIRKRRSPDDELLYPVNGRETYEMLKIKESLET 329
 Db 292 PPPGSTRALPPST---SSTPQKKKPLDGEYFTLQIRGRERFEREMLNLEL 343

RESULT 11

P53_TETMU STANDARD: PRT; 367 AA.
 AC Q9W679;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Tetradon mirus (Congo puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=94908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RA Bhaskaran A.; May D.; Rand-Weaver M.; Tyler C.R.;
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 CC "Evolutionary conservation of p53 gene sequences in fish."
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC cell cycle arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF071571; AAD34213.1; -
 CC DR HSSP: P04637; ITUP
 CC DR InterPro: IPR002117; P53.
 CC DR Pfam: PF00870; P53; 1.
 CC DR PRINTS: PR00386; P53SUPPRESSR.
 CC DR PRODOM: PD002681; P53; 1.
 CC DR PROSITE: PS00348; P53; 1.
 CC KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 CC Nuclear protein; Phosphorylation; Apoptosis.
 CC KM
 CC FT DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
 CC FT DNA_BIND 86 273 BY SIMILARITY.
 CC FT DOMAIN 308 337 OLIGOMERIZATION.
 CC FT DOMAIN 342 363 BASIC (REPRESSION OF DNA-BINDING).
 CC FT DOMAIN 288 301 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC FT MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
 CC SQ SEQUENCE 367 AA; 41266 MW; ACCIOEEEF59FCDF CRC64;

Query Match 24.0%; Score 745; DB 1; Length 367;
 Best Local Similarity 51.9%; Pred. No. 5, 2e-44;
 Matches 148; Conservative 43; Mismatches 76; Indels 18; Gaps 3;

OY 57 QPSTFDALSPSPALPSNTDYPGPHSFDVSPFOOSTAKSATVYSTELKLYQIAKCP 116
 Db 67 EPPSDGANSSSPTVPTDTPDYGEGFKIRPKSGSTASVTSTYELINKLCOIAKSL 126
 OY 117 IQIKVTPPGAVIRAMPVYKAEHVEVYKRCNHELREFNGQIAPSHLIRVEGN 176
 Db 127 VVLLGKDPMPGAVIRATVYAKTEHVAEVVRCFHHQ-----NEDSAEHRSHLLRMGS 181
 OY 177 SHAQVVEDPIRGROSVLYPEPPQVGTETTVLYLNFMCSSCGVMNRRLIYVLETR 236
 Db 182 ERAQYFEHPHTKRQSVLYPEPPQVGTETTVLYLNFMCSSCGVMNRRLIYVLETR 241
 OY 237 DGOVLRRCFEARIACPGDRKRADEDSIRKQVSDSTKNGDGTAKRFRONTGICMTSI 296
 Db 242 EGVLAGRCFEVYRVCACPGDRKRADEDSIRKQVSDSTKNGDGTAKRFRONTGICMTSI 294
 OY 297 KRRRS-----PDDELLYPVNGRETYEMLKIKESLETMOYLPQ 335
 Db 295 KSKTASSAEDNNEVYTLQIRGRKRYEMLKIKINDGLDLENKPK 339

RESULT 12

P53_CANFA STANDARD: PRT; 381 AA.

AC Q29537; Q9TV78;
 DT 01-NOV-1997 (Rel. 35, Created).
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=98178696; PubMed=9519881;
 RA Veldhoen N.; Milner J.;
 RT "Isolation of canine p53 cDNA and detailed characterization of the
 RT full length canine p53 protein."
 RL Oncogene 16:1077-1084(1998).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Setoguchi A.; Sakai T.; Okuda M.; Minehata K.; Yazawa M.; Ishizaka T.;
 RA Watarai T.; Hasegawa A.; Tsujimoto H.;
 RT "Aberrations of p53 tumor suppressor gene in various spontaneous
 RT tumors in the dog."
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
 RL [3]
 RP SEQUENCE OF 25-300 FROM N.A.
 RC STRAIN=Beagle;
 RX MEDLINE=95323915; PubMed=7600529;
 RA Kraegel S.A.; Pazzi K.A.; Madewell B.R.;
 RT "Sequence analysis of canine p53 in the region of exons 3-8."
 RL Cancer Lett. 92:181-186(1995).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression.
 CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DISEASE: p53 is found in increased amounts in a wide variety


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FT CONFLICT 380 380 R -> T (IN REF. 2).
SQ SEQUENCE 386 AA: 43255 MW: 22247328C548F31 CRC64:
Query Match 24.0%; Score 744; DB 1; Length 386;
Best Local Similarity 41.5%; Pred. No. 6.5e-44;
Matches 164; Conservative 65; Mismatches 120; Indels 46; Gaps 12;

OY 5 ENNAOTQSEPOYNTLGLT-----NSMDQIONGSSSTSPYN-----TDAQNSVAP--- 52
DB 7 ELNVEPPLSQETFDLWMLLPENNLLSELSELPVDDLPIYDVATWDECPNE--APQMP 64
OY 53 ---SPYAPQSTFEDALSPSPA-----IPSNIDYPGPHSFVDFQOOSTAKSATWTYS 101
DB 65 EPSAPAAPPPAT-----PAPATSMPLSEFVSQKPYPNYGRLGLFQSGAKSVTCYTS 119
OY 102 TELKLYQIAKTCPIQIKVMPROGAVIRAMPYKKAHVTEVVKRCNHELRENE 161
DB 120 PSLNKLFCQIAKTCVQLWVDSPPPGRRVRAIMAYIKKLEHMTVEVRRCPHERSSDYSD 179
OY 162 GQIAPPSHLIRVEGNSHAQYEDPTTGRQSVLYPEPQVGTETVLYNFCNCSYVG 221
DB 180 G-LAPQQLIVEGRLRAEYIDDRTEFRHSVYVPESEIDSECTIHNFCNCSCKMG 238
OY 222 MNRPIILITVLETRDQVLCGRCEARICACPGDRKADSDSIRKQVSDSTKNGDGT 281
DB 229 MNRPIILITVLEDSQGLIRNSEFEVYACPGDRKTEENELKKGQSCPEPPRSTK 298
OY 282 RPFQNTGIGMTSLIKRRSP--DDELLYPRGRTYEMLKIKSLTMOVLPHQHTET 340
DB 299 RALPNT-----SSSQPKKPLDGEYFTLQIRGFRKRYEMFRLNDALEL---KDALDG 349
OY 341 YRQOQOQH-OHLQKQTSIQSPSSYGNSSPLNK 374
DB 350 REPGESRAHSHLSK-----KRPSCKHKKPKMLK 380

RESULT 14
P53_MARMO STANDARD; PRT; 391 AA.
AC 036006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97376996; PubMed=9233767;
RA Feltelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
RT Partial characterization of the woodchuck tumor suppressor, p53, and
RT its interaction with woodchuck hepatitis virus X antigen in
RT hepatocarcinogenesis.
RT Oncogene 15:327-336(1997).
RL -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and BAX antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC -----
DR EMBL: AJ001022; CA04478.1; -.
DR HSP: P04637; ITUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DNA_BIND 1 44 TRANSSCRIPTION ACTIVATION (ACIDIC).
FT DOMAIN 100 290 OLIGOMERIZATION.
FT DOMAIN 323 354 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 366 385 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 309 321 PHOSPHORYLATION (BY PRPK) (BY
FT MOD_RES 15 15 SIMILARITY).
FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 391 AA: 43468 MW: 45508484A0182 CRC64:
Query Match 23.8%; Score 738.5; DB 1; Length 391;
Best Local Similarity 41.3%; Pred. No. 1.6e-43;
Matches 158; Conservative 65; Mismatches 117; Indels 43; Gaps 9;

OY 5 ENNAOTQSEPOYNTLGLTGLNSMDQIONGSSSTSPYNTHQNSTAPYAQSPSTDA 64
DB 28 ENNVLSPLVSPMDL-LIASED--VENWPK-----GDEALQNSAPAPKAPTPAASTL 80
OY 65 LSPSPA-----IPSNIDYPGPHSFVDFQOOSTAKSATWTYSTELKLYCQIAKTC 116
DB 81 AAPSPATSMPLSSSVSQNTYGVYGFRLGHSQTAKSVCTYPSLNLKLCQIAKTC 140
OY 117 IQIKVMPROGAVIRAMPYKKAHVTEVVKRCNHELRENEGQIAPPSHLIRVEGN 176
DB 141 VOLWVDSPPPGRRVRAIMAYIKKQHMTEVVRRCPHNE--RCSDSGLAPQHLIRVEGN 198
OY 177 SHAQVDEPITGRQSVLYPEPQVGTETVLYNFCNCSYGNMNRPIILITLFR 236
DB 199 LRAETLDNRNTRFHSVVPYEPPEVSECTIHNFCNCSYGNMNRPIILITLFR 258
OY 237 DGOVLGRRCFEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPFPRONT-----HGI 291
DB 259 SGNLGRNRSFEVRCACPGDRKTEENFRK-----GRCPEPPRSTRKALPNGT 310
OY 292 QMTSTIKRRSPDDELLYPRGRTYEMLKIKESLELMQVLPQHT-----IET 341
DB 311 SSSPPKPKPLDGEYFTLQIRGFRKRYEMFRLNDALELKDQAQKEGSESRPHPSLYSK 370
OY 342 RQOQOQOQH-OHLQKQTSIQSPSS 364
DB 371 KGQSTSRHKIITFR--EGPDS 390

RESULT 15
P53_ORYLA STANDARD; PRT; 352 AA.
AC P79620; O9PSU7; O9PSU8;
DT 01-NOV-1997 (Rel. 35; Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei;

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CC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianiichthyidae; Oryziatidae; Oryziatidae;
OX NCBI_Taxid=8090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: Liver;
RA MEDLINE=97305153; Pubmed=9161419;
RX Krause M.K., Rhodes L.D., van Beneden R.J.;
RT "Cloning of the p53 tumor suppressor gene from the Japanese medaka
RT (Oryzias latipes) and evaluation of mutational hotspots in MNN-
RT exposed fish.";
RL Gene 189:101-106(1997).
[2]
RP SEQUENCE FROM N.A., AND VARIANT THR-91.
RC STRAIN-Himedaka;
RA Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;
RT "Isolation of cDNAs encoding the p53 tumor suppressor gene in the
RT Japanese Medaka (Oryzias latipes)."
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL: U57306; AAC60146.1; -;
DR EMBL: AF003949; AAD01195.1; -;
DR EMBL: AF003950; AAD01196.1; -;
DR HSSP: P04637; IYCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR Prodom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.
FT DOMAIN 1 48 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 87 273 BY SIMILARITY.
FT DOMAIN 302 331 OLIGOMERIZATION.
FT DOMAIN 334 350 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 283 295 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 351 351 PHOSPHORYLATION (BY SIMILARITY).
FT VARIANT 91 91 S->T.
FT CONFLICT 22 22 MISSING (IN REF. 1).
SQ SEQUENCE 352 AA; 39753 MW; 196868A66351BFF5 CRC64;
Query Match 23.88; Score 737.5; DB 1; Length 352;
Best Local Similarity 52.5%; Pred. No. 1.6e-43;
Matches 148; Conservative 40; Mismatches 67; Indels 27; Gaps 5;
QY 57 QPSTFDALSPSPAIPTNTDYPGHSFDVYFQOSTAKSATWYSTELKLYCOIATCP 116
DB 68 EPPVPTNEVNDPPTVTPTDTPGSELELRFQSGTAKSVTSYSETLNKLXCOLAKTSP 127
QY 117 IQIKVMTPPQAGVIRAMPYKKAHEVTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGN 176
DB 128 IEVYKSKPEPKGAILRATAYKTKTEHVADYVRCPHHQ-----NEDSEVHRSHLIRVEGS 182

QY 177 SHAQYVEDPITGQSVLVPYEPQVGTETFTVLYNEMCNSSCVGNNRRPILITVLETR 236
DB 183 QLAQYFEDPYTKRSQSVVPEYEPQVGTETFTVLYNEMCNSSCVGNNRRPILITVLETR 241
QY 237 DGQYLGRCFEARICACPGDRKRADESIKQVSDSTKNGDGTKKRFRONTGICMTSI 296
DB 242 EGVLGRCFEARICACPGDRKRADESIKQVSDSTKNGDGTKKRFRONTGICMTSI 297
QY 297 KKRSS-----PDDELLYLPVGRREYEMULIKESLEIMO 331
DB 288 KKKSHSSGDEEDNREYFHEVYGRERYEFLKINDGLELLE 329

Search completed: August 7, 2003, 09:47:27
Job time : 11.3921 secs

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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:41:09 ; Search time 47.1494 Seconds
(without alignments)
3207.225 Million cell updates/sec

Title: US-09-538-106-16

Perfect score: 3104
Sequence: 1 MLYLENNMQTQSEPPQYTNL.....FNEFDARRNNKQRIKEGE 586

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp_invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp_unclassified:*
- 15: sp-virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3104	100.0	586	4 Q9UBV9	Q9UBV9 homo sapien
2	3100	99.9	586	4 Q9P1B4	Q9P1B4 homo sapien
3	3087	99.5	586	4 Q75080	Q75080 homo sapien
4	3066	98.8	586	11 Q89097	Q89097 mus musculus
5	3057	98.5	586	11 Q99J82	Q99J82 rattus norv
6	3033	97.7	680	4 Q8H3D4	Q8H3D4 homo sapien
7	3029	97.6	641	4 Q75195	Q75195 homo sapien
8	3025	97.5	680	4 Q9UE10	Q9UE10 homo sapien
9	2995	96.5	680	11 Q88898	Q88898 mus musculus
10	2991	96.4	663	11 Q99J83	Q99J83 rattus norv
11	2991	96.4	680	11 Q99J86	Q99J86 rattus norv
12	2962	95.4	582	13 Q9DEC7	Q9DEC7 gallus gall
13	2601.5	83.8	501	4 Q9H3P8	Q9H3P8 homo sapien
14	2421	78.0	461	4 Q9P1B5	Q9P1B5 homo sapien
15	2421	78.0	461	4 Q9UP26	Q9UP26 homo sapien
16	2398	77.3	461	11 Q9QWY9	Q9QWY9 mus musculus

17	2389	77.0	461	11 Q99J86	Q99J86 rattus norv
18	2350	75.7	516	4 Q9P1B7	Q9P1B7 homo sapien
19	2350	75.7	556	4 Q9H3D3	Q9H3D3 homo sapien
20	2344	75.5	576	13 Q8JFE3	Q8JFE3 brachydanio
21	2330	75.1	588	13 Q8JH26	Q8JH26 brachydanio
22	2327	75.0	555	11 Q9QWZ0	Q9QWZ0 mus musculus
23	2323	74.8	538	11 Q99J87	Q99J87 rattus norv
24	2323	74.8	555	11 Q99J88	Q99J88 rattus norv
25	2148	69.2	416	4 Q9P1B6	Q9P1B6 homo sapien
26	2077	66.9	471	4 Q9NPH7	Q9NPH7 homo sapien
27	1884	60.7	393	4 Q75922	Q75922 homo sapien
28	1872	60.3	356	4 Q9UP74	Q9UP74 homo sapien
29	1868	60.2	393	11 Q99J89	Q99J89 rattus norv
30	1837	59.2	389	11 Q88899	Q88899 mus musculus
31	1826	58.8	457	13 Q8JH25	Q8JH25 brachydanio
32	1813	58.4	487	4 Q9H3D2	Q9H3D2 homo sapien
33	1802	58.1	470	11 Q99J81	Q99J81 rattus norv
34	1802	58.1	487	11 Q99J80	Q99J80 rattus norv
35	1777	57.2	641	13 Q9W664	Q9W664 barbus barb
36	1766	56.9	483	11 Q88897	Q88897 mus musculus
37	1748.5	56.3	590	11 Q99J81	Q99J81 mus musculus
38	1746	56.2	587	4 Q8TDX6	Q8TDX6 homo sapien
39	1744.5	56.2	631	11 Q99J82	Q99J82 mus musculus
40	1730.5	55.8	365	13 Q98SW0	Q98SW0 xenopus lae
41	1562	50.3	514	11 Q9CU77	Q9CU77 mus musculus
42	1489	48.0	284	11 Q8C826	Q8C826 mus musculus
43	1459.5	47.0	497	11 Q9WUJ0	Q9WUJ0 mus musculus
44	1420.5	45.8	450	4 Q8TDX5	Q8TDX5 homo sapien
45	1256	40.5	426	4 Q8NHW9	Q8NHW9 homo sapien

ALIGNMENTS

RESULT 1
Q9UBV9 PRELIMINARY: PRT: 586 AA.

AC Q9UBV9
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE DN P63 alpha.
GN P63.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE:98448095; PubMed:9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "P63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lee L.A., Walsh P., Prater C.A., Su L., Marchbank A., Egbert T.B.,
RA DellaValle R.P., Targoff I.N., Kaufman K.M., Chorzelski T.P.,
RA Jablonska S.;
RT "Characterization of an autoantigen associated with chronic ulcerative
RT stomatitis: The CUSP autoantigen is a member of the p53 family.";
RL J. Invest. Dermatol. 0:0-0(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Hagihara K., McMenamin M.G., Harris C.C.;
RA Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF075431; AAC62636.1; -;
DR EMBL: AF091627; AAC43038.1; -;
DR EMBL: AF124539; AAG45610.1; -;
DR EMBL: AF124530; AAG45610.1; JOINED.

DR EMBL; AF124531; AAG45610.1; JOINED.
 DR EMBL; AF124532; AAG45610.1; JOINED.
 DR EMBL; AF124533; AAG45610.1; JOINED.
 DR EMBL; AF124534; AAG45610.1; JOINED.
 DR EMBL; AF124535; AAG45610.1; JOINED.
 DR EMBL; AF124536; AAG45610.1; JOINED.
 DR EMBL; AF124537; AAG45610.1; JOINED.
 DR EMBL; AF124538; AAG45610.1; JOINED.
 DR HSSP; P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53; SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nucleic protein.
 SO SEQUENCE 586 AA; 65756 MW; 2E2F92ABF1AF8629 CRC64;

Query Match 100.0%; Score 3104; DB 4; Length 586;
 Best Local Similarity 100.0%; Pred. No. 1.5e-256;
 Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLYENNAAQTFSEBQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 |||||||
 DB 1 MLYENNAAQTFSEBQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 |||||||
 OY 61 TFDALSPSPALPSTNDYDGPSPFVSFOQSTAKSATWTYTELTKLYCOIAKCPQIOIK 120
 |||||||
 DB 61 TFDALSPSPALPSTNDYDGPSPFVSFOQSTAKSATWTYTELTKLYCOIAKCPQIOIK 120
 |||||||
 OY 121 VMTPEPGAVIRAMPVYKKAHVTEVYKRCPNHLSREFNGQIAPSHLIRVGNSHAQ 180
 |||||||
 DB 121 VMTPEPGAVIRAMPVYKKAHVTEVYKRCPNHLSREFNGQIAPSHLIRVGNSHAQ 180
 |||||||
 OY 181 YVEDPIGRQSVLVYEPPOVGTETTYLVNFMCNSSCVGGMNRPILITVLETRDGOV 240
 |||||||
 DB 181 YVEDPIGRQSVLVYEPPOVGTETTYLVNFMCNSSCVGGMNRPILITVLETRDGOV 240
 |||||||
 OY 241 LGRRCFEARICACGRDKADEDSIRKQOVSSTKNGDGTGRPRPRONTGHIOMTSIKRR 300
 |||||||
 DB 241 LGRRCFEARICACGRDKADEDSIRKQOVSSTKNGDGTGRPRPRONTGHIOMTSIKRR 300
 |||||||
 OY 301 SPDELLYLPRKGETYEMLIKIKESLELMQYLPQHTIETRYROOQOOHHLQKQTSIQ 360
 |||||||
 DB 301 SPDELLYLPRKGETYEMLIKIKESLELMQYLPQHTIETRYROOQOOHHLQKQTSIQ 360
 |||||||
 OY 361 SPSSYGNSPPLNKMNSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
 |||||||
 DB 361 SPSSYGNSPPLNKMNSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
 |||||||
 OY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIVSFARLGGSSCLDYFTTQGLTTIY 480
 |||||||
 DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIVSFARLGGSSCLDYFTTQGLTTIY 480
 |||||||
 OY 481 QIEHYSMDLALSLKIPROFRAIKGILDHROLHEFSSPHLRTPPSSASTVSGSSETR 540
 |||||||
 DB 481 QIEHYSMDLALSLKIPROFRAIKGILDHROLHEFSSPHLRTPPSSASTVSGSSETR 540
 |||||||
 OY 541 GERVIDAVRFTLROTISFPPRDEMNDFMDARNRKQORKEGE 586
 |||||||
 DB 541 GERVIDAVRFTLROTISFPPRDEMNDFMDARNRKQORKEGE 586
 |||||||

RESULT 2

O9P1B4 PRELIMINARY: PRT: 586 AA.
 AC O9P1B4
 DT 01-OCT-2000 (TIREMBLrel. 15, Created)
 DT 01-OCT-2000 (TIREMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TIREMBLrel. 22, Last annotation update)
 DE P51 isoform delNalpa.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20388515; PubMed=10935472;
 RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
 RA Yokota J.;
 RT "Mutation and expression of the p51 gene in human lung cancer.";
 RL Neoplasia 1:71-79(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AF116769; AAF43491.1; JOINED.
 DR EMBL; AF116758; AAF43491.1; JOINED.
 DR EMBL; AF116759; AAF43491.1; JOINED.
 DR EMBL; AF116760; AAF43491.1; JOINED.
 DR EMBL; AF116761; AAF43491.1; JOINED.
 DR EMBL; AF116762; AAF43491.1; JOINED.
 DR EMBL; AF116763; AAF43491.1; JOINED.
 DR EMBL; AF116764; AAF43491.1; JOINED.
 DR EMBL; AF116765; AAF43491.1; JOINED.
 DR EMBL; AF116766; AAF43491.1; JOINED.
 DR EMBL; AF116767; AAF43491.1; JOINED.
 DR EMBL; AF116768; AAF43491.1; JOINED.
 DR HSSP; P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53; SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nucleic protein.
 SO SEQUENCE 586 AA; 65726 MW; 9A2316B631AF8634 CRC64;

Query Match 99.9%; Score 3100; DB 4; Length 586;
 Best Local Similarity 99.8%; Pred. No. 3.2e-256;
 Matches 585; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLYENNAAQTFSEBQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 |||||||
 DB 1 MLYENNAAQTFSEBQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 |||||||
 OY 61 TFDALSPSPALPSTNDYDGPSPFVSFOQSTAKSATWTYTELTKLYCOIAKCPQIOIK 120
 |||||||
 DB 61 TFDALSPSPALPSTNDYDGPSPFVSFOQSTAKSATWTYTELTKLYCOIAKCPQIOIK 120
 |||||||
 OY 121 VMTPEPGAVIRAMPVYKKAHVTEVYKRCPNHLSREFNGQIAPSHLIRVGNSHAQ 180
 |||||||
 DB 121 VMTPEPGAVIRAMPVYKKAHVTEVYKRCPNHLSREFNGQIAPSHLIRVGNSHAQ 180
 |||||||
 OY 181 YVEDPIGRQSVLVYEPPOVGTETTYLVNFMCNSSCVGGMNRPILITVLETRDGOV 240
 |||||||
 DB 181 YVEDPIGRQSVLVYEPPOVGTETTYLVNFMCNSSCVGGMNRPILITVLETRDGOV 240
 |||||||
 OY 241 LGRRCFEARICACGRDKADEDSIRKQOVSSTKNGDGTGRPRPRONTGHIOMTSIKRR 300
 |||||||
 DB 241 LGRRCFEARICACGRDKADEDSIRKQOVSSTKNGDGTGRPRPRONTGHIOMTSIKRR 300
 |||||||
 OY 241 LGRRCFEARICACGRDKADEDSIRKQOVSSTKNGDGTGRPRPRONTGHIOMTSIKRR 300
 |||||||
 DB 241 LGRRCFEARICACGRDKADEDSIRKQOVSSTKNGDGTGRPRPRONTGHIOMTSIKRR 300
 |||||||
 OY 301 SPDELLYLPRKGETYEMLIKIKESLELMQYLPQHTIETRYROOQOOHHLQKQTSIQ 360
 |||||||
 DB 301 SPDELLYLPRKGETYEMLIKIKESLELMQYLPQHTIETRYROOQOOHHLQKQTSIQ 360
 |||||||
 OY 301 SPDELLYLPRKGETYEMLIKIKESLELMQYLPQHTIETRYROOQOOHHLQKQTSIQ 360
 |||||||
 DB 301 SPDELLYLPRKGETYEMLIKIKESLELMQYLPQHTIETRYROOQOOHHLQKQTSIQ 360
 |||||||
 OY 361 SPSSYGNSPPLNKMNSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
 |||||||
 DB 361 SPSSYGNSPPLNKMNSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
 |||||||
 OY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIVSFARLGGSSCLDYFTTQGLTTIY 480
 |||||||
 DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIVSFARLGGSSCLDYFTTQGLTTIY 480
 |||||||
 OY 481 QIEHYSMDLALSLKIPROFRAIKGILDHROLHEFSSPHLRTPPSSASTVSGSSETR 540
 |||||||

Db 481 QIEHYSMDLASLKIPEQFRHAIWKGIIDHRLHEFSSPSHLRPPSSASTVSGSSETR 540
OY 541 GERVIDAVFTLRKOTISPPREMDNFMDARRNKQORIKEGE 586
Db 541 GERVIDAVFTLRKOTISPPREMDNFMDARRNKQORIKEGE 586

RESULT 3

ID 075080 PRELIMINARY; PRT: 586 AA.
AC 075080;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE P73H.
GN P73H.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98369596; PubMed-9703973;
RA Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,
Tanaka T., Shinkai Y., Kato H.;
RT "A second p53-related protein, p73L, with high homology to p73.";
RT Biochem. Biophys. Res. Commun. 248:603-607(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AB010153; BAA32433.1; -;
DR HSSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRODOM: PD002681; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 586 AA; 65734 MW; 9DC102AB57120C0F CRC64;

Query Match 99.5%; Score 3087; DB 4; Length 586;
Best Local Similarity 99.5%; Pred. No. 4, 1e-255;
Matches 583; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MYLENNMOTQSEFOYTNLGLNSMDQIQNGSSSTSYNTDHAONSTYASPTAOPSS 60
Db 1 MYLENNMOTQSEFOYTNLGLNSMDQIQNGSSSTSYNTDHAONSTYASPTAOPSS 60
OY 61 TFDALSPSPALPSNTDYGPHSFDVSPFOSSSTAKSATWTYSELKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNTDYGPHSFDVSPFOSSSTAKSATWTYSELKLYCQIAKTCPIQIK 120
OY 121 VMTPPQGAIVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
OY 181 YVEDDITIGROSIVLYEPPOVTEFTTYLYNFMCSNCCYGGNNRRPILITVLETRDQV 240
Db 181 YVEDDITIGROSIVLYEPPOVTEFTTYLYNFMCSNCCYGGNNRRPILITVLETRDQV 240
OY 241 IGRREFEIRICACPRDRKADSDIRKOOVSDSTKNGDGTKPRFONFHGIDMTSTKKRR 300
Db 241 IGRREFEIRICACPRDRKADSDIRKOOVSDSTKNGDGTKPRFONFHGIDMTSTKKRR 300
OY 301 SPDELLLYLVYRGRETYEMLTIKESLELMQYLPQHTIETTYRQOQOQHLLQKQTSIQ 360
Db 301 SPDELLLYLVYRGRETYEMLTIKESLELMQYLPQHTIETTYRQOQOQHLLQKQTSIQ 360
OY 361 SSSSYGNSSPPLTNKNSMKNLPSVSQILNPOORNALPTTTPDGGAGNIPMGTHMPAG 420
Db 361 SSSSYGNSSPPLTNKNSMKNLPSVSQILNPOORNALPTTTPDGGAGNIPMGTHMPAG 420

OY 421 DNKGLSPQALPPLSPMSTSHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTITY 480
Db 421 DNKGLSPQALPPLSPMSTSHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTITY 480
OY 481 QIEHYSMDLASLKIPEQFRHAIWKGIIDHRLHEFSSPSHLRPPSSASTVSGSSETR 540
Db 481 QIEHYSMDLASLKIPEQFRHAIWKGIIDHRLHEFSSPSHLRPPSSASTVSGSSETR 540
OY 541 GERVIDAVFTLRKOTISPPREMDNFMDARRNKQORIKEGE 586
Db 541 GERVIDAVFTLRKOTISPPREMDNFMDARRNKQORIKEGE 586

RESULT 4

ID 089097 PRELIMINARY; PRT: 586 AA.
AC 089097;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE DN p63 alpha.
GN TRP63 OR P73H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98448095; PubMed-9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
Caput D., McKoon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RT Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE-98369596; PubMed-9703973;
RA Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,
Tanaka T., Shinkai Y., Kato H.;
RT "A second p53-related protein, p73L, with high homology to p73.";
RT Biochem. Biophys. Res. Commun. 248:603-607(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF075439; AAC62644.1; -;
DR EMBL: AB010152; BAA32432.1; -;
DR HSSP: P04637; 1YCS.
DR MGD: MGI:1330810; Trp63.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 586 AA; 65789 MW; 622E24085B8BCB7 CRC64;

Query Match 98.8%; Score 3066; DB 11; Length 586;
Best Local Similarity 98.5%; Pred. No. 2, 6e-253;
Matches 577; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 MYLENNMOTQSEFOYTNLGLNSMDQIQNGSSSTSYNTDHAONSTYASPTAOPSS 60
Db 1 MYLENNMOTQSEFOYTNLGLNSMDQIQNGSSSTSYNTDHAONSTYASPTAOPSS 60
OY 61 TFDALSPSPALPSNTDYGPHSFDVSPFOSSSTAKSATWTYSELKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNTDYGPHSFDVSPFOSSSTAKSATWTYSELKLYCQIAKTCPIQIK 120
OY 121 VMTPPQGAIVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180

QY 181 YVEDPITGRQSVLPVPEPVGTEFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETDRGOV 240
DB 181 YVEDPITGRQSVLPVPEPVGTEFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETDRGOV 240
QY 241 LGRRCFARICACGRRKAKDEDSIRKQOVSSTKNGDGTGRRPRONTHTGIQMTSIRKRR 300
DB 241 LGRRCFARICACGRRKAKDEDSIRKQOVSSTKNGDGTGRRPRONTHTGIQMTSIRKRR 300
QY 301 SPDELLYLPRVGRRETEMLKIKESLELMQYLPQHTIEFYRQOQOQHLLQKOTSIO 360
DB 301 SPDELLYLPRVGRRETEMLKIKESLELMQYLPQHTIEFYRQOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLNKMNSMKNLPSVSQILNPOORNALPTPTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLNKMNSMKNLPSVSQILNPOORNALPTPTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSMPSSTHCTPPPYPTDCSIVSFARLGCSSCLDFTTQGLTTTY 480
DB 421 DMNGLSPTQALPPLSMPSSTHCTPPPYPTDCSIVSFARLGCSSCLDFTTQGLTTTY 480
QY 481 QIEHYSMDDLASLKIPEQFRHAIWKGLDHRQLHEFSPSHLRTPPSASTVSQSSSETR 540
DB 481 QIEHYSMDDLASLKIPEQFRHAIWKGLDHRQLHEFSPSHLRTPPSASTVSQSSSETR 540
QY 541 GERVIDAVRFTLRQTISSPPRDEWDFNFDMDARRNKQOIRKEGE 586
DB 541 GERVIDAVRFTLRQTISSPPRDEWDFNFDMDARRNKQOIRKEGE 586

RESULT 5

Q99J2 PRELIMINARY; PRT; 586 AA.
ID 099J2
AC 099J2;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE DN KER alpha protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KER/p63 splice
variants";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AJ277447; CAC37099.1; -
DR HSSP; P04637; ICSC.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SMO0454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 586 AA; 65732 MW; 78AB8C4F52BA743 CRC64;

Query Match 98.5%; Score 3057; DB 11; Length 586;
Best Local Similarity 98.1%; Pred. No. 1.5e-252;
Matches 575; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 MYLENNAGQFSEPOYTINGLNLSMDQIQNGSSSTSPYNTDAQNSVYAPSPYAPSS 60
DB 1 MYLENNAGQFSEPOYTINGLNLSMDQIQNGSSSTSPYNTDAQNSVYAPSPYAPSS 60

QY 61 TFDALSPSPALPSNTDYPGSHSEDFVSFOQSSSTAKSATWTYSTELKLYCOIANTCPIQK 120
DB 61 TFDALSPSPALPSNTDYPGSHSEDFVSFOQSSSTAKSATWTYSTELKLYCOIANTCPIQK 120
QY 121 VMPPPGAVIRAMPYKKAHEVYKRCPNHELSSEFNEGQIAPSHLIRREGNSHAQ 180
DB 121 VMPPPGAVIRAMPYKKAHEVYKRCPNHELSSEFNEGQIAPSHLIRREGNSHAQ 180
QY 181 YVEDPITGRQSVLPVPEPVGTEFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETDRGOV 240
DB 181 YVEDPITGRQSVLPVPEPVGTEFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETDRGOV 240
QY 241 LGRRCFARICACGRRKAKDEDSIRKQOVSSTKNGDGTGRRPRONTHTGIQMTSIRKRR 300
DB 241 LGRRCFARICACGRRKAKDEDSIRKQOVSSTKNGDGTGRRPRONTHTGIQMTSIRKRR 300
QY 301 SPDELLYLPRVGRRETEMLKIKESLELMQYLPQHTIEFYRQOQOQHLLQKOTSIO 360
DB 301 SPDELLYLPRVGRRETEMLKIKESLELMQYLPQHTIEFYRQOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLNKMNSMKNLPSVSQILNPOORNALPTPTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLNKMNSMKNLPSVSQILNPOORNALPTPTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSMPSSTHCTPPPYPTDCSIVSFARLGCSSCLDFTTQGLTTTY 480
DB 421 DMNGLSPTQALPPLSMPSSTHCTPPPYPTDCSIVSFARLGCSSCLDFTTQGLTTTY 480
QY 481 QIEHYSMDDLASLKIPEQFRHAIWKGLDHRQLHEFSPSHLRTPPSASTVSQSSSETR 540
DB 481 QIEHYSMDDLASLKIPEQFRHAIWKGLDHRQLHEFSPSHLRTPPSASTVSQSSSETR 540
QY 541 GERVIDAVRFTLRQTISSPPRDEWDFNFDMDARRNKQOIRKEGE 586
DB 541 GERVIDAVRFTLRQTISSPPRDEWDFNFDMDARRNKQOIRKEGE 586

RESULT 6

Q9H3D4 PRELIMINARY; PRT; 680 AA.
ID Q9H3D4
AC Q9H3D4; Q9UP28;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE TA p63 alpha (Tumor protein p63).
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kadhad M., Wang Y., Gillett E., Fleming M.D., Dotach V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph.
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF124539; AAG45607.1; -
DR EMBL; AF124528; AAG45607.1; JOINED.
DR EMBL; AF124529; AAG45607.1; JOINED.
DR EMBL; AF124531; AAG45607.1; JOINED.

DR EMBL: AF124532; AAG45607.1; JOINED.
 DR EMBL: AF124533; AAG45607.1; JOINED.
 DR EMBL: AF124534; AAG45607.1; JOINED.
 DR EMBL: AF124535; AAG45607.1; JOINED.
 DR EMBL: AF124536; AAG45607.1; JOINED.
 DR EMBL: AF124537; AAG45607.1; JOINED.
 DR EMBL: AF124538; AAG45607.1; JOINED.
 DR EMBL: AF075430; AAC62635.1; JOINED.
 DR EMBL: BC039815; AAH39815.1; -.
 DR HSP: P04637; IYCS.
 DR Genew; HGNC:15979; TP63.
 DR InterPro; IPR002117; P53.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR SMART; SM0054; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 DR Nuclear protein.
 SQ SEQUENCE 680 AA; 76785 MW; F66BCD45E87D9799 CRC64;

Query Match 97.7%; Score 3033; DB 4; Length 680;
 Best Local Similarity 100.0%; Pred. No. 2,1e-250;
 Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSPSTFDALSPSPAIPSN 74
 DB 109 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSPSTFDALSPSPAIPSN 168
 QY 75 TDYPGHSPDVSVFOQSSSTAKSATWTYSTELKLYCOIATCPDIQIKVMPPPGAVIRAM 134
 DB 169 TDYPGHSPDVSVFOQSSSTAKSATWTYSTELKLYCOIATCPDIQIKVMPPPGAVIRAM 228
 QY 135 PYYKKAHEVTEVVKRCPNHLSREFNEGOIAPSHLIRVEGNSHAQYVEDPTIGRSVLY 194
 DB 229 PYYKKAHEVTEVVKRCPNHLSREFNEGOIAPSHLIRVEGNSHAQYVEDPTIGRSVLY 288
 QY 195 PYEPPOVGTETFTVLYNFMCNSSCVGAMNRPDLITVLETRDGYLGRCEARICACP 254
 DB 289 PYEPPOVGTETFTVLYNFMCNSSCVGAMNRPDLITVLETRDGYLGRCEARICACP 348
 QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIOMTSIKRRSPDELLYLPVGR 314
 DB 349 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIOMTSIKRRSPDELLYLPVGR 408
 QY 315 EYTEMILKIKESLELMQYLPQHTIETYROOQOQHLLQKQTSIOSPSYGNSSPPLNK 374
 DB 409 EYTEMILKIKESLELMQYLPQHTIETYROOQOQHLLQKQTSIOSPSYGNSSPPLNK 468
 QY 375 MNSMNLPSVSQLINQORNALPTTIPGMGANIPMGTHMPMAGDMGLSPTOLAPP 434
 DB 469 MNSMNLPSVSQLINQORNALPTTIPGMGANIPMGTHMPMAGDMGLSPTOLAPP 528
 QY 435 LMPSTSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIHYSMNDLASLK 494
 DB 529 LMPSTSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIHYSMNDLASLK 588
 QY 495 IPEQFHAIWKGLDHRQLHEFSSPSHLIRPSASATVSGSSETRGEYIDAIVRTLLQ 554
 DB 589 IPEQFHAIWKGLDHRQLHEFSSPSHLIRPSASATVSGSSETRGEYIDAIVRTLLQ 648
 QY 555 TISFPREDMNFNDMARKNKOIRKEGE 586
 DB 649 TISFPREDMNFNDMARKNKOIRKEGE 680

RESULT 7
 075195
 ID 075195 PRELIMINARY; PRT; 641 AA.
 AC 075195;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, last annotation update)

DE P51 isoform TAP63ALPHA (P51B protein).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE=98324755; PubMed=9662378;
 RA Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katch I.,
 RA Ikawa Y., Nimura Y., Nakagawara A., Odinata M.,
 RT "Cloning and functional analysis of human p51, which structurally and
 RT functionally resembles p53.";
 RL Nat. Med. 4:839-844(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20388515; PubMed=10935472;
 RA Tanl M., Shimitzu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
 RA Yokota J.,
 RT "Mutation and expression of the p51 gene in human lung cancer.";
 RL Neoplasia 1:71-79(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AB016073; BAA32593.1; -.
 DR EMBL; AF116769; AAF43487.1; -.
 DR EMBL; AF116756; AAF43487.1; JOINED.
 DR EMBL; AF116757; AAF43487.1; JOINED.
 DR EMBL; AF116759; AAF43487.1; JOINED.
 DR EMBL; AF116760; AAF43487.1; JOINED.
 DR EMBL; AF116761; AAF43487.1; JOINED.
 DR EMBL; AF116762; AAF43487.1; JOINED.
 DR EMBL; AF116763; AAF43487.1; JOINED.
 DR EMBL; AF116764; AAF43487.1; JOINED.
 DR EMBL; AF116765; AAF43487.1; JOINED.
 DR EMBL; AF116766; AAF43487.1; JOINED.
 DR EMBL; AF116767; AAF43487.1; JOINED.
 DR EMBL; AF116768; AAF43487.1; JOINED.
 DR HSP: P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR SMART; SM0054; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 DR Nuclear protein.
 SQ SEQUENCE 641 AA; 72019 MW; 97AE61F66B63618 CRC64;

Query Match 97.6%; Score 3029; DB 4; Length 641;
 Best Local Similarity 99.8%; Pred. No. 4,2e-250;
 Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSPSTFDALSPSPAIPSN 74
 DB 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSPSTFDALSPSPAIPSN 129
 QY 75 TDYPGHSPDVSVFOQSSSTAKSATWTYSTELKLYCOIATCPDIQIKVMPPPGAVIRAM 134
 DB 130 TDYPGHSPDVSVFOQSSSTAKSATWTYSTELKLYCOIATCPDIQIKVMPPPGAVIRAM 189
 QY 135 PYYKKAHEVTEVVKRCPNHLSREFNEGOIAPSHLIRVEGNSHAQYVEDPTIGRSVLY 194
 DB 190 PYYKKAHEVTEVVKRCPNHLSREFNEGOIAPSHLIRVEGNSHAQYVEDPTIGRSVLY 249
 QY 195 PYEPPOVGTETFTVLYNFMCNSSCVGAMNRPDLITVLETRDGYLGRCEARICACP 254
 DB 250 PYEPPOVGTETFTVLYNFMCNSSCVGAMNRPDLITVLETRDGYLGRCEARICACP 309
 QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIOMTSIKRRSPDELLYLPVGR 314
 DB 310 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIOMTSIKRRSPDELLYLPVGR 369
 QY 315 EYTEMILKIKESLELMQYLPQHTIETYROOQOQHLLQKQTSIOSPSYGNSSPPLNK 374

Db 370 EYEMLKIKESLELMQYLPOHTIETRYROOOOHOHLKOTSIQSSSYGNSPPLNK 429
QY 375 MNSMNLKPSVSQILNPOORNLPTTIPDGGANIPMGTHMPAGDMNGLSPQALPP 434
Db 430 MNSMNLKPSVSQILNPOORNLPTTIPDGGANIPMGTHMPAGDMNGLSPQALPP 489
QY 435 LSPSTSHCTPPPPYPTDCISVSLFARLGCSSCLDYFTTQGLTIYQIEHYSMDLASLK 494
Db 490 LSPSTSHCTPPPPYPTDCISVSLFARLGCSSCLDYFTTQGLTIYQIEHYSMDLASLK 549
QY 495 IPEQFRAIWKGIIDHRQLHEFSSPSHLRTPSSASTVSGSSETRGERVIDAVFTLRQ 554
Db 550 IPEQFRAIWKGIIDHRQLHEFSSPSHLRTPSSASTVSGSSETRGERVIDAVFTLRQ 609
QY 555 TISFPPEMDNDFPMDDARRNKQORIKEGE 586
Db 610 TISFPPEMDNDFPMDDARRNKQORIKEGE 641

RESULT 8

09UE10 PRELIMINARY: PRT: 680 AA.

AC 09UE10
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE KEY protein.
GN KEY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle, and Keratinocytes;
RX MEDLINE=99018225; PubMed=9799841;
RA Augustin M., Bamberger C., Paul D., Schmale H.;
RT "Cloning and chromosomal mapping of the human p53-related KET gene to
RT chromosome 3q27 and its murine homolog Ket to mouse chromosome 16.";
RL Mamm. Genome 9:899-902(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: Y16961; CAAT6562.1; -.
DR HSSP: P04637; IYCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF008070; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76776 MW; 6548A6F218D852E CRC64;

Query Match 97.5%; Score 3025; DB 4; Length 680;
Best Local Similarity 99.8%; Pred. No. 1e-249;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PQTNLGLNLSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSSFTDALSPSPALPSN 74
Db 109 PQTNLGLNLSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSSFTDALSPSPALPSN 168
QY 75 TDYGPSPFDVSPFOOSSTAKSATWTSTELKKLYCOIAKTCPIQIKVTPPGQAVIRAM 134
Db 169 TDYGPSPFDVSPFOOSSTAKSATWTSTELKKLYCOIAKTCPIQIKVTPPGQAVIRAM 228
QY 135 PYTKAHVTEVYKRCNHELISREFNEGQIAPSPHLIRVEGNSHAQYVEDPITGRQSVLV 194
Db 229 PYTKAHVTEVYKRCNHELISREFNEGQIAPSPHLIRVEGNSHAQYVEDPITGRQSVLV 288
QY 195 PYEPQVGTETTYLYNFKCNSSCYVGNNRPILITVLETRDQVUGRCFEARICACP 254

Db 289 PYEPQVGTETTYLYNFKCNSSCYVGNNRPILITVLETRDQVUGRCFEARICACP 348
QY 255 GRDRKADSDSLRKOQVSDSTKNGDGTKPRPONTGHOITSIKKRNSPDDELLYLPVGR 314
Db 349 GRDRKADSDSLRKOQVSDSTKNGDGTKPRPONTGHOITSIKKRNSPDDELLYLPVGR 408
QY 315 EYEMLKIKESLELMQYLPOHTIETRYROOOOHOHLKOTSIQSSSYGNSPPLNK 374
Db 409 EYEMLKIKESLELMQYLPOHTIETRYROOOOHOHLKOTSIQSSSYGNSPPLNK 468
QY 375 MNSMNLKPSVSQILNPOORNLPTTIPDGGANIPMGTHMPAGDMNGLSPQALPP 434
Db 469 MNSMNLKPSVSQILNPOORNLPTTIPDGGANIPMGTHMPAGDMNGLSPQALPP 528
QY 435 LSPSTSHCTPPPPYPTDCISVSLFARLGCSSCLDYFTTQGLTIYQIEHYSMDLASLK 494
Db 529 LSPSTSHCTPPPPYPTDCISVSLFARLGCSSCLDYFTTQGLTIYQIEHYSMDLASLK 588
QY 495 IPEQFRAIWKGIIDHRQLHEFSSPSHLRTPSSASTVSGSSETRGERVIDAVFTLRQ 554
Db 589 IPEQFRAIWKGIIDHRQLHEFSSPSHLRTPSSASTVSGSSETRGERVIDAVFTLRQ 648
QY 555 TISFPPEMDNDFPMDDARRNKQORIKEGE 586
Db 649 TISFPPEMDNDFPMDDARRNKQORIKEGE 680

RESULT 9

088898 PRELIMINARY: PRT: 680 AA.

AC 088898
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Trp63.
GN Trp63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kagnad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF075436; AAC62641.1; -.
DR HSSP: P04637; IYCS.
DR MGD: MGI:1330810; Trp63.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF008070; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76788 MW; 8DF0284F247C68A CRC64;

Query Match 96.5%; Score 2995; DB 11; Length 680;
Best Local Similarity 98.4%; Pred. No. 3.7e-247;
Matches 563; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 15 PQTNLGLNLSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSSFTDALSPSPALPSN 74
Db 109 PQTNLGLNLSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSSFTDALSPSPALPSN 168
QY 75 TDYGPSPFDVSPFOOSSTAKSATWTSTELKKLYCOIAKTCPIQIKVTPPGQAVIRAM 134

```
DB      169 TDYPGHSHFDVFOOOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVIRAM 228
QY      135 PVYKKAHEHTEVYKRCPNHELISREFNEGOIAPPSHLIRVEGNSHAQYEDPTTGQSVLY 194
DB      229 PVYKKAHEHTEVYKRCPNHELISREFNEGOIAPPSHLIRVEGNSHAQYEDPTTGQSVLY 288
QY      195 PYEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILIIIVLETEDGOVLGRCEARICACP 254
DB      289 PYEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILIIIVLETEDGOVLGRCEARICACP 348
QY      255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSICKRRSPDDELLYLPVGR 314
DB      349 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSICKRRSPDDELLYLPVGR 408
QY      315 EYEMILKIKESLEIMQYLPQHTIETTYRQOQOQHLLQKOTSIOSSPSYGNSSPPLNK 374
DB      409 EYEMILKIKESLEIMQYLPQHTIETTYRQOQOQHLLQKOTSIOSSPSYGNSSPPLNK 468
QY      375 NMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
DB      469 NMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 528
QY      435 LSMSTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTITTYOIEHYSMDLASIK 494
DB      529 LSMSTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTITTYOIEHYSMDLASIK 588
QY      495 IPEOFRRHAIWKILDHROLHEFSSPHILRTSSASTVSGSSETRGERVIDAVRFTLQ 554
DB      589 IPEOFRRHAIWKILDHROLHEFSSPHILRTSSASTVSGSSETRGERVIDAVRFTLQ 648
QY      555 TISPPRDEWMDNFMDARNRKQORIKEGE 586
DB      649 TISPPRDEWMDNFMDARNRKQORIKEGE 680

RESULT 10
Q99JTE3 PRELIMINARY: PRT: 663 AA.
AC 099JTE3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE TAI KET alpha protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Wistar: TISSUE-Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C.; Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
RT variants."
RT FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DB EMBL: AJ277446; CAC37098.1; -.
DB HSSP: P04637; IYCS.
DB InterPro: IPR002117; P53.
DB InterPro: IPR001660; SAM.
DB Pfam: PF00870; P53; 1.
DB PRINTS: PR00386; P53SUPPRESSR.
DB PRODom: PD002681; P53; 1.
DB SMART: SM00454; SAM; 1.
DB PROSITE: PS00348; P53; 1.
DB Nuclear protein.
SQ SEQUENCE 663 AA: 74660 MW: C953BBA6C389D5B70 CRC64;

Query Match 96.4%; Score 2991; DB 11; Length 663;
Best Local Similarity 98.3%; Pred. No. 7,8e-247;
Matches 562; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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QY      15 POTNLGLINSMDOOLIONGSSSTSPYNTDHAONVTAAPSPASTPDALSPPAISN 74
DB      92 POTNLGLINSMDOOLIONGSSSTSPYNTDHAONVTAAPSPASTPDALSPPAISN 151
QY      75 TDYPGHSHFDVFOOOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVIRAM 134
DB      152 TDYPGHSHFDVFOOOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVIRAM 211
QY      135 PVYKKAHEHTEVYKRCPNHELISREFNEGOIAPPSHLIRVEGNSHAQYEDPTTGQSVLY 194
DB      212 PVYKKAHEHTEVYKRCPNHELISREFNEGOIAPPSHLIRVEGNSHAQYEDPTTGQSVLY 271
QY      195 PYEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILIIIVLETEDGOVLGRCEARICACP 254
DB      272 PYEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILIIIVLETEDGOVLGRCEARICACP 331
QY      255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSICKRRSPDDELLYLPVGR 314
DB      332 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSICKRRSPDDELLYLPVGR 391
QY      315 EYEMILKIKESLEIMQYLPQHTIETTYRQOQOQHLLQKOTSIOSSPSYGNSSPPLNK 374
DB      392 EYEMILKIKESLEIMQYLPQHTIETTYRQOQOQHLLQKOTSIOSSPSYGNSSPPLNK 451
QY      375 NMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
DB      452 NMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 511
QY      435 LSMSTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTITTYOIEHYSMDLASIK 494
DB      512 LSMSTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTITTYOIEHYSMDLASIK 571
QY      495 IPEOFRRHAIWKILDHROLHEFSSPHILRTSSASTVSGSSETRGERVIDAVRFTLQ 554
DB      572 IPEOFRRHAIWKILDHROLHEFSSPHILRTSSASTVSGSSETRGERVIDAVRFTLQ 631
QY      555 TISPPRDEWMDNFMDARNRKQORIKEGE 586
DB      632 TISPPRDEWMDNFMDARNRKQORIKEGE 663

RESULT 11
Q99JTE6 PRELIMINARY: PRT: 680 AA.
AC 099JTE6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE TAI KET alpha.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Lingual epithelium;
RX MEDLINE=97460723; PubMed=9315105;
RA Schmale H.; Bamberger C.;
RT "A novel protein with strong homology to the tumor suppressor p53."
RT Oncogene 15:1363-1367(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Lingual epithelium;
RA Schmale H.;
RT Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DB EMBL: Y10258; CAB88216.1; -.
DB HSSP: P04637; IYCS.
DB InterPro: IPR002117; P53.
DB InterPro: IPR001660; SAM.
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DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 680 AA; 76760 MW; AC45DAB88F61400 CRC64;
 Query Match 96.4%; Score 2991; DB 11; Length 680;
 Best Local Similarity 98.3%; Pred. No. 8,1e-247;
 Matches 562; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPDSSFDALSPSPALPSN 74
 DB PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPDSSFDALSPSPALPSN 168
 QY 75 TDYGPSPFVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIKWTTPPGCAVIRAM 134
 DB TDYGPSPFVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIKWTTPPGCAVIRAM 228
 QY 135 PVYKKAHYTEVYKRCNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
 DB PVYKKAHYTEVYKRCNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 288
 QY 229 PVYKKAHYTEVYKRCNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 288
 DB PVYKKAHYTEVYKRCNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 348
 QY 195 PYEPPOVGETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQOVLGRRCFEARICAC 254
 DB PYEPPOVGETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQOVLGRRCFEARICAC 348
 QY 289 PYEPPOVGETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQOVLGRRCFEARICAC 348
 DB PYEPPOVGETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQOVLGRRCFEARICAC 314
 QY 255 GRDRAEDSIRKQOVSASTKRGDGTGRPRONTGHIOMTSIKRRSPDDELTLVPRGR 314
 DB GRDRAEDSIRKQOVSASTKRGDGTGRPRONTGHIOMTSIKRRSPDDELTLVPRGR 408
 QY 349 GRDRAEDSIRKQOVSASTKRGDGTGRPRONTGHIOMTSIKRRSPDDELTLVPRGR 408
 DB GRDRAEDSIRKQOVSASTKRGDGTGRPRONTGHIOMTSIKRRSPDDELTLVPRGR 374
 QY 315 EYEMMLIKESLELMQYLPQHTIETRYROOQOHOHLQKQTSIQSPSSVGNSSPPLNK 374
 DB EYEMMLIKESLELMQYLPQHTIETRYROOQOHOHLQKQTSIQSPSSVGNSSPPLNK 468
 QY 409 EYEMMLIKESLELMQYLPQHTIETRYROOQOHOHLQKQTSIQSPSSVGNSSPPLNK 468
 DB EYEMMLIKESLELMQYLPQHTIETRYROOQOHOHLQKQTSIQSPSSVGNSSPPLNK 434
 QY 375 MNSMKNKLPVSQOLNPOORNALPTTIPDGGANIPMAGTHMPAGMNGSLPQALPPR 434
 DB MNSMKNKLPVSQOLNPOORNALPTTIPDGGANIPMAGTHMPAGMNGSLPQALPPR 528
 QY 469 MNSMKNKLPVSQOLNPOORNALPTTIPDGGANIPMAGTHMPAGMNGSLPQALPPR 528
 DB MNSMKNKLPVSQOLNPOORNALPTTIPDGGANIPMAGTHMPAGMNGSLPQALPPR 494
 QY 435 LSMSTSHCTPPPPYPTDCSIVSFILARLGSSCLDYFTTQGLTIYQIEHYSMDLASLK 494
 DB LSMSTSHCTPPPPYPTDCSIVSFILARLGSSCLDYFTTQGLTIYQIEHYSMDLASLK 588
 QY 529 LSMSTSHCTPPPPYPTDCSIVSFILARLGSSCLDYFTTQGLTIYQIEHYSMDLASLK 588
 DB LSMSTSHCTPPPPYPTDCSIVSFILARLGSSCLDYFTTQGLTIYQIEHYSMDLASLK 554
 QY 495 IPEOFRAIWKGLDHRQLHEFSSPSHLRTSSASTVSVSSSTREGRVDAVFTLRQ 554
 DB IPEOFRAIWKGLDHRQLHEFSSPSHLRTSSASTVSVSSSTREGRVDAVFTLRQ 648
 QY 589 IPEOFRAIWKGLDHRQLHEFSSPSHLRTSSASTVSVSSSTREGRVDAVFTLRQ 648
 DB IPEOFRAIWKGLDHRQLHEFSSPSHLRTSSASTVSVSSSTREGRVDAVFTLRQ 586
 QY 555 TISPPRDENWDFMDARNNKQRIKEGE 586
 DB TISPPRDENWDFMDARNNKQRIKEGE 680
 QY 649 TISPPRDENWDFMDARNNKQRIKEGE 680
 DB TISPPRDENWDFMDARNNKQRIKEGE 680
 RESULT 12
 Q9DEC7 PRELIMINARY; PRT; 582 AA.
 AC Q9DEC7;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE DN p63 alpha.
 GN DNF63A.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP MEDLINE FROM N.A.
 RX MEDLINE-20568966; PubMed-11118893;
 RA Yasue A., Tao H., Nohno T., Moriyama K., Noji S., Ohuchi H.:
 RT "Cloning and expression of a chick p63 gene".
 RL Mech. Dev. 100:105-108(2001).

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AB045224; BAB20631.1; -.
 DR HSSP; P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 582 AA; 65213 MW; 9D1C356B99CAEC3 CRC64;
 Query Match 95.4%; Score 2962; DB 13; Length 582;
 Best Local Similarity 95.6%; Pred. No. 2e-244;
 Matches 560; Conservative 9; Mismatches 13; Indels 4; Gaps 1;
 QY 1 MLYENNAQGFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPDSS 60
 DB MLYENNAQGFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPDSS 60
 QY 61 TFDALSSPAIPSTNDYPGHSHSPVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 DB TFDALSSPAIPSTNDYPGHSHSPVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 QY 61 TFDALSSPAIPSTNDYPGHSHSPVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 DB TFDALSSPAIPSTNDYPGHSHSPVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 180
 QY 121 VMPPPGCAVIRAMPYKKAHYTEVYKRCNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
 DB VMPPPGCAVIRAMPYKKAHYTEVYKRCNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
 QY 121 VMPPPGCAVIRAMPYKKAHYTEVYKRCNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
 DB VMPPPGCAVIRAMPYKKAHYTEVYKRCNHELSEFNEGQIAPPSHLIRVEGNSHAQ 240
 QY 181 YVEDPITGRQSVLVYEPPOVGETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQOVL 240
 DB YVEDPITGRQSVLVYEPPOVGETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQOVL 240
 QY 181 YVEDPITGRQSVLVYEPPOVGETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQOVL 240
 DB YVEDPITGRQSVLVYEPPOVGETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQOVL 300
 QY 241 IGRRCFEARICACGRRAKDEDSIRKQOVSASTKRGDGTGRPRONTGHIOMTSIKRR 300
 DB IGRRCFEARICACGRRAKDEDSIRKQOVSASTKRGDGTGRPRONTGHIOMTSIKRR 256
 QY 241 IGRRCFEARICACGRRAKDEDSIRKQOVSASTKRGDGTGRPRONTGHIOMTSIKRR 256
 DB IGRRCFEARICACGRRAKDEDSIRKQOVSASTKRGDGTGRPRONTGHIOMTSIKRR 360
 QY 301 SPDELLYLPVGRHTEYEMMLIKESLELMQYLPQHTIETRYROOQOHOHLQKQTSIQ 360
 DB SPDELLYLPVGRHTEYEMMLIKESLELMQYLPQHTIETRYROOQOHOHLQKQTSIQ 356
 QY 297 SPDELLYLPVGRHTEYEMMLIKESLELMQYLPQHTIETRYROOQOHOHLQKQTSIQ 356
 DB SPDELLYLPVGRHTEYEMMLIKESLELMQYLPQHTIETRYROOQOHOHLQKQTSIQ 420
 QY 361 SPSSYGNSSPPLNKMNSMKNKLPVSQOLNPOORNALPTTIPDGGANIPMAGTHMPAG 420
 DB SPSSYGNSSPPLNKMNSMKNKLPVSQOLNPOORNALPTTIPDGGANIPMAGTHMPAG 416
 QY 357 SQSSYGNSSPPLNKMNSMKNKLPVSQOLNPOORNALPTTIPDGGANIPMAGTHMPAG 416
 DB SQSSYGNSSPPLNKMNSMKNKLPVSQOLNPOORNALPTTIPDGGANIPMAGTHMPAG 480
 QY 421 DMNGLSTQALPPLSMPTSHCTPPPPYPTDCSIVSFILARLGSSCLDYFTTQGLTIY 480
 DB DMNGLSTQALPPLSMPTSHCTPPPPYPTDCSIVSFILARLGSSCLDYFTTQGLTIY 476
 QY 417 DMNGLSTQALPPLSMPTSHCTPPPPYPTDCSIVSFILARLGSSCLDYFTTQGLTIY 476
 DB DMNGLSTQALPPLSMPTSHCTPPPPYPTDCSIVSFILARLGSSCLDYFTTQGLTIY 540
 QY 481 QIEHYSMDLASLKIPQOFRAIWKGLDHRQLHEFSSPSHLRTSSASTVSVSSSETR 540
 DB QIEHYSMDLASLKIPQOFRAIWKGLDHRQLHEFSSPSHLRTSSASTVSVSSSETR 536
 QY 477 HIEHYSMDLASLKIPQOFRAIWKGLDHRQLHEFSSPSHLRTSSASTVSVSSSETR 536
 DB HIEHYSMDLASLKIPQOFRAIWKGLDHRQLHEFSSPSHLRTSSASTVSVSSSETR 586
 QY 541 GERVIDAVFTLRQTIISPPRDENWDFMDARNNKQRIKEGE 586
 DB GERVIDAVFTLRQTIISPPRDENWDFMDARNNKQRIKEGE 582
 QY 537 GERVIDAVFTLRQTIISPPRDENWDFMDARNNKQRIKEGE 582
 DB GERVIDAVFTLRQTIISPPRDENWDFMDARNNKQRIKEGE 582
 RESULT 13
 Q9H3P8 PRELIMINARY; PRT; 501 AA.
 AC Q9H3P8;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Delta N p73L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE FROM N.A.
 RX MEDLINE-20568966; PubMed-11118893;
 RA Yasue A., Tao H., Nohno T., Moriyama K., Noji S., Ohuchi H.:
 RT "Cloning and expression of a chick p63 gene".
 RL Mech. Dev. 100:105-108(2001).

RA Senoo M., Tsuchiya I., Matsumura Y., Mori T., Saito Y., Kato H.,
 RA Okamoto T., Habu S.;
 RT "Transcriptional dysregulation of the p73L/p63/p51/p40/KMT gene in
 RT human squamous cell carcinomas - Expression of delta N p73L, a novel
 RT dominant negative isoform, and loss of expression of a potential tumor
 RT suppressor p51-";
 CC Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL: AB042841; BAB20591.1; -.
 DR HSSP: P04637; 1YCS.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 DR Nucleic protein.
 SQ SEQUENCE 501 AA; 56749 MW; 31E1BEA3CA305B88 CRC64;

Query Match 83.8%; Score 2601.5; DB 4; Length 501;
 Best Local Similarity 85.5%; Pred. No. 1e-213;
 Matches 501; Conservative 0; Mismatches 0; Indels 85; Gaps 1;

OY 1 MLYLENNMOTQFSEPOQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 DB 1 MLYLENNMOTQFSE----- 14
 OY 61 TFDALSPSPALPNSNDYDGPSPFDVSPFOSSSTAKSATWTYSTELKKLYCQIAKTPQIQK 120
 DB 15 -----YSTELKKLYCQIAKTPQIQK 35
 OY 121 VMTPPQGAIVIRAMPYVYKKAHVTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 180
 DB 36 VMTPPQGAIVIRAMPYVYKKAHVTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 95
 OY 181 YVEDPITGRQSVLYVEEPQVGTETFTVLYNFMNCSSCYGNNRRPILITVLETRDQV 240
 DB 96 YVEDPITGRQSVLYVEEPQVGTETFTVLYNFMNCSSCYGNNRRPILITVLETRDQV 155
 OY 241 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGDGTKRPFQONTHGIDMTSIRKKR 300
 DB 156 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGDGTKRPFQONTHGIDMTSIRKKR 215
 OY 301 SPDDLLLYLPVGRGRTYEMLKIKESLELMQYLPQHTIETYROQOQOQHLLQKOTSIO 360
 DB 216 SPDDLLLYLPVGRGRTYEMLKIKESLELMQYLPQHTIETYROQOQOQHLLQKOTSIO 275
 OY 361 SPSSYGNSPPLNKNKNSNKLPSVSQILNPOORNALPTTIPDGGANIPMGTHMPAG 420
 DB 276 SPSSYGNSPPLNKNKNSNKLPSVSQILNPOORNALPTTIPDGGANIPMGTHMPAG 335
 OY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIVSEFLARLGSSCLDYFTTQGLTIIY 480
 DB 336 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIVSEFLARLGSSCLDYFTTQGLTIIY 395
 OY 481 QIEHNSMDLASLKTPEQFRRAIKGIIDHRLHEFSSPSHLIRPPSSASIVSSSETR 540
 DB 396 QIEHNSMDLASLKTPEQFRRAIKGIIDHRLHEFSSPSHLIRPPSSASIVSSSETR 455
 OY 541 GERVIDAVRFTLROTIISFPPEDEMDNFMDARANKOORTKEE 586
 DB 456 GERVIDAVRFTLROTIISFPPEDEMDNFMDARANKOORTKEE 501

RESULT 14
 O9P1B5 PRELIMINARY: PRT: 461 AA.
 AC O9P1B5:
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)

DE P51 isoform delNbeta.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2038515; PubMed=10935472;
 RA Tanai M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
 RA Yokota J.;
 RT "Mutation and expression of the p51 gene in human lung cancer.";
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL: AF116769; AAF43492.1; JOINED.
 DR EMBL: AF116768; AAF43492.1; JOINED.
 DR EMBL: AF116759; AAF43492.1; JOINED.
 DR EMBL: AF116760; AAF43492.1; JOINED.
 DR EMBL: AF116761; AAF43492.1; JOINED.
 DR EMBL: AF116762; AAF43492.1; JOINED.
 DR EMBL: AF116763; AAF43492.1; JOINED.
 DR EMBL: AF116764; AAF43492.1; JOINED.
 DR EMBL: AF116765; AAF43492.1; JOINED.
 DR EMBL: AF116766; AAF43492.1; JOINED.
 DR EMBL: AF116767; AAF43492.1; JOINED.
 DR HSSP: P04637; 1YCS.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR PROSITE: PS00348; P53; 1.
 DR Nucleic protein.
 SQ SEQUENCE 461 AA; 51305 MW; 68B63547B81C1B05 CRC64;

Query Match 78.0%; Score 2421; DB 4; Length 461;
 Best Local Similarity 100.0%; Pred. No. 2.5e-198;
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLYLENNMOTQFSEPOQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 DB 1 MLYLENNMOTQFSEPOQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 OY 61 TFDALSPSPALPNSNDYDGPSPFDVSPFOSSSTAKSATWTYSTELKKLYCQIAKTPQIQK 120
 DB 61 TFDALSPSPALPNSNDYDGPSPFDVSPFOSSSTAKSATWTYSTELKKLYCQIAKTPQIQK 120
 OY 121 VMTPPQGAIVIRAMPYVYKKAHVTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPPQGAIVIRAMPYVYKKAHVTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 180
 OY 181 YVEDPITGRQSVLYVEEPQVGTETFTVLYNFMNCSSCYGNNRRPILITVLETRDQV 240
 DB 181 YVEDPITGRQSVLYVEEPQVGTETFTVLYNFMNCSSCYGNNRRPILITVLETRDQV 240
 OY 241 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGDGTKRPFQONTHGIDMTSIRKKR 300
 DB 241 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGDGTKRPFQONTHGIDMTSIRKKR 300
 OY 301 SPDDLLLYLPVGRGRTYEMLKIKESLELMQYLPQHTIETYROQOQOQHLLQKOTSIO 360
 DB 301 SPDDLLLYLPVGRGRTYEMLKIKESLELMQYLPQHTIETYROQOQOQHLLQKOTSIO 360
 OY 361 SPSSYGNSPPLNKNKNSNKLPSVSQILNPOORNALPTTIPDGGANIPMGTHMPAG 420
 DB 361 SPSSYGNSPPLNKNKNSNKLPSVSQILNPOORNALPTTIPDGGANIPMGTHMPAG 420
 OY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456
 DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456

RESULT 15
 O9UP26

ID Q9UP26 PRELIMINARY; PRT: 461 AA.
AC Q9UP26;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE DN P63 beta.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Haglwaara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF075433; AAC62638.1; -.
DR EMBL: AF124539; AAG45611.1; JOINED.
DR EMBL: AF124530; AAG45611.1; JOINED.
DR EMBL: AF124531; AAG45611.1; JOINED.
DR EMBL: AF124532; AAG45611.1; JOINED.
DR EMBL: AF124533; AAG45611.1; JOINED.
DR EMBL: AF124534; AAG45611.1; JOINED.
DR EMBL: AF124535; AAG45611.1; JOINED.
DR EMBL: AF124536; AAG45611.1; JOINED.
DR EMBL: AF124537; AAG45611.1; JOINED.
DR HSSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51404 MW; 68B6347A46C1B05 CRC64;

Query Match 78.0%; Score 2421; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.5e-198;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db |||||
Qy 361 SPSSYGNSSPPLNKNMNSMKNLPVSQILNPOQRNALPTTIPDGMGNIIPMGTHMPMAG 420
Db 421 DMNGLSPTQALPPLPPLMPSSTSHCTPPPPPTDCSTV 456
Db 421 DMNGLSPTQALPPLPPLMPSSTSHCTPPPPPTDCSTV 456

Search completed: August 7, 2003, 09:51:41
Job time : 48.1494 secs

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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:31:28 ; Search time 31.7931 Seconds
(without alignments)
2301.535 Million cell updates/sec

Title: US-09-538-106-17

Perfect score: 2450

Sequence: 1 MLYLENNAQTFSEPOYTNL.....HCTPPPYPTDCSIVRIWQV 461

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_19Jun03:*

1: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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14: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2450	100.0	461	21	AA11362
2	2450	100.0	461	23	ABG95138
3	2450	100.0	461	23	ABP61914
4	2450	100.0	461	23	ABP74994
5	2443	99.7	461	23	ABG95131
6	2427	99.1	461	20	AA105963
7	2421	98.8	586	20	AA105956
8	2421	98.8	586	23	ABG95132
9	2421	98.8	586	23	ABG95140

10	2404	98.1	586	21	AA11357	Human p63 protein
11	2404	98.1	586	23	ABP61909	Human lung cancer
12	2404	98.1	586	23	ABP74989	Human p53 homologue
13	2398	97.9	586	20	AA105962	Mouse cell regulat
14	2397	97.8	586	20	AA141032	Human lung tumor a
15	2397	97.8	586	21	AA113117	Human lung cancer-
16	2397	97.8	586	23	ABP61869	Human lung cancer
17	2397	97.8	586	23	ABP74949	Human lung tumour
18	2379	97.1	516	20	AA105954	Human cell regulat
19	2379	97.1	516	21	AA113363	Human p63 protein
20	2379	97.1	516	23	ABG95141	Human oncogene p63
21	2379	97.1	516	23	ABP61915	Human lung cancer
22	2379	97.1	516	23	ABP74995	Human p53 homologue
23	2372	96.8	516	23	ABG95135	Human oncogene p51
24	2350	95.9	641	20	AA145247	Human p51 protein
25	2350	95.9	641	20	AA105953	Human cell regulat
26	2350	95.9	641	21	AA113358	Human p63 protein
27	2350	95.9	641	22	AA182129	Human protein #2 u
28	2350	95.9	641	23	ABG95128	Human oncogene p58
29	2350	95.9	641	23	ABG95136	Human oncogene p51
30	2350	95.9	641	23	ABG95142	Human oncogene p63
31	2350	95.9	641	23	ABP61910	Human lung cancer
32	2350	95.9	641	23	ABP74990	Human p53 homologue
33	2342	95.6	680	21	AA113361	Human p63 protein
34	2342	95.6	680	21	AA150997	Human KET protein.
35	2342	95.6	680	23	ABP61913	Human lung cancer
36	2342	95.6	680	23	ABP74993	Human p53 homologue
37	2327	95.0	680	20	AA105958	Human cell regulat
38	2323	94.8	680	21	AA150998	Human KET protein.
39	2148	87.7	416	23	ABG95130	Human oncogene p51
40	2077	84.8	471	23	ABG95129	Human oncogene p51
41	2077	84.8	471	23	ABG95134	Human oncogene p51
42	1884	76.9	393	20	AA105957	Human cell regulat
43	1884	76.9	393	23	ABG95133	Human oncogene p51
44	1884	76.9	393	23	ABG95139	Human oncogene p63
45	1872	76.4	356	20	AA143135	Human p40 protein

ALIGNMENTS

RESULT 1	AA11362	AA11362 standard; protein; 461 AA.
ID	AA11362	
AC	AA11362	
XX		
XX		
DT	21-FEB-2001	(first entry)
DE		Human p63 protein isoform #6.
XX		
XX		
KW		Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW		vacine; detection.
XX		
OS		Homo sapiens.
XX		
PN		W0200061612-A2.
XX		
PD		19-OCT-2000.
XX		
PF		03-APR-2000; 2000MO-US08896.
XX		
PR		02-APR-1999; 99US-0285479.
XX		
PR		17-DEC-1999; 99US-0466396.
XX		
PR		30-DEC-1999; 99US-0476496.
XX		
PR		10-JAN-2000; 2000US-0480884.
XX		
PR		22-FEB-2000; 2000US-0510376.
XX		
PA		(CORI-) CORIXA CORP.
XX		
XX		
PI		Wang T, Fan L;
XX		
DR		WPI; 2000-628399/60.

DR N-PSDB; AAC66032.
 XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
 PT protein is used for detecting and monitoring progression of lung cancer
 PT in a patient -
 XX
 PS Disclosure: Page 253-254; 261pp; English.
 XX
 CC This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.
 CC
 XX Sequence 461 AA;
 SQ
 Query Match 100.0%; Score 2450; DB 21; Length 461;
 Best Local Similarity 100.0%; Pred. No. 6.6e-195;
 Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 DB 1 MLYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 QY 61 TFDALSPSPALPSTWDYPGHSPDVSVFOQSSSTAKSAWTSTELKRLKYCIATCPYQIK 120
 DB 61 TFDALSPSPALPSTWDYPGHSPDVSVFOQSSSTAKSAWTSTELKRLKYCIATCPYQIK 120
 QY 121 VMTPPGAGAVIRAMPYVYKKAHEVYKRCPNHLSRENEGOIAPPSHLIRVGNSHAQ 180
 DB 121 VMTPPGAGAVIRAMPYVYKKAHEVYKRCPNHLSRENEGOIAPPSHLIRVGNSHAQ 180
 QY 181 YVEDPITGRQSVLYVPEPPVGTETTVLYNFMKNSSCVGMNRRPILITVLETRDGOV 240
 DB 181 YVEDPITGRQSVLYVPEPPVGTETTVLYNFMKNSSCVGMNRRPILITVLETRDGOV 240
 QY 241 LGRRCFARICACGRRKRADEDSIRKQVSDSTKNDGTRKPRRONTHTGQMTSIKRR 300
 DB 241 LGRRCFARICACGRRKRADEDSIRKQVSDSTKNDGTRKPRRONTHTGQMTSIKRR 300
 QY 301 SPDELLYLTVRGRETEYEMLIKESLELMQYLPQHTIETRYROQOQOQHLLQKTSIQ 360
 DB 301 SPDELLYLTVRGRETEYEMLIKESLELMQYLPQHTIETRYROQOQOQHLLQKTSIQ 360
 QY 361 SPSSYGNSSPPLNKMNSMNLPSYSQILNPOQRNALPTPTIPDGMGANIPMGTHMPMAG 420
 DB 361 SPSSYGNSSPPLNKMNSMNLPSYSQILNPOQRNALPTPTIPDGMGANIPMGTHMPMAG 420
 QY 421 DMNGLSPTQALPPLSMPTSHCPPPYPPDGSIVIMQY 461
 DB 421 DMNGLSPTQALPPLSMPTSHCPPPYPPDGSIVIMQY 461
 RESULT 2
 ID ABG95138 standard; Protein; 461 AA.
 AC ABG95138;
 DT 04-DEC-2002 (first entry)
 XX Human oncogene p63 isoform delta n p63 beta.
 XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW Proliferative disease; cellular protein isoform; heat shock protein 90;
 KM HSP-90; Rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;

KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX
 OS Homo sapiens.
 XX WO200269900-A2.
 PN 12-SEP-2002.
 PD 01-MAR-2002; 2002WO-US06518.
 XX 01-MAR-2001; 2001US-272751P.
 PR (CONF-) CONFORMA THERAPEUTICS CORP.
 PA Filtz LC, Burrows FJ;
 PI WPI; 2002-698710/75.
 DR N-PSDB; ABS73330.
 XX
 PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90
 PT.
 XX
 PS Disclosure: Page 342-344; 389pp; English.
 XX
 CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (i) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (ii) dependent on heat shock
 CC protein (HSP)-90, or selectively treating cells expressing (ii)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (ii). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.
 XX
 SQ Sequence 461 AA;
 Query Match 100.0%; Score 2450; DB 23; Length 461;
 Best Local Similarity 100.0%; Pred. No. 6.6e-195;
 Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 DB 1 MLYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 QY 61 TFDALSPSPALPSTWDYPGHSPDVSVFOQSSSTAKSAWTSTELKRLKYCIATCPYQIK 120
 DB 61 TFDALSPSPALPSTWDYPGHSPDVSVFOQSSSTAKSAWTSTELKRLKYCIATCPYQIK 120
 QY 121 VMTPPGAGAVIRAMPYVYKKAHEVYKRCPNHLSRENEGOIAPPSHLIRVGNSHAQ 180
 DB 121 VMTPPGAGAVIRAMPYVYKKAHEVYKRCPNHLSRENEGOIAPPSHLIRVGNSHAQ 180
 QY 181 YVEDPITGRQSVLYVPEPPVGTETTVLYNFMKNSSCVGMNRRPILITVLETRDGOV 240
 DB 181 YVEDPITGRQSVLYVPEPPVGTETTVLYNFMKNSSCVGMNRRPILITVLETRDGOV 240
 QY 241 LGRRCFARICACGRRKRADEDSIRKQVSDSTKNDGTRKPRRONTHTGQMTSIKRR 300

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DB 241 IGRCFEARIACPGDRKRADEDSIRKQOVSDSTKNGDGTFRPQNTHTGIQMTSIRKRR 300
QY 301 SPDDDELIVPVGRGRTYEMLLKIKESLELMQYLPQHTTETTRQOQOQOHOHLQKOTSIO 360
DB 301 SPDDDELIVPVGRGRTYEMLLKIKESLELMQYLPQHTTETTRQOQOQOHOHLQKOTSIO 360
QY 361 SPSSYGNSSPPLNKNKNSMKNKLPSVSQILNPOQRNALPTTIPDGGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLNKNKNSMKNKLPSVSQILNPOQRNALPTTIPDGGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPPTDCSIVRIQOV 461
DB 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPPTDCSIVRIQOV 461

```

RESULT 3

ABP61914
ID ABP61914 standard; Protein; 461 AA.

AC ABP61914;

XX 07-OCT-2002 (first entry)

DE Human lung cancer associated protein sequence SEQ ID NO:343.

XX Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.

OS Homo sapiens.

XX WO200247534-A2.

XX 20-JUN-2002.

XX 30-NOV-2001; 2001WO-US47576.

XX 12-DEC-2000; 2000US-0735705.

XX 07-MAY-2001; 2001US-0850716.

XX 28-JUN-2001; 2001US-0897778.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Durham MD, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;

XX WPI: 2002-583465/62.

XX N-PSDB; ABQ92437.

XX Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT by the polynucleotides, useful in pharmaceutical compositions such as
PT vaccines and as markers to indicate the presence of lung cancer
XX

PS Example 2; Page 333-334; 381pp; English.

XX The present invention describes isolated human lung carcinoma
CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC activity, and can be used in gene therapy and in vaccines. Compositions
CC comprising (I) or (II) can be used for stimulating an immune response in
CC a patient and for treating lung cancer in a patient. Oligonucleotides of
CC (I) can be used for detecting the presence of a cancer in a patient, by
CC obtaining a biological sample from the patient, contacting the
CC biological sample with the oligonucleotide, detecting in the sample, an
CC amount of polynucleotide that hybridises to the oligonucleotide and
CC comparing the amount of polynucleotide that hybridises to the
CC oligonucleotide to a predetermined cut-off value, and determining the
CC presence of a cancer in the patient. (I) and (II) are useful in
CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
CC indicate the presence or absence of a cancer such as lung cancer.
CC ABQ924145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used
CC in the exemplification of the present invention.

XX Sequence 461 AA;

Query Match 100.0%; Score 2450; DB 23; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.6e-195;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLYENNAQTOPSEPOQYTNGLINSMDOOIQNGSSSTSPYNTDHAQNSVTAPSPYADPS 60
DB 1 MLYENNAQTOPSEPOQYTNGLINSMDOOIQNGSSSTSPYNTDHAQNSVTAPSPYADPS 60
QY 61 TEDALSPSPALPNSNDYDQPHSFVDSFOQSSATAKATWTYSTELKKLYCOIAKTCPIQIK 120
DB 61 TEDALSPSPALPNSNDYDQPHSFVDSFOQSSATAKATWTYSTELKKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGVIRAMVYVYKAEHVTYVRCRPHHELHRENEGOIAPPSHLIVBENSHAQ 180
DB 121 VMTPPQGVIRAMVYVYKAEHVTYVRCRPHHELHRENEGOIAPPSHLIVBENSHAQ 180
QY 181 YVEDPITGRQSVLYVEPPQVTEFTTVLYNFMCSGCVGKRRPILITVLETRDCOV 240
DB 181 YVEDPITGRQSVLYVEPPQVTEFTTVLYNFMCSGCVGKRRPILITVLETRDCOV 240
QY 241 IGRCFEARIACPGDRKRADEDSIRKQOVSDSTKNGDGTFRPQNTHTGIQMTSIRKRR 300
DB 241 IGRCFEARIACPGDRKRADEDSIRKQOVSDSTKNGDGTFRPQNTHTGIQMTSIRKRR 300
QY 301 SPDDDELIVPVGRGRTYEMLLKIKESLELMQYLPQHTTETTRQOQOQOHOHLQKOTSIO 360
DB 301 SPDDDELIVPVGRGRTYEMLLKIKESLELMQYLPQHTTETTRQOQOQOHOHLQKOTSIO 360
QY 361 SPSSYGNSSPPLNKNKNSMKNKLPSVSQILNPOQRNALPTTIPDGGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLNKNKNSMKNKLPSVSQILNPOQRNALPTTIPDGGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPPTDCSIVRIQOV 461
DB 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPPTDCSIVRIQOV 461

```

RESULT 4

ABB74994
ID ABB74994 standard; Protein; 461 AA.

XX ABB74994;

XX 01-MAY-2002 (first entry)

XX Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:343.

XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;

XX Immune response.

XX Homo sapiens.

XX WO200200174-A2.

XX 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

XX 28-JUN-2000; 2000US-0606421.

XX 02-AUG-2000; 2000US-0630940.

XX 21-AUG-2000; 2000US-0643597.

XX 15-SEP-2000; 2000US-0662786.

XX 09-OCT-2000; 2000US-0685696.

XX 12-DEC-2000; 2000US-0735705.

XX 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;

XX McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;

XX Vedvick TS, Carter D, Watanabe Y, Peckham DW;

DR WPI: 2002-090513/12.
 DR N-PSDB: ABL49251.
 XX
 PT Polynucleotides encoding lung tumor polypeptides, useful for treating
 PT lung cancer or stimulating an immune response -
 XX
 PS Example 2: Page 326-327; 374pp; English.
 XX
 CC The present invention describes human lung tumour proteins. Human lung
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumour proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumour proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL49251 to ABL49300 and ABL74946 to
 CC ABL75070 represent sequences used in the exemplification of the present
 CC invention.
 CC
 XX Sequence 461 AA:
 SQ
 Query Match 100.0%; Score 2450; DB 23; Length 461;
 Best Local Similarity 100.0%; Pred. No. 6, 6e-195;
 Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPPQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSS 60
 DB 1 MLYENNAQTOFSEPPQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSS 60
 QY 61 TFDALSPSPALPSTVDYPGHSPFVSFOQSTAKSATWTSTELKLYCOIAKCPQIQK 120
 DB 61 TFDALSPSPALPSTVDYPGHSPFVSFOQSTAKSATWTSTELKLYCOIAKCPQIQK 120
 QY 121 VMPPPOGAVIRAMPVYKKAHEVTEVYKRCPNHLSREFNEGOIAPSHLIRVGNSHAQ 180
 DB 121 VMPPPOGAVIRAMPVYKKAHEVTEVYKRCPNHLSREFNEGOIAPSHLIRVGNSHAQ 180
 QY 181 YVEDPITGRQSVLVYRPPQVGEFTTVLYLNFMKNSSCVGMNRPILLIYVLETRDGOV 240
 DB 181 YVEDPITGRQSVLVYRPPQVGEFTTVLYLNFMKNSSCVGMNRPILLIYVLETRDGOV 240
 QY 241 LGRRCFARICACGRKADSDIRKQVSDSTKNGDGRPRPROMTHGIOMTSIKRR 300
 DB 241 LGRRCFARICACGRKADSDIRKQVSDSTKNGDGRPRPROMTHGIOMTSIKRR 300
 QY 301 SPDELLYLPRYGRRETEMLKIKESLELMQYLPQHTIETRRQOQOQHILQKQTSIQ 360
 DB 301 SPDELLYLPRYGRRETEMLKIKESLELMQYLPQHTIETRRQOQOQHILQKQTSIQ 360
 QY 361 SPSSYGNSPPPLMKNMKNKLPSVSQILNPOQRNALPPTTIPDGMGANIPMGTHMPYAG 420
 DB 361 SPSSYGNSPPPLMKNMKNKLPSVSQILNPOQRNALPPTTIPDGMGANIPMGTHMPYAG 420
 QY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPPDGSIVRLIMOV 461
 DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPPDGSIVRLIMOV 461

RESULT 5
 ABG95131
 ID ABG95131 standard; Protein: 461 AA.
 XX
 AC ABG95131;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human oncogene p51 isoform delnbeta.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;

KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200269900-A2.
 XX
 PD 12-SEP-2002.
 XX
 PE 01-MAR-2002; 2002WO-US06518.
 XX
 PR 01-MAR-2001; 2001US-272751P.
 XX
 PA (CONF-) CONFORMA THERAPEUTICS CORP.
 XX
 PI Fritzt LC, Burrows FU;
 XX
 DR WPI: 2002-698710/75.
 XX
 PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90
 PT
 Disclosure; Page 329-331; 389pp; English.
 XX
 PS The invention describes a method of treating genetically-defined disease
 XX associated with chromosomal aberrations yielding oncogenic fusion
 XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
 XX cell population, treating proliferative diseases associated with mutant
 XX protein or cellular protein isoforms (II) dependent on heat shock
 XX protein (HSP)-90, or selectively treating cells expressing (II)
 XX involving administering HSP90-inhibitor. The method is useful for
 XX treating genetically-defined disease with chromosomal aberration yielding
 XX oncogenic fusion protein, treating cancerous cells containing fusion
 XX protein in heterogeneous cell population, treating proliferative disease
 XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 XX p53), or selectively treating cells expressing mutant protein or cellular
 XX protein isoform in a patient heterozygous for (II). The method is useful
 XX for treating a disease e.g. haematopoietic disorder such as T or B cell
 XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
 XX or a disease characterised by a solid tumour such as papillary thyroid
 XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 XX synovial sarcoma. The method is also useful for treating viral
 XX infections. This is the amino acid sequence of a human oncogenic protein.
 SQ Sequence 461 AA:
 Query Match 99.7%; Score 2443; DB 23; Length 461;
 Best Local Similarity 99.8%; Pred. No. 2, 5e-194;
 Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPPQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSS 60
 DB 1 MLYENNAQTOFSEPPQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSS 60
 QY 61 TFDALSPSPALPSTVDYPGHSPFVSFOQSTAKSATWTSTELKLYCOIAKCPQIQK 120
 DB 61 TFDALSPSPALPSTVDYPGHSPFVSFOQSTAKSATWTSTELKLYCOIAKCPQIQK 120
 QY 121 VMPPPOGAVIRAMPVYKKAHEVTEVYKRCPNHLSREFNEGOIAPSHLIRVGNSHAQ 180
 DB 121 VMPPPOGAVIRAMPVYKKAHEVTEVYKRCPNHLSREFNEGOIAPSHLIRVGNSHAQ 180
 QY 181 YVEDPITGRQSVLVYRPPQVGEFTTVLYLNFMKNSSCVGMNRPILLIYVLETRDGOV 240
 DB 181 YVEDPITGRQSVLVYRPPQVGEFTTVLYLNFMKNSSCVGMNRPILLIYVLETRDGOV 240
 QY 241 LGRRCFARICACGRKADSDIRKQVSDSTKNGDGRPRPROMTHGIOMTSIKRR 300
 DB 241 LGRRCFARICACGRKADSDIRKQVSDSTKNGDGRPRPROMTHGIOMTSIKRR 300

QY 301 SPDELLLYPVGRGTEYEMLLIKESLELMOYLPOHTIETRYQOQOQHLLQKQTSIQ 360
 DB 301 SPDELLLYPVGRGTEYEMLLIKESLELMOYLPOHTIETRYQOQOQHLLQKQTSIQ 360
 QY 361 SPSSYGNSSPPLNKNMKNKLPSVSQOLINPOORNALPTTIPDGAGANIPMGTHMPAG 420
 DB 361 SPSSYGNSSPPLNKNMKNKLPSVSQOLINPOORNALPTTIPDGAGANIPMGTHMPAG 420
 QY 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIVRIWQV 461
 DB 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIVRIWQV 461

RESULT 6
 AAY05963
 ID AAY05963 standard; Protein; 461 AA.
 AC AAY05963;
 XX 16-AUG-1999 (first entry)
 DT Mouse cell regulatory protein p63, isoform delta p63 beta, cDNA.
 DE Cell regulatory protein; p63; mu-delta p63 beta; mouse;
 KM cancer; tumour suppressor; cell cycle control; apoptosis;
 KM cell proliferation; cell differentiation; therapy.
 XX Mus sp.
 OS WO9919357-A2.
 PM 22-APR-1999.
 PD 02-OCT-1998; 98MO-US21992.
 PF 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 XX (HARD) HARVARD COLLEGE.
 PA McKeon F, Yang A;
 PI WPI: 1999-277595/23.
 DR N-PSDB; AAX58582.
 XX New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 PS Claim 23; Fig 19; 161pp; English.
 XX The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
 CC RACE. Sequencing of the amplification product indicated that the
 CC amplified cDNA possessed a truncated N-terminus, i.e. the
 CC transactivation domain was absent. Additional splice variants were
 CC identified by screening a cDNA library with a probe corresponding
 CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
 CC variants differing at the C-terminus are designated as alpha, beta
 CC and gamma forms, while p63 members differing in the N-terminus are
 CC designated as delta and 7A forms, where the delta form lacks the
 CC transactivation domain. The present sequence represents mouse p63
 CC isoform mu-delta p63 beta. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. Delta isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in hematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05963-64), polynucleotides (see

CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 XX Sequence 461 AA:
 SQ
 Query Match 99.1%; Score 2427; DB 20; Length 461;
 Best Local Similarity 98.9%; Pred No. 5.3e-193;
 Matches 456; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYENNAQTQSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSAQPS 60
 DB 1 MLYENNAQTQSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSAQPS 60
 QY 61 TFDALSPSPALPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
 DB 61 TFDALSPSPALPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
 QY 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHLSRENEGQIAPPSHLIRVGNASHAQ 180
 DB 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHLSRENEGQIAPPSHLIRVGNASHAQ 180
 QY 181 YVEDPITGRQSVLYVPEPPQVGTETTYVLYNFMCNSSCVGNNRRPILITVLETRDGQV 240
 DB 181 YVEDPITGRQSVLYVPEPPQVGTETTYVLYNFMCNSSCVGNNRRPILITVLETRDGQV 240
 QY 241 IGRRCFARICACPGDRKADSDIRKQOVSSTKNGDGTAKRPFONTHGICMTSTKRR 300
 DB 241 IGRRCFARICACPGDRKADSDIRKQOVSSTKNGDGTAKRPFONTHGICMTSTKRR 300
 QY 301 SPDELLLYPVGRGTEYEMLLIKESLELMOYLPOHTIETRYQOQOQHLLQKQTSIQ 360
 DB 301 SPDELLLYPVGRGTEYEMLLIKESLELMOYLPOHTIETRYQOQOQHLLQKQTSIQ 360
 QY 361 SPSSYGNSSPPLNKNMKNKLPSVSQOLINPOORNALPTTIPDGAGANIPMGTHMPAG 420
 DB 361 SPSSYGNSSPPLNKNMKNKLPSVSQOLINPOORNALPTTIPDGAGANIPMGTHMPAG 420
 QY 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIVRIWQV 461
 DB 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIVRIWQV 461

RESULT 7
 AAY05956
 ID AAY05956 standard; Protein; 586 AA.
 AC AAY05956;
 XX 16-AUG-1999 (first entry)
 DT Human cell regulatory protein p63, isoform delta p63 alpha.
 DE Cell regulatory protein; p63; hu-delta p63 alpha; human;
 KM cancer; tumour suppressor; cell cycle control; apoptosis;
 KM cell proliferation; cell differentiation; therapy.
 XX Homo sapiens.
 OS WO9919357-A2.
 PM 22-APR-1999.
 PD 02-OCT-1998; 98MO-US21992.
 PF 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 XX (HARD) HARVARD COLLEGE.
 PA McKeon F, Yang A;
 PI

ID	Accession	Standard	Protein	Length (AA)
Db	1	MYLENNAPQTQSE	QTYTNLGLNSMDQIQNGSSSTSPYNDHQAQNSTAPSAQPS	60
Qy	61	TFDALS	SPSAIPSNNDYDGPSPDPVSVFQOASSTAKSATWTYSTELKALYQIAKTCPIQIK	120
Db	61	TFDALS	SPSAIPSNNDYDGPSPDPVSVFQOASSTAKSATWTYSTELKALYQIAKTCPIQIK	120
Qy	121	VMT	PPQGAIVIRAMPYKKAEHYEVYKRCNHELSEFNEGOIAPPSHLIRVGNASHAQ	180
Db	121	VMT	PPQGAIVIRAMPYKKAEHYEVYKRCNHELSEFNEGOIAPPSHLIRVGNASHAQ	180
Qy	181	YVBD	PLTGTGQSVLYVPEPPQVSTFEFTYLVLYNFCNSSCGAMNRPILLIVLETSDGV	240
Db	181	YVBD	PLTGTGQSVLYVPEPPQVSTFEFTYLVLYNFCNSSCGAMNRPILLIVLETSDGV	240
Qy	241	LGRN	CFEARIACPGHDKRADEDSIRKQOVSDFKTNQDGTTRPPRQNTHGIGMTSIKRR	300
Db	241	LGRN	CFEARIACPGHDKRADEDSIRKQOVSDFKTNQDGTTRPPRQNTHGIGMTSIKRR	300
Qy	301	SPDE	LLYLVVRGEHYEMLLIKESIELMQYLPOHTIETRYRQOQOQHLLQKQTSIQ	360
Db	301	SPDE	LLYLVVRGEHYEMLLIKESIELMQYLPOHTIETRYRQOQOQHLLQKQTSIQ	360
Qy	361	SPSS	YGNSSPEPLKMSNMKLPESVSQLINPQORNLLPTTIPDGGANIPMAGTHMPAG	420
Db	361	SPSS	YGNSSPEPLKMSNMKLPESVSQLINPQORNLLPTTIPDGGANIPMAGTHMPAG	420
Qy	421	DMNG	LSPTQALPPLSMPTSHCTPPPPYPTDCSIY	456
Db	421	DMNG	LSPTQALPPLSMPTSHCTPPPPYPTDCSIY	456

RESULT 9

ABG95140

ID ABG95140 standard: Protein: 586 AA.

AC ABG95140:

DT 04-DEC-2002 (first entry)

DE Human oncogene p63 isoform delta n p63 alpha.

XX Chromosome aberration: oncogenic fusion protein; cancer; Oncogene;

KW proliferative disease; cellular protein isoform; heat shock protein 90;

KW HSP-90; Rheumatoid arthritis; cancer; haematopoietic disorder;

KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;

KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;

KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;

KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;

KW rhabdomyosarcoma; synovial sarcoma; viral infection.

OS Homo sapiens.

PN WO200269900-A2.

XX 12-SEP-2002.

PD 01-MAR-2002; 2002WO-US06518.

PF 01-MAR-2001; 2001US-272751P.

PR (CONF-) CONFORMA THERAPEUTICS CORP.

PA Fritz LC, Burrows FJ;

PI WPI, 2002-698710/75.

XX N-PSDB; ABS73332.

DR Treating genetically-defined disease associated with chromosomal

XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative

PT diseases, involves administering an inhibitor of heat shock protein 90

DISCLOSURE; PAGE 346-348; 389PP; ENGLISH.

THE INVENTION DESCRIBES A METHOD OF TREATING GENETICALLY-DEFINED DISEASE ASSOCIATED WITH CHROMOSOMAL ABERRATIONS YIELDING ONCOGENIC FUSION PROTEINS (I), TREATING CANCEROUS CELLS CONTAINING (I) IN A HETEROGENEOUS CELL POPULATION, TREATING PROLIFERATIVE DISEASES ASSOCIATED WITH MUTANT PROTEIN OR CELLULAR PROTEIN ISOFORMS (II) DEPENDENT ON HEAT SHOCK PROTEIN (HSP)-90, OR SELECTIVELY TREATING CELLS EXPRESSING (II) INVOLVING ADMINISTERING HSP90-INHIBITOR. THE METHOD IS USEFUL FOR TREATING GENETICALLY-DEFINED DISEASE WITH CHROMOSOMAL ABERRATION YIELDING ONCOGENIC FUSION PROTEIN, CELL POPULATION, TREATING PROLIFERATIVE DISEASE OR (E.G. RHEUMATOID ARTHRITIS OR CANCER) ASSOCIATED WITH MUTANT PROTEIN OR CELLULAR PROTEIN ISOFORM DEPENDENT ON HEAT SHOCK PROTEIN (HSP)-90 (E.G. P53), OR SELECTIVELY TREATING CELLS EXPRESSING SUCH AS T OR B CELL FOR TREATING A DISEASE E.G. HEMATOPOIETIC DISORDER SUCH AS T OR B CELL LYMPHOMA, CHRONIC MYELOID LEUKAEMIA (CM), APL, ALL, ANL, NHL AND CML, OR A DISEASE CHARACTERISED BY A SOLID TUMOUR SUCH AS PAPILLARY THYROID CARCINOMA, EWING'S SARCOMA, MELANOMA, LIPOSARCOMA, RHABDYOYSARCOMA AND SYNOVIAL SARCOMA. THE METHOD IS ALSO USEFUL FOR TREATING VIRAL INFECTIONS. THIS IS THE AMINO ACID SEQUENCE OF A HUMAN ONCOGENIC PROTEIN.

SEQUENCE 586 AA:

Query Match . 98.8%; Score 2421; DB 23; Length 586;
Best Local Similarity 100.0%; Pred. No. 2,3e+192;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTLENNAAQOFSEPOYTNLGLNSMDOIOIGSSSTSYNTDHQNVSVAAPYAOPSS 60
1 MTLENNAAQOFSEPOYTNLGLNSMDOIOIGSSSTSYNTDHQNVSVAAPYAOPSS 60

1 TPVALSPPAIPSNTRYPGPHSDVFSFOOSTAKSATWTYSTELKLYCOLAKTCPIOK 120
1 TPVALSPPAIPSNTRYPGPHSDVFSFOOSTAKSATWTYSTELKLYCOLAKTCPIOK 120

61 TFEDRLSPRAIPSNTRYPGPHSDVFSFOOSTAKSATWTYSTELKLYCOLAKTCPIOK 120
61 TFEDRLSPRAIPSNTRYPGPHSDVFSFOOSTAKSATWTYSTELKLYCOLAKTCPIOK 120

121 VMTPPVGAVIRAMPYKKAEHTVEYKRCPNHELRENEGAIAPSHLIVEGNSHAQ 180
121 VMTPPVGAVIRAMPYKKAEHTVEYKRCPNHELRENEGAIAPSHLIVEGNSHAQ 180

121 VMTPPVGAVIRAMPYKKAEHTVEYKRCPNHELRENEGAIAPSHLIVEGNSHAQ 180
121 VMTPPVGAVIRAMPYKKAEHTVEYKRCPNHELRENEGAIAPSHLIVEGNSHAQ 180

181 YVEPTGTROSVALPYEPPOVGTETFTVLTYNEMCNSSCVGMNRRIILTVILETDDGV 240
181 YVEPTGTROSVALPYEPPOVGTETFTVLTYNEMCNSSCVGMNRRIILTVILETDDGV 240

181 YVEPTGTROSVALPYEPPOVGTETFTVLTYNEMCNSSCVGMNRRIILTVILETDDGV 240
181 YVEPTGTROSVALPYEPPOVGTETFTVLTYNEMCNSSCVGMNRRIILTVILETDDGV 240

241 IGRRCFEARICACGRDRKADEDSIRKOQVSDSKKNDDGTRRPFROWTHGIOWTSIKRR 300
241 IGRRCFEARICACGRDRKADEDSIRKOQVSDSKKNDDGTRRPFROWTHGIOWTSIKRR 300

241 IGRRCFEARICACGRDRKADEDSIRKOQVSDSKKNDDGTRRPFROWTHGIOWTSIKRR 300
241 IGRRCFEARICACGRDRKADEDSIRKOQVSDSKKNDDGTRRPFROWTHGIOWTSIKRR 300

301 SPDDLTLPLVPGARETYEMLLKIKESIELMAYLPQHTLEYRDOOOOHLLQOTSIQ 360
301 SPDDLTLPLVPGARETYEMLLKIKESIELMAYLPQHTLEYRDOOOOHLLQOTSIQ 360

301 SPDDLTLPLVPGARETYEMLLKIKESIELMAYLPQHTLEYRDOOOOHLLQOTSIQ 360
301 SPDDLTLPLVPGARETYEMLLKIKESIELMAYLPQHTLEYRDOOOOHLLQOTSIQ 360

361 SPSSYGNSPPLANKNSMNKLPSYSQLNPQORNALPTTIPDGMGANIPMGTHMPAG 420
361 SPSSYGNSPPLANKNSMNKLPSYSQLNPQORNALPTTIPDGMGANIPMGTHMPAG 420

361 SPSSYGNSPPLANKNSMNKLPSYSQLNPQORNALPTTIPDGMGANIPMGTHMPAG 420
361 SPSSYGNSPPLANKNSMNKLPSYSQLNPQORNALPTTIPDGMGANIPMGTHMPAG 420

421 DMNGLSPTQALPPPLSMPESTSHCTPPPEYPIDCSIV 456
421 DMNGLSPTQALPPPLSMPESTSHCTPPPEYPIDCSIV 456

421 DMNGLSPTQALPPPLSMPESTSHCTPPPEYPIDCSIV 456
421 DMNGLSPTQALPPPLSMPESTSHCTPPPEYPIDCSIV 456

RESULT 10
AAB11357 standard; Protein; 586 AA.
ID AAB11357
XX AAB11357;
AC AAB11357;
XX 21-FEB-2001 (first entry)
DT 21-FEB-2001 (first entry)
XX Human p63 protein isoform #1.
DE Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;

KW vaccine; detection.
 XX OS Homo sapiens.
 XX PN WO200061612-A2.
 XX PD 19-OCT-2000.
 XX PF 03-APR-2000; 2000WO-US08896.
 XX PR 02-APR-1999; 99US-0285479.
 XX PR 17-DEC-1999; 99US-0466396.
 XX PR 30-DEC-1999; 99US-0476496.
 XX PR 10-JAN-2000; 2000US-0480886.
 XX PR 22-FEB-2000; 2000US-0510376.
 XX PA (CORI-) CORIXA CORP.
 XX PI Wang T, Fan L;
 XX DR WPI; 2000-628399/60.
 XX DR N-PSDB; AAC66027.
 PT Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of a lung cancer in a patient -
 XX
 PS Disclosure; Page 243-245; 261pp; English.
 CC This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.
 CC
 XX
 SO Sequence 586 AA;
 Query Match 98.1%; Score 2404; DB 21; Length 586;
 Best Local Similarity 99.3%; Pred. No. 6e-191;
 Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MLYENNAQTFSEPOYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSYAPSPYAQPS 60
 DB 1 MLYENNAQTFSEPOYTNLGLNSMDQOIRNGSSSTSPYNTDHAQNSYAPSPYAQPS 60
 QY 61 TFDALSPSPALPSTWDYRGPHSPDVSRQSSSTAKSATWTYSTEKLKLYCOIAATCPYQIK 120
 DB 61 TFDALSPSPALPSTWDYRGPHSPDVSRQSSSTAKSATWTYSTEKLKLYCOIAATCPYQIK 120
 QY 121 VMTPEPGAVIRAMPVYKKAHEYTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPEPGAVIRAMPVYKKAHEYTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRGSOVLVPEPPGVGTEFTTYLYNEMCNSSCGVGNRRPILITVLEFRDQV 240
 DB 181 YVEDPITGRGSOVLVPEPPGVGTEFTTYLYNEMCNSSCGVGNRRPILITVLEFRDQV 240
 QY 241 LGRRCPEARICACPGDRKRADEDSIRKQOVSDSTNGCTKPFQNTNGIOMTSIKRR 300
 DB 241 LGRRCPEARICACPGDRKRADEDSIRKQOVSDSTNGCTKPFQNTNGIOMTSIKRR 300
 QY 301 SPDDLLIYVARGRETYEMLKIKSLDELMOYLPQHTLETYRQOQOHOHLQKOTSIQ 360
 DB 301 SPDDLLIYVARGRETYEMLKIKSLDELMOYLPQHTLETYRQOQOHOHLQKOTSIQ 360
 QY 361 SPSSYGNSSPPLNKNKNSMKLPSVSQLNPOORNALPTTTPDGMGANIPMGTHFMAG 420
 DB 361 SPSSYGNSSPPLNKNKNSMKLPSVSQLNPOORNALPTTTPDGMGANIPMGTHFMAG 420

DB 361 SPSSYGNSSPPLNKNKNSMKLPSVSQLNPOORNALPTTTPDGMGANIPMGTHFMAG 420
 QY 421 DMNGLSPTQALPPLSMPTSHCPTPPPYPDSCIV 456
 DB 421 DMNGLSPTQALPPLSMPTSHCPTPPPYPDSCIV 456
 RESULT 11
 ID ABP61909 standard; Protein; 586 AA.
 XX AC ABP61909;
 XX DT 07-OCT-2002 (first entry)
 XX DE Human lung cancer associated protein sequence SEQ ID NO:338.
 XX KW Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
 XX OS Homo sapiens.
 XX PN WO200247534-A2.
 XX PD 20-JUN-2002.
 XX PF 30-NOV-2001; 2001WO-US47576.
 XX PR 12-DEC-2000; 2000US-0735705.
 XX PR 07-MAY-2001; 2001US-0850716.
 XX PR 28-JUN-2001; 2001US-0897778.
 XX PA (CORI-) CORIXA CORP.
 XX PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA,
 XX PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS,
 XX PI Carter D, Watanabe Y, Peckham DW, Cal F, Foy TW;
 XX DR WPI; 2002-583465/62.
 XX DR N-PSDB; ABQ92432.
 PT Novel lung carcinoma polynucleotide sequences and polypeptides encoded
 PT by the polynucleotides, useful in pharmaceutical compositions such as
 PT vaccines and as markers to indicate the presence of lung cancer -
 XX
 PS Example 2; Page 326-328; 381pp; English.
 CC The present invention describes isolated human lung carcinoma
 CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
 CC activity, and can be used in gene therapy and in vaccines. Compositions
 CC comprising (I) or (II) can be used for stimulating an immune response in
 CC a patient and for treating lung cancer in a patient. Oligonucleotides of
 CC (I) can be used for detecting lung cancer in a patient. Oligonucleotides of
 CC obtaining a biological sample from the presence of a cancer in a patient, by
 CC biological sample with the oligonucleotide, detecting in the sample, an
 CC amount of polynucleotide that hybridises to the oligonucleotide and
 CC comparing the amount of polynucleotide to the oligonucleotide and
 CC oligonucleotide to a predetermined cut-off value, and determining the
 CC presence of a cancer in the patient. (I) and (II) are useful in
 CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
 CC indicate the presence or absence of a cancer such as lung cancer.
 CC ABQ92445 to ABQ92486 and ABP61866 to ABP61992 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SO Sequence 586 AA;
 Query Match 98.1%; Score 2404; DB 23; Length 586;
 Best Local Similarity 99.3%; Pred. No. 6e-191;
 Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MLYENNAQTFSEPOYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSYAPSPYAQPS 60
 DB 1 MLYENNAQTFSEPOYTNLGLNSMDQOIRNGSSSTSPYNTDHAQNSYAPSPYAQPS 60

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QY 61 TFDALSPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
   |||||
Db 61 TFDALSPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
   |||||
Db 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVPEPPQVGTETFTVLYNFMCNSSCVGAMRRRILLIIVLETFDGOV 240
   |||||
Db 181 YVEDPITGRQSVLVPEPPQVGTETFTVLYNFMCNSSCVGAMRRRILLIIVLETFDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDCKRPFRONTGIGIOMTSIKRR 300
   |||||
Db 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDCKRPFRONTGIGIOMTSIKRR 300
QY 301 SPDDLLELYPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIO 360
   |||||
Db 301 SPDDLLELYPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLNKNSMKNKLPSVSQLINPQORNALPTTIPDGMGANIPMGTHMPMAG 420
   |||||
Db 361 SPSSYGNSSPPLNKNSMKNKLPSVSQLINPQORNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIV 456
   |||||
Db 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIV 456

```

RESULT 12

ABR74989
ABR74989 standard; Protein; 586 AA.

AC ABR74989;
XX

DT 01-MAY-2002 (first entry)
XX

DE Human p53 homologue isoform, p63 (L530S) protein seq ID NO:338.
XX

KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW immune response.
XX

OS Homo sapiens.
XX

PN WO200200174-A2.
XX

PD 03-JAN-2002.
XX

PF 28-JUN-2001; 2001WO-US21065.
XX

PR 28-JUN-2000; 2000US-0606421.
XX

PR 02-AUG-2000; 2000US-0630940.
XX

PR 21-AUG-2000; 2000US-0643597.
XX

PR 15-SEP-2000; 2000US-0662786.
XX

PR 09-OCT-2000; 2000US-0685696.
XX

PR 12-DEC-2000; 2000US-0735705.
XX

PR 07-MAY-2001; 2001US-0850716.
XX

PA (CORI-) CORIXA CORP.
XX

PI Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Warnerakis M, Fanger GR;
PI Vedvick JS, Carter D, Watanabe Y, Peckham DW;
XX

DR MPI: 2002-090513/12.
XX

DR N-PSDB; ABL49246.
XX

PT Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX

PS Example 2; Page 319-320; 374pp; English.
XX

CC The present invention describes human lung tumour proteins. Human lung
CC

CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABR74946 to
CC ABR75070 represent sequences used in the exemplification of the present
CC invention.

XX SQ Sequence 586 AA;

Query Match 98.1%; Score 2404; DB 23; Length 586;
Best local Similarity 99.3%; Pred. No. 6e-191;

Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MYLENNAOTOFSEPOYTNLGLNSDDQOIONGSSSTSPYNTDHAONSTAPSPYAPSS 60
   |||||
Db 1 MYLENNAOTOFSEPOYTNLGLNSDDQOIONGSSSTSPYNTDHAONSTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
   |||||
Db 61 TFDALSPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
   |||||
Db 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVPEPPQVGTETFTVLYNFMCNSSCVGAMRRRILLIIVLETFDGOV 240
   |||||
Db 181 YVEDPITGRQSVLVPEPPQVGTETFTVLYNFMCNSSCVGAMRRRILLIIVLETFDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDCKRPFRONTGIGIOMTSIKRR 300
   |||||
Db 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDCKRPFRONTGIGIOMTSIKRR 300
QY 301 SPDDLLELYPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIO 360
   |||||
Db 301 SPDDLLELYPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLNKNSMKNKLPSVSQLINPQORNALPTTIPDGMGANIPMGTHMPMAG 420
   |||||
Db 361 SPSSYGNSSPPLNKNSMKNKLPSVSQLINPQORNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIV 456
   |||||
Db 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIV 456

```

RESULT 13

AAAY05962
ID AAAY05962 standard; Protein; 586 AA.

AC AAAY05962;
XX

DT 16-AUG-1999 (first entry)
XX

DE Mouse cell regulatory protein p63, isoform deltaNp63 alpha.
XX

KW Cell regulatory protein; p63; mu-deltaNp63 alpha; mouse;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy.
XX

OS Mus sp.
XX

PN WO9919357-A2.
XX

PD 22-APR-1999.
XX

PF 02-OCT-1998; 98WO-US21992.
XX

PR 29-MAY-1998; 98US-0087216.
XX

PR 15-OCT-1997; 97US-0062076.
XX

XX

PA (HARD) HARVARD COLLEGE.
 XX
 PI McKeon F, Yang A;
 XX
 DR WPI; 1999-277595/23.
 DR N-PSDB; AAX58581.
 XX
 PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 PS
 XX Claim 23; Fig 18; 161pp; English.
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
 CC RACE. Sequencing of the amplification product indicated that the
 CC amplified cDNA possessed a truncated N-terminus, i.e. the
 CC transactivation domain was absent. Additional splice variants were
 CC identified by screening a cDNA library with a probe corresponding
 CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
 CC variants differing at the C-terminus are designated as alpha, beta
 CC and gamma forms, while p63 members differing in the N-terminus are
 CC designated as delta and TA forms, where the delta form lacks the
 CC transactivation domain. The present sequence represents mouse p63
 CC isoform mu-delta/p63 alpha. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. Delta isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 CC
 XX
 XX Sequence 586 AA;
 SO
 Query Match 97.98; Score 2398; DB 20; Length 586;
 Best Local Similarity 98.94; Pred. No. 1.9e-190;
 Matches 451; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MLYENNAQOFSPPOYTNGILNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
 DB 1 MLYENNAQOFSPPOYTNGILNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
 QY 61 TFDALSPSPALPSNTDYPGPHSPDVFSFOQSTAKSATWTSTELKRLKLYCOIAKTCPIQIK 120
 DB 61 TFDALSPSPALPSNTDYPGPHSPDVFSFOQSTAKSATWTSTELKRLKLYCOIAKTCPIQIK 120
 QY 121 VMTPPGAVIRAMPYVYKKAHEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPPGAVIRAMPYVYKKAHEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLVYPPEPVGTEFTTVLYNFMCNSSCVGGMNRRPLLIIVTLETBRGOV 240
 DB 181 YVEDPITGRQSVLVYPPEPVGTEFTTVLYNFMCNSSCVGGMNRRPLLIIVTLETBRGOV 240
 QY 241 LGRRCFEARACACPGDRKADKEDSIRKQVSDSTKNGDGTKRPRTWHTGIOMTSIKRR 300
 DB 241 LGRRCFEARACACPGDRKADKEDSIRKQVSDSTKNGDGTKRPRTWHTGIOMTSIKRR 300
 QY 301 SPDELLIYLVGRRETYEMLTIKESLELMQYLPQHTIETRYRQOQOHOHLQKOTSIQ 360
 DB 301 SPDELLIYLVGRRETYEMLTIKESLELMQYLPQHTIETRYRQOQOHOHLQKOTSIQ 360
 QY 361 SPSPSYGSSPPLKNNKSMNKLPSVSQILNPOQRNALPTTIPGGMGNIIMMGTHMAG 420
 DB 361 SPSPSYGSSPPLKNNKSMNKLPSVSQILNPOQRNALPTTIPGGMGNIIMMGTHMAG 420

QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
 DB 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
 RESULT 14
 AAY41032
 ID AAY41032 standard; protein; 586 AA.
 XX
 AC AAY41032;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Human lung tumor antigen L503S.
 XX
 KW Human; lung tumor; lung cancer; T cell stimulation.
 XX
 OS Homo sapiens.
 XX
 PN WO9947674-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 17-MAR-1999; 99WO-US05798.
 XX
 PR 18-MAR-1998; 98US-0040802.
 PR 18-MAR-1998; 98US-0040984.
 PR 27-JUL-1998; 98US-0123912.
 PR 27-JUL-1998; 98US-0123933.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Reed SG, Wang T;
 XX
 DR WPI; 1999-571839/48.
 DR N-PSDB; AAZ24648.
 XX
 PT New isolated lung tumor polynucleotides, used to develop products for
 PT the treatment, prevention and monitoring the progression of lung cancer
 XX
 XX Example 2; Page 130-131; 148pp; English.
 PS The invention provides isolated human lung tumor nucleic acids and
 XX polypeptides. The polypeptides can be used for the treatment of lung
 XX cancer. The polypeptides and polynucleotides can be used to stimulate T
 XX cells or antigen presenting cells for use in the treatment of lung
 XX cancer. The polypeptides and monoclonal antibodies specific for the
 XX polypeptides can also be used to inhibit the development of lung cancer.
 CC Agents which bind the polypeptides can be used for detecting lung cancer
 CC and for monitoring the progression of lung cancer.
 CC
 XX
 SO Sequence 586 AA;
 Query Match 97.98; Score 2397; DB 20; Length 586;
 Best Local Similarity 99.14; Pred. No. 2.3e-190;
 Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MLYENNAQOFSPPOYTNGILNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
 DB 1 MLYENNAQOFSPPOYTNGILNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
 QY 61 TFDALSPSPALPSNTDYPGPHSPDVFSFOQSTAKSATWTSTELKRLKLYCOIAKTCPIQIK 120
 DB 61 TFDALSPSPALPSNTDYPGPHSPDVFSFOQSTAKSATWTSTELKRLKLYCOIAKTCPIQIK 120
 QY 121 VMTPPGAVIRAMPYVYKKAHEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPPGAVIRAMPYVYKKAHEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLVYPPEPVGTEFTTVLYNFMCNSSCVGGMNRRPLLIIVTLETBRGOV 240
 DB 181 YVEDPITGRQSVLVYPPEPVGTEFTTVLYNFMCNSSCVGGMNRRPLLIIVTLETBRGOV 240

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Db      181 YVEDPITGRQSVLYVEPPQVGETTEFTVLYNFKCNSSCVGANNRPILLIYVLETRDQV 240
QY      241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRR 300
Db      241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRR 300
QY      301 SPDELLYLPRGRRETYEMLIKESLELMQYLPORHTIETRYRQOQOQOHOHLQKOTSIO 360
Db      301 SPDELLYLPRGRRETYEMLIKESLELMQYLPORHTIETRYRQOQOQOHOHLQKOTSIO 360
QY      361 SPSSYGNSPPLKMNKSNKLPVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
Db      361 SPSSYGNSPPLKMNKSNKLPVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY      421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIV 456
Db      421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIV 456

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RESULT 15

AAB11317
ID AAB11317 standard; Protein; 586 AA.

XX AC AAB11317;

DT 21-FEB-2001. (first entry)

XX DE Human lung cancer-associated protein L530S.

XX KM Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;

XX KM vaccine; detection.

OS Homo sapiens.

XX PN WO200061612-A2.

XX PD 19-OCT-2000.

XX PF 03-APR-2000; 2000MO-US08896.

XX PR 02-APR-1999; 99US-0285479.

XX PR 17-DEC-1999; 99US-0466386.

XX PR 30-DEC-1999; 99US-0476496.

XX PR 10-JAN-2000; 2000US-0480884.

XX PR 22-FEB-2000; 2000US-0510376.

XX FA (CORI-) CORIXA CORP.

XX PI Wang T, Fan L;

XX DR WPI; 2000-628399/60.

XX DR N-PSDB; AAC65887.

XX PT Isolated polypeptide comprising an immunogenic portion of a lung tumor

XX PT protein is used for detecting and monitoring progression of lung cancer

XX PT in a patient -

XX PS Claim 3; Page 163-164; 261pp; English.

XX CC This invention describes a novel isolated polypeptide (1) which

XX CC comprising an immunogenic portion of a lung tumor protein or variant (P2)

XX CC which have cytostatic activity. The polypeptides and polynucleotides are

XX CC used in compositions and vaccines to inhibit the development of cancer,

XX CC especially lung cancer, in a patient. Methods described in the invention

XX CC can be used to monitor the progression of a cancer by carrying out the

XX CC detection at subsequent time points and comparing the results from the

XX CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient

XX CC are treated with P2, polynucleotides encoding P2 or antigen presenting

XX CC cells expressing P2 and then administered to the patient to inhibit

XX CC development of cancer.

XX CC Sequence 586 AA;

XX SQ

Query Match 97.88; Score 2397; DB 21; Length 586;
Best Local Similarity 99.1%; Pred. No. 2.3e-190;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db      1 MLTYENNAQIOFESPQYNTNLGLNSMDQOIQONSSSTSPYNTDHAONSVTAASPYAQPS 60
QY      61 TFDAISPSPALPSNTDYPGPHSPFVSFOQSSSTAKSATWTSTELKKLYCOIAKTCPIQIK 120
Db      61 TFDAISPSPALPSNTDYPGPHSPFVSFOQSSSTAKSATWTSTELKKLYCOIAKTCPIQIK 120
QY      121 VMTPPPGQAVLRAMPVYKKAHVTEYVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQ 180
Db      121 VMTPPPGQAVLRAMPVYKKAHVTEYVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQ 180
QY      181 YVEDPITGRQSVLYVEPPQVGETTEFTVLYNFKCNSSCVGANNRPILLIYVLETRDQV 240
Db      181 YVEDPITGRQSVLYVEPPQVGETTEFTVLYNFKCNSSCVGANNRPILLIYVLETRDQV 240
QY      241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRR 300
Db      241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRR 300
QY      301 SPDELLYLPRGRRETYEMLIKESLELMQYLPORHTIETRYRQOQOQOHOHLQKOTSIO 360
Db      301 SPDELLYLPRGRRETYEMLIKESLELMQYLPORHTIETRYRQOQOQOHOHLQKOTSIO 360
QY      361 SPSSYGNSPPLKMNKSNKLPVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
Db      361 SPSSYGNSPPLKMNKSNKLPVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY      421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIV 456
Db      421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIV 456

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Search completed: August 7, 2003, 09:46:27
Job time : 32.7931 secs

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241 LGRCFEARICACPGGRKAEDEDSIRKQVSDSINMGDGINFPRKNTLHGLVGGD.....

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Db      241  LGRCEAFARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHGLOMTSIRKRR 300
QY      301  SPDELLIYLPVRGRETYEMILKIKESLEMOYLPOHTIETRYRQOQOQHHLQKQTSIQ 360
Db      301  SPDELLIYLPVRGRETYEMILKIKESLEMOYLPOHTIETRYRQOQOQHHLQKQTSIQ 360
QY      361  SPSSYGNSSPPLKNKSNMKNLPVSQOLNPOORNALPTTTIPDGMGANIPMGTHMPMAG 420
Db      361  SPSSYGNSSPPLKNKSNMKNLPVSQOLNPOORNALPTTTIPDGMGANIPMGTHMPMAG 420
QY      421  DMNGLSPTQALPPLSMSTSHCTPPPPYPIDCSIVRIMQV 461
Db      421  DMNGLSPTQALPPLSMSTSHCTPPPPYPIDCSIVRIMQV 461

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RESULT 2

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US-09-542-615A-343
; Sequence 343, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Pan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hoeken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-343

```

```

Query Match      100.0%; Score 2450; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1,2e-216;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  MLYENNQOTSEPOYNILGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
Db      1  MLYENNQOTSEPOYNILGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
QY      61  TFDALSPSPAIPSTNDYGPSPHSPVDFVFSQOSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
Db      61  TFDALSPSPAIPSTNDYGPSPHSPVDFVFSQOSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY      121  VMTPEPGAVIRAMPYVYKKAHYTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db      121  VMTPEPGAVIRAMPYVYKKAHYTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY      181  YVEPITGRQSVLVYEPPOVGTETTVLYNFMCNSSCVGMMRRPILITVLETRDQV 240
Db      181  YVEPITGRQSVLVYEPPOVGTETTVLYNFMCNSSCVGMMRRPILITVLETRDQV 240
QY      241  LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHGLOMTSIRKRR 300
Db      241  LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHGLOMTSIRKRR 300
QY      301  SPDELLIYLPVRGRETYEMILKIKESLEMOYLPOHTIETRYRQOQOQHHLQKQTSIQ 360
Db      301  SPDELLIYLPVRGRETYEMILKIKESLEMOYLPOHTIETRYRQOQOQHHLQKQTSIQ 360
QY      361  SPSSYGNSSPPLKNKSNMKNLPVSQOLNPOORNALPTTTIPDGMGANIPMGTHMPMAG 420
Db      361  SPSSYGNSSPPLKNKSNMKNLPVSQOLNPOORNALPTTTIPDGMGANIPMGTHMPMAG 420
QY      421  DMNGLSPTQALPPLSMSTSHCTPPPPYPIDCSIVRIMQV 461
Db      421  DMNGLSPTQALPPLSMSTSHCTPPPPYPIDCSIVRIMQV 461

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Db      421  DMNGLSPTQALPPLSMSTSHCTPPPPYPIDCSIVRIMQV 461

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RESULT 3

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US-09-606-421B-343
; Sequence 343, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Pan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hoeken, Nancy A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-343

```

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Query Match      100.0%; Score 2450; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1,2e-216;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  MLYENNQOTSEPOYNILGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
Db      1  MLYENNQOTSEPOYNILGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
QY      61  TFDALSPSPAIPSTNDYGPSPHSPVDFVFSQOSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
Db      61  TFDALSPSPAIPSTNDYGPSPHSPVDFVFSQOSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
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Db      121  VMTPEPGAVIRAMPYVYKKAHYTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY      181  YVEPITGRQSVLVYEPPOVGTETTVLYNFMCNSSCVGMMRRPILITVLETRDQV 240
Db      181  YVEPITGRQSVLVYEPPOVGTETTVLYNFMCNSSCVGMMRRPILITVLETRDQV 240
QY      241  LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHGLOMTSIRKRR 300
Db      241  LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHGLOMTSIRKRR 300
QY      301  SPDELLIYLPVRGRETYEMILKIKESLEMOYLPOHTIETRYRQOQOQHHLQKQTSIQ 360
Db      301  SPDELLIYLPVRGRETYEMILKIKESLEMOYLPOHTIETRYRQOQOQHHLQKQTSIQ 360
QY      361  SPSSYGNSSPPLKNKSNMKNLPVSQOLNPOORNALPTTTIPDGMGANIPMGTHMPMAG 420
Db      361  SPSSYGNSSPPLKNKSNMKNLPVSQOLNPOORNALPTTTIPDGMGANIPMGTHMPMAG 420
QY      421  DMNGLSPTQALPPLSMSTSHCTPPPPYPIDCSIVRIMQV 461
Db      421  DMNGLSPTQALPPLSMSTSHCTPPPPYPIDCSIVRIMQV 461

```

RESULT 4

```

US-09-643-597-338
; Sequence 338, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:

```



```

1 TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
2 FILE REFERENCE: 210121.455C8
3 CURRENT APPLICATION NUMBER: US/09/542,615A
4 CURRENT FILING DATE: 2000-04-14
5 NUMBER OF SEQ ID NOS: 350
6 SOFTWARE: FastSeq for Windows Version 3.0
7 SEQ ID NO 338
8 LENGTH: 586
9 TYPE: PRT
10 ORGANISM: Homo sapiens
11 US-09-542-615A-338
12
13 Query Match          98.1%; Score 2404; DB 4; Length 586;
14 Best Local Similarity 99.3%; Pred. No. 2,9e-212;
15 Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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32 QY
33 181 VVEDPITGRQSVLVYEPPOVTEETETVLYLNPNCSSCVGGMNRPILLITVLETBEGVY 240
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66 421 DMNGISPTQALPPPLSMPSHCHCPPPYPTDCSIY 456
67
68 Db
69 421 DMNGISPTQALPPPLSMPSHCHCPPPYPTDCSIY 456
70 421 DMNGISPTQALPPPLSMPSHCHCPPPYPTDCSIY 456
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72 RESULT 6
73 US-09-606-421B-338
74 ; Sequence 338, Application US/09606421B
75 ; Patent No. 6531315
76 ; GENERAL INFORMATION:
77 ; APPLICANT: Wang, Tongtong
78 ; APPLICANT: Fan, Liqun
79 ; APPLICANT: Kalos, Michael D.
80 ; APPLICANT: Bangur, Chaltanya S.
81 ; APPLICANT: Hosken, Nancy
82 ; APPLICANT: Fanger, Gary R.
83 ; APPLICANT: Li, Samuel X.
84 ; APPLICANT: Wang, Aijun
85 ; APPLICANT: Skeiky, Yasir A.W.
86 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
87 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
88 ; FILE REFERENCE: 210121.455C9
89 ; CURRENT APPLICATION NUMBER: US/09/606,421B
90 ; CURRENT FILING DATE: 2000-06-28
91 ; NUMBER OF SEQ ID NOS: 358
92 ; SOFTWARE: FastSeq for Windows Version 3.0
93 ; SEQ ID NO 338
94 ; LENGTH: 586
95 ; TYPE: PRT

```

ORGANISM: Homo sapiens
US-09-606-421B-338

Query Match 98.1%; Score 2404; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 2,9e-212;
Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MLYLENNAAQTGFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYLENNAAQTGFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPBHSFDVSVFOOSSSTAKSATWTSTELKKLYCOIAKTCPIQIK 120
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DB 121 VMTPPGAGAVIRAMPYVYKKAHEVTEVYKRCPNHLSREFNEGQIAPSHLIRVGNASHQ 180
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DB 181 YVEDPITGRQSVLYVEPPQVGTETTVLYNFMKNSCVGGMNRRPILITVLETRDGOV 240
QY 241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRFONTHGIQWTSIKRR 300
DB 241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRFONTHGIQWTSIKRR 300
QY 301 SPDELLYLPVGRRETEYEMLIKESLELMQYLPQHTIETRYRQOQOQOHHLOKQTSIQ 360
DB 301 SPDELLYLPVGRRETEYEMLIKESLELMQYLPQHTIETRYRQOQOQOHHLOKQTSIQ 360
QY 361 SPSSYGNSSPPLKMNMSMNLPSVSQILNQORNALPTTIPDGAGANIPMGTHMPAG 420
DB 361 SPSSYGNSSPPLKMNMSMNLPSVSQILNQORNALPTTIPDGAGANIPMGTHMPAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456

```

RESULT 7

US-09-643-597-152
Sequence 152, Application US/09643597
Patent No. 6426072

GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-643-597-152

Query Match 97.8%; Score 2397; DB 4; Length 586;
Best Local Similarity 99.1%; Pred. No. 1.3e-211;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MLYLENNAAQTGFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYLENNAAQTGFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPBHSFDVSVFOOSSSTAKSATWTSTELKKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNDYDGPBHSFDVSVFOOSSSTAKSATWTSTELKKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAGAVIRAMPYVYKKAHEVTEVYKRCPNHLSREFNEGQIAPSHLIRVGNASHQ 180
DB 121 VMTPPGAGAVIRAMPYVYKKAHEVTEVYKRCPNHLSREFNEGQIAPSHLIRVGNASHQ 180
QY 181 YVEDPITGRQSVLYVEPPQVGTETTVLYNFMKNSCVGGMNRRPILITVLETRDGOV 240
DB 181 YVEDPITGRQSVLYVEPPQVGTETTVLYNFMKNSCVGGMNRRPILITVLETRDGOV 240
QY 241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRFONTHGIQWTSIKRR 300
DB 241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRFONTHGIQWTSIKRR 300
QY 301 SPDELLYLPVGRRETEYEMLIKESLELMQYLPQHTIETRYRQOQOQOHHLOKQTSIQ 360
DB 301 SPDELLYLPVGRRETEYEMLIKESLELMQYLPQHTIETRYRQOQOQOHHLOKQTSIQ 360
QY 361 SPSSYGNSSPPLKMNMSMNLPSVSQILNQORNALPTTIPDGAGANIPMGTHMPAG 420
DB 361 SPSSYGNSSPPLKMNMSMNLPSVSQILNQORNALPTTIPDGAGANIPMGTHMPAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456

```

RESULT 8

US-09-480-884A-152
Sequence 152, Application US/0948084A
Patent No. 6482597

GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-480-884A-152

Query Match 97.8%; Score 2397; DB 4; Length 586;
Best Local Similarity 99.1%; Pred. No. 1.3e-211;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MLYLENNAAQTGFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYLENNAAQTGFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPBHSFDVSVFOOSSSTAKSATWTSTELKKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNDYDGPBHSFDVSVFOOSSSTAKSATWTSTELKKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAGAVIRAMPYVYKKAHEVTEVYKRCPNHLSREFNEGQIAPSHLIRVGNASHQ 180
DB 121 VMTPPGAGAVIRAMPYVYKKAHEVTEVYKRCPNHLSREFNEGQIAPSHLIRVGNASHQ 180
QY 181 YVEDPITGRQSVLYVEPPQVGTETTVLYNFMKNSCVGGMNRRPILITVLETRDGOV 240

```

```
Db      181 YVEDITGRQSVLYVEPPQVGTTEFTTVLYNFMCNSSCGVGNRRPILITVLETRDGV 240
QY      241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDSTKRPFRONTGIGTOMTSIKRR 300
Db      241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDSTKRPFRONTGIGTOMTSIKRR 300
QY      301 SPDDLLYLPVGRGRETYEMLKIKESLELMOYLPOHTIETTYRQOOOQHLLQKOTSIO 360
Db      301 SPDDLLYLPVGRGRETYEMLKIKESLELMOYLPOHTIETTYRQOOOQHLLQKOTSIO 360
QY      361 SPSSYGNSPPLNKNMKNKLPSVSQOLINPOQRNALPTPTIPDGAGANIPMGTHMPAG 420
Db      361 SPSSYGNSPPLNKNMKNKLPSVSQOLINPOQRNALPTPTIPDGAGANIPMGTHMPAG 420
QY      421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456
Db      421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456
```

RESULT 9

```
US-09-542-615A-152
; Sequence 152, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-542-615A-152
```

```
Query Match      97.8%; Score 2397; DB 4; Length 586;
Best Local Similarity 99.1%; Pred. No. 1.3e-211;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 MLYENNATQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
Db      1 MLYENNATQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY      61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
Db      61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY      121 VMTPPQGAIVIRAMPVYKKAHEVTEVVKRCPMHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db      121 VMTPPQGAIVIRAMPVYKKAHEVTEVVKRCPMHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY      181 YVEDITGRQSVLYVEPPQVGTTEFTTVLYNFMCNSSCGVGNRRPILITVLETRDGV 240
Db      181 YVEDITGRQSVLYVEPPQVGTTEFTTVLYNFMCNSSCGVGNRRPILITVLETRDGV 240
QY      241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDSTKRPFRONTGIGTOMTSIKRR 300
Db      241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDSTKRPFRONTGIGTOMTSIKRR 300
QY      301 SPDDLLYLPVGRGRETYEMLKIKESLELMOYLPOHTIETTYRQOOOQHLLQKOTSIO 360
Db      301 SPDDLLYLPVGRGRETYEMLKIKESLELMOYLPOHTIETTYRQOOOQHLLQKOTSIO 360
QY      421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456
Db      421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456
```

```
Db      361 SPSSYGNSPPLNKNMKNKLPSVSQOLINPOQRNALPTPTIPDGAGANIPMGTHMPAG 420
QY      421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456
Db      421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456
```

RESULT 10

```
US-09-606-421B-152
; Sequence 152, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-606-421B-152
```

```
Query Match      97.8%; Score 2397; DB 4; Length 586;
Best Local Similarity 99.1%; Pred. No. 1.3e-211;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 MLYENNATQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
Db      1 MLYENNATQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY      61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
Db      61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY      121 VMTPPQGAIVIRAMPVYKKAHEVTEVVKRCPMHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db      121 VMTPPQGAIVIRAMPVYKKAHEVTEVVKRCPMHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY      181 YVEDITGRQSVLYVEPPQVGTTEFTTVLYNFMCNSSCGVGNRRPILITVLETRDGV 240
Db      181 YVEDITGRQSVLYVEPPQVGTTEFTTVLYNFMCNSSCGVGNRRPILITVLETRDGV 240
QY      241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDSTKRPFRONTGIGTOMTSIKRR 300
Db      241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDSTKRPFRONTGIGTOMTSIKRR 300
QY      301 SPDDLLYLPVGRGRETYEMLKIKESLELMOYLPOHTIETTYRQOOOQHLLQKOTSIO 360
Db      301 SPDDLLYLPVGRGRETYEMLKIKESLELMOYLPOHTIETTYRQOOOQHLLQKOTSIO 360
QY      361 SPSSYGNSPPLNKNMKNKLPSVSQOLINPOQRNALPTPTIPDGAGANIPMGTHMPAG 420
Db      361 SPSSYGNSPPLNKNMKNKLPSVSQOLINPOQRNALPTPTIPDGAGANIPMGTHMPAG 420
QY      421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456
Db      421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456
```

RESULT 11

```
US-09-643-597-344
; Sequence 344, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-344

Query Match      97.1%; Score 2379; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 4.8e-210;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDALSPSPALPSN 74
DB 70 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDALSPSPALPSN 129
QY 75 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVTPPPGAVIRAM 134
DB 130 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVTPPPGAVIRAM 189
QY 135 PVYKKAHEVYEVRCRNHLSREFNEGQIAPPSHLRVEGNSHAQYVEDPITGRQSVLV 194
DB 190 PVYKKAHEVYEVRCRNHLSREFNEGQIAPPSHLRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIYLETFRDQVILGRRCFEARICACP 254
DB 250 PYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIYLETFRDQVILGRRCFEARICACP 309
QY 255 GRDKKADSDIRKQOVSDSTKNGDGTKRPRQNTHGQIOMTSIKRRSPDDELLYLPVGR 314
DB 310 GRDKKADSDIRKQOVSDSTKNGDGTKRPRQNTHGQIOMTSIKRRSPDDELLYLPVGR 369
QY 315 ETYEMLKIKESLEIMQYLPQHTIETVYRQOQOQOQHLLQKQTSIQSPSSYGNSSPPLNK 374
DB 370 ETYEMLKIKESLEIMQYLPQHTIETVYRQOQOQOQHLLQKQTSIQSPSSYGNSSPPLNK 429
QY 375 MNSMKNKLPSVSQLINPOQRNALPPTTIPDGGANIPMGGTHMPAGDMNGISPTQALPPP 434
DB 430 MNSMKNKLPSVSQLINPOQRNALPPTTIPDGGANIPMGGTHMPAGDMNGISPTQALPPP 489
QY 435 LSMSTSHCHTTPPPYPTDCSIVRIWQV 461
DB 490 LSMSTSHCHTTPPPYPTDCSIVRIWQV 516

RESULT 12
US-09-542-615A-344
; Sequence 344, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
```

```
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-344

Query Match      97.1%; Score 2379; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 4.8e-210;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDALSPSPALPSN 74
DB 70 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDALSPSPALPSN 129
QY 75 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVTPPPGAVIRAM 134
DB 130 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVTPPPGAVIRAM 189
QY 135 PVYKKAHEVYEVRCRNHLSREFNEGQIAPPSHLRVEGNSHAQYVEDPITGRQSVLV 194
DB 190 PVYKKAHEVYEVRCRNHLSREFNEGQIAPPSHLRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIYLETFRDQVILGRRCFEARICACP 254
DB 250 PYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIYLETFRDQVILGRRCFEARICACP 309
QY 255 GRDKKADSDIRKQOVSDSTKNGDGTKRPRQNTHGQIOMTSIKRRSPDDELLYLPVGR 314
DB 310 GRDKKADSDIRKQOVSDSTKNGDGTKRPRQNTHGQIOMTSIKRRSPDDELLYLPVGR 369
QY 315 ETYEMLKIKESLEIMQYLPQHTIETVYRQOQOQOQHLLQKQTSIQSPSSYGNSSPPLNK 374
DB 370 ETYEMLKIKESLEIMQYLPQHTIETVYRQOQOQOQHLLQKQTSIQSPSSYGNSSPPLNK 429
QY 375 MNSMKNKLPSVSQLINPOQRNALPPTTIPDGGANIPMGGTHMPAGDMNGISPTQALPPP 434
DB 430 MNSMKNKLPSVSQLINPOQRNALPPTTIPDGGANIPMGGTHMPAGDMNGISPTQALPPP 489
QY 435 LSMSTSHCHTTPPPYPTDCSIVRIWQV 461
DB 490 LSMSTSHCHTTPPPYPTDCSIVRIWQV 516

RESULT 13
US-09-606-421B-344
; Sequence 344, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
```

```

SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-344

Query Match      97.1%; Score 2379; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 4.8e-210;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

15 PQTMLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 74
   |||||||
70 PQTMLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 129
   |||||||
75 TDYPPGHSFDVSVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVRAM 189
   |||||||
130 TDYPPGHSFDVSVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVRAM 189
   |||||||
135 PYKKAHEVTEVYKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 194
   |||||||
190 PYKKAHEVTEVYKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 249
   |||||||
195 PYKKAHEVTEVYKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 254
   |||||||
250 PYKKAHEVTEVYKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 309
   |||||||
255 GDRKRADEDSIRKQVSDSTKNGDTKRPFRONTNGIOMTSIKKRRSPDDELLYLPVGR 314
   |||||||
310 GDRKRADEDSIRKQVSDSTKNGDTKRPFRONTNGIOMTSIKKRRSPDDELLYLPVGR 369
   |||||||
315 EYEMMLKIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
   |||||||
370 EYEMMLKIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 429
   |||||||
375 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 434
   |||||||
430 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 489
   |||||||
435 LSMSTSHCTPPPPYPTDCSIVRIMQV 461
   |||||||
490 LSMSTSHCTPPPPYPTDCSIVRIMQV 516

```

```

RESULT 14
US-09-643-597-339
; Sequence 339, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Bangur, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-339

```

```

Query Match      95.9%; Score 2350; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 3e-207;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

15 PQTMLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 74
   |||||||
70 PQTMLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 129
   |||||||
75 TDYPPGHSFDVSVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVRAM 134
   |||||||
130 TDYPPGHSFDVSVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVRAM 189
   |||||||
135 PYKKAHEVTEVYKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 194
   |||||||
190 PYKKAHEVTEVYKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 249
   |||||||
195 PYKKAHEVTEVYKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 254
   |||||||
250 PYKKAHEVTEVYKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 309
   |||||||
255 GDRKRADEDSIRKQVSDSTKNGDTKRPFRONTNGIOMTSIKKRRSPDDELLYLPVGR 314
   |||||||
310 GDRKRADEDSIRKQVSDSTKNGDTKRPFRONTNGIOMTSIKKRRSPDDELLYLPVGR 369
   |||||||
315 EYEMMLKIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
   |||||||
370 EYEMMLKIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 429
   |||||||
375 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 434
   |||||||
430 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 489
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435 LSMSTSHCTPPPPYPTDCSIV 456
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490 LSMSTSHCTPPPPYPTDCSIV 511

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RESULT 15
US-09-542-615A-339
; Sequence 339, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Bangur, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-339

Query Match      95.9%; Score 2350; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 3e-207;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 190 PVYKKAHEVTEVVKRCBNHLSREPNEGOTAPPSHLIRVBGNSHAQYVEDPITGRQSVLY 249
QY 195 PYEPPOVGTETTVLYNFMGNSCVGMMNRPLLIVTLETTRDGQVIGRRCFEARIACAP 254
Db 250 PYEPPOVGTETTVLYNFMGNSCVGMMNRPLLIVTLETTRDGQVIGRRCFEARIACAP 309
QY 255 GRDRKADEDSIRKQOYSDSTKNGDGTKRPFONTGHIQMTSIKKRRSPDDELLYLPVNGR 314
Db 310 GRDRKADEDSIRKQOYSDSTKNGDGTKRPFONTGHIQMTSIKKRRSPDDELLYLPVNGR 369
QY 315 EYEMLLTKESLELMQYLPQHTIETYYROOQOQOHLQKOTSIQSPSSYGNSSPPLNK 374
Db 370 EYEMLLTKESLELMQYLPQHTIETYYROOQOQOHLQKOTSIQSPSSYGNSSPPLNK 429
QY 375 MNSMNLPSVSQOLINPOORNALPTTIPDGMGANTPMGTHMPMAGDMNGLSPTQALPpp 434
Db 430 MNSMNLPSVSQOLINPOORNALPTTIPDGMGANTPMGTHMPMAGDMNGLSPTQALPpp 489
QY 435 LSMPSSTSHCTPPPPPTDCSIV 456
Db 490 LSMPSSTSHCTPPPPPTDCSIV 511

Search completed: August 7, 2003, 09:54:55
JOD time : 13.7172 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:46:34 ; Search time 19.6814 Seconds
(without alignments)
2781.719 Million cell updates/sec

Title: US-09-538-106-17
Perfect score: 2450
Sequence: 1 MLYENNAQTQFSEPOYTNL.....HCTPPPPYPCDSIVIMQV 461

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 451899 seqs, 118759770 residues
Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications-AA:*

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18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2450	100.0	461	9	US-09-735-705-343 Sequence 343, App
2	2450	100.0	461	10	US-09-850-716A-343 Sequence 343, App
3	2450	100.0	461	10	US-09-897-778-343 Sequence 343, App
4	2404	98.1	586	9	US-09-735-705-338 Sequence 338, App
5	2404	98.1	586	10	US-09-850-716A-338 Sequence 338, App
6	2404	98.1	586	9	US-09-897-778-338 Sequence 338, App
7	2397	97.8	586	9	US-09-735-705-152 Sequence 152, App
8	2397	97.8	586	10	US-09-850-716A-152 Sequence 152, App
9	2397	97.8	586	10	US-09-897-778-152 Sequence 152, App
10	2397	97.8	586	11	US-09-466-396A-152 Sequence 152, App
11	2379	97.1	516	9	US-09-735-705-344 Sequence 344, App
12	2379	97.1	516	10	US-09-850-716A-344 Sequence 344, App
13	2379	97.1	516	10	US-09-897-778-344 Sequence 344, App
14	2350	95.9	641	9	US-09-735-705-339 Sequence 339, App
15	2350	95.9	641	10	US-09-850-716A-339 Sequence 339, App

16	2350	95.9	641	10	US-09-897-778-339	Sequence 339, App
17	2342	95.6	680	9	US-09-735-705-342	Sequence 342, App
18	2342	95.6	680	10	US-09-850-716A-342	Sequence 342, App
19	2342	95.6	680	10	US-09-897-778-342	Sequence 342, App
20	1893	77.3	426	15	US-10-274-874-19	Sequence 19, App
21	1872	76.4	356	9	US-09-735-705-341	Sequence 341, App
22	1872	76.4	356	10	US-09-850-716A-341	Sequence 341, App
23	1872	76.4	356	10	US-09-897-778-341	Sequence 341, App
24	1872	76.4	356	15	US-10-274-874-2	Sequence 2, App
25	1813	74.0	448	10	US-09-735-705-340	Sequence 340, App
26	1813	74.0	448	10	US-09-850-716A-340	Sequence 340, App
27	1813	74.0	448	10	US-09-897-778-340	Sequence 340, App
28	1415.5	57.8	635	14	US-10-155-053-10	Sequence 10, App
29	1415.5	57.8	635	14	US-09-732-384-10	Sequence 10, App
30	1279.5	52.2	420	15	US-10-274-874-20	Sequence 20, App
31	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
32	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
33	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
34	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
35	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
36	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
37	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
38	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
39	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
40	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
41	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
42	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
43	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
44	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App
45	1279.5	52.2	420	15	US-09-732-384-3	Sequence 32, App

ALIGNMENTS

1	US-09-735-705-343	Application US/09735705
2	Sequence 343, App	Sequence 343, App
3	Patent No. US20020052329A1	Patent No. US20020052329A1
4	GENERAL INFORMATION:	GENERAL INFORMATION:
5	APPLICANT: Wang, Tongtong	APPLICANT: Wang, Tongtong
6	APPLICANT: Fan, Liqun	APPLICANT: Fan, Liqun
7	APPLICANT: Kalos, Michael D.	APPLICANT: Kalos, Michael D.
8	APPLICANT: Baquer, Chaitanya S.	APPLICANT: Baquer, Chaitanya S.
9	APPLICANT: Hosken, Nancy	APPLICANT: Hosken, Nancy
10	APPLICANT: Fanger, Gary R.	APPLICANT: Fanger, Gary R.
11	APPLICANT: Li, Samuel X.	APPLICANT: Li, Samuel X.
12	APPLICANT: Wang, Aljun	APPLICANT: Wang, Aljun
13	APPLICANT: Skelky, Yasir A.W.	APPLICANT: Skelky, Yasir A.W.
14	APPLICANT: Henderson, Robert A.	APPLICANT: Henderson, Robert A.
15	APPLICANT: McNeill, Patricia D.	APPLICANT: McNeill, Patricia D.
16	APPLICANT: Fanger, Neil	APPLICANT: Fanger, Neil
17	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
18	FILE REFERENCE: 210121.456C14	FILE REFERENCE: 210121.456C14
19	CURRENT APPLICATION NUMBER: US/09/735,705	CURRENT APPLICATION NUMBER: US/09/735,705
20	CURRENT FILING DATE: 2000-12-12	CURRENT FILING DATE: 2000-12-12
21	NUMBER OF SEQ ID NOS: 419	NUMBER OF SEQ ID NOS: 419
22	SOFTWARE: FASTSEQ for Windows Version 3.0	SOFTWARE: FASTSEQ for Windows Version 3.0
23	SEQ ID NO 343	SEQ ID NO 343
24	LENGTH: 461	LENGTH: 461
25	ORGANISM: Homo sapiens	ORGANISM: Homo sapiens
26	Query Match	Query Match
27	Best Local Similarity 100.0%; Score 2450; DB 9; Length 461;	Best Local Similarity 100.0%; Score 2450; DB 9; Length 461;
28	Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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30	1 MLYENNAQTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNDHAQNSVTASPTAPOS 60	1 MLYENNAQTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNDHAQNSVTASPTAPOS 60

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DB 61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPSHLIRVGENSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPSHLIRVGENSHAQ 180
QY 181 YVEDPITGROSVALPYEPPOVGTETFTVLYNFMCMSSCVGGMNRRPILITVLETRDGOV 240
DB 181 YVEDPITGROSVALPYEPPOVGTETFTVLYNFMCMSSCVGGMNRRPILITVLETRDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPRFRONTHTGIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPRFRONTHTGIOMTSIKRR 300
QY 301 SPDELLLYLPVGRRETYEMLLKIKESLEMOYLPQHTLETYRQOQOQHLLQKOTSIO 360
DB 301 SPDELLLYLPVGRRETYEMLLKIKESLEMOYLPQHTLETYRQOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLKNKMSNMKLPSVSQOLINPOORNALPFTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLKNKMSNMKLPSVSQOLINPOORNALPFTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLPSMSTSHCTPPPPYPTDCSIVRMQV 461
DB 421 DMNGLSPTQALPPLPSMSTSHCTPPPPYPTDCSIVRMQV 461
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RESULT 2
US-09-850-716A-343
; Sequence 343, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Reiter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; NUMBER OF FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-850-716A-343
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Query Match 100.0%; Score 2450; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.5e-197;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLYENNAQOTSEPOYTINGLNSMDQOIONGSSSTPYNTDHAONSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIK 120
QY 181 YVEDPITGROSVALPYEPPOVGTETFTVLYNFMCMSSCVGGMNRRPILITVLETRDGOV 240
DB 181 YVEDPITGROSVALPYEPPOVGTETFTVLYNFMCMSSCVGGMNRRPILITVLETRDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPRFRONTHTGIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPRFRONTHTGIOMTSIKRR 300
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QY 301 SPDELLLYLPVGRRETYEMLLKIKESLEMOYLPQHTLETYRQOQOQHLLQKOTSIO 360
DB 301 SPDELLLYLPVGRRETYEMLLKIKESLEMOYLPQHTLETYRQOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLKNKMSNMKLPSVSQOLINPOORNALPFTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLKNKMSNMKLPSVSQOLINPOORNALPFTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLPSMSTSHCTPPPPYPTDCSIVRMQV 461
DB 421 DMNGLSPTQALPPLPSMSTSHCTPPPPYPTDCSIVRMQV 461
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RESULT 3
US-09-897-778-343
; Sequence 343, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Margerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; NUMBER OF FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-897-778-343
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Query Match 100.0%; Score 2450; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.5e-197;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIK 120
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DB 181 YVEDPITGROSVALPYEPPOVGTETFTVLYNFMCMSSCVGGMNRRPILITVLETRDGOV 240
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DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPRFRONTHTGIOMTSIKRR 300
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DB 301 SPDELLLYLPVGRRETYEMLLKIKESLEMOYLPQHTLETYRQOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLKNKMSNMKLPSVSQOLINPOORNALPFTTIPDGMGANIPMGTHMPMAG 420
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QY 421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIVRMQV 461
Db 421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIVRMQV 461

RESULT 4

US-09-735-705-338
; Sequence 338, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Baugur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-338

Query Match 98.1%; Score 2404; DB 9; Length 586;
Best Local Similarity 99.3%; Pred. No. 2,6e-193;
Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNMOTOFSEPOYTNLGLNSMDQOIONGSSSTSYNTDHAONSTYAPSPYAPSS 60
Db 1 MYLENNMOTOFSEPOYTNLGLNSMDQOIONGSSSTSYNTDHAONSTYAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOSSSTAKSATWTYSTEKLKLYQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOSSSTAKSATWTYSTEKLKLYQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYVYKKAHEVTEVYKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPYVYKKAHEVTEVYKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPTTGROSLVLYPEPPOVGTETFTVLYXNFMCSNCGVGMNRRPILITVLETTRDQV 240
Db 181 YVEDPTTGROSLVLYPEPPOVGTETFTVLYXNFMCSNCGVGMNRRPILITVLETTRDQV 240
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Db 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTAKRPFRONTHGIONTSIKRR 300
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Db 301 SPDDLILYLVYRGRTYEMLLKIKESLEIMQYLPQHTTETTYRQOQOQOHOHLQKOTSIO 360
QY 361 SPSSYGNSSPPLNKNKSNMKNLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLNKNKSNMKNLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPMAG 420
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Db 421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456

RESULT 5

US-09-850-716A-338
; Sequence 338, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-338

Query Match 98.1%; Score 2404; DB 10; Length 586;
Best Local Similarity 99.3%; Pred. No. 2,6e-193;
Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNMOTOFSEPOYTNLGLNSMDQOIONGSSSTSYNTDHAONSTYAPSPYAPSS 60
Db 1 MYLENNMOTOFSEPOYTNLGLNSMDQOIONGSSSTSYNTDHAONSTYAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOSSSTAKSATWTYSTEKLKLYQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOSSSTAKSATWTYSTEKLKLYQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYVYKKAHEVTEVYKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPYVYKKAHEVTEVYKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPTTGROSLVLYPEPPOVGTETFTVLYXNFMCSNCGVGMNRRPILITVLETTRDQV 240
Db 181 YVEDPTTGROSLVLYPEPPOVGTETFTVLYXNFMCSNCGVGMNRRPILITVLETTRDQV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTAKRPFRONTHGIONTSIKRR 300
Db 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTAKRPFRONTHGIONTSIKRR 300
QY 301 SPDDLILYLVYRGRTYEMLLKIKESLEIMQYLPQHTTETTYRQOQOQOHOHLQKOTSIO 360
Db 301 SPDDLILYLVYRGRTYEMLLKIKESLEIMQYLPQHTTETTYRQOQOQOHOHLQKOTSIO 360
QY 361 SPSSYGNSSPPLNKNKSNMKNLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLNKNKSNMKNLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456

RESULT 6

US-09-897-778-338
; Sequence 338, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Mainerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Neil
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

```
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897.778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PR
; ORGANISM: Homo sapiens
; US-09-897-778-338

Query Match      98.1%; Score 2404; DB 10; Length 586;
Best Local Similarity 99.3%; Pred. No. 2,6e-193;
Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNGILNSMDQIQIONGSSSTSPYNTDHAQNSVTAAPSPYAPQSS 60
DB 1 MLYENNAQTOFSEPOYTNGILNSMDQIQIONGSSSTSPYNTDHAQNSVTAAPSPYAPQSS 60
QY 61 TFDALSPSPAIPSTNDYPGHSEFVSPQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSTNDYPGHSEFVSPQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
QY 121 VMPPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGQIAPSSHILIREGNSHAQ 180
DB 121 VMPPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGQIAPSSHILIREGNSHAQ 180
QY 181 YVEDPITGRQSVLPYEPPOVGTETTVLYNFMCNSSCVGAMNRPILLITVLETRDGOV 240
DB 181 YVEDPITGRQSVLPYEPPOVGTETTVLYNFMCNSSCVGAMNRPILLITVLETRDGOV 240
QY 241 LGRRCFARICACGDRKKADEDSIRKQOYSDSTKNGDGTKRPRRONTGHIQMTSIKRR 300
DB 241 LGRRCFARICACGDRKKADEDSIRKQOYSDSTKNGDGTKRPRRONTGHIQMTSIKRR 300
QY 301 SPDELLYLVRGRTYEMLKIKESLELMQYLPQHTIEYRQOQOQHLLQKQTSIQ 360
DB 301 SPDELLYLVRGRTYEMLKIKESLELMQYLPQHTIEYRQOQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLKMNKMLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLKMNKMLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456

RESULT 7
US-09-735-705-152
; Sequence 152, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735.705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
```

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; LENGTH: 586
; TYPE: PR
; ORGANISM: Homo sapien
; US-09-735-705-152

Query Match      97.8%; Score 2397; DB 9; Length 586;
Best Local Similarity 99.1%; Pred. No. 1e-192;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNGILNSMDQIQIONGSSSTSPYNTDHAQNSVTAAPSPYAPQSS 60
DB 1 MLYENNAQTOFSEPOYTNGILNSMDQIQIONGSSSTSPYNTDHAQNSVTAAPSPYAPQSS 60
QY 61 TFDALSPSPAIPSTNDYPGHSEFVSPQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSTNDYPGHSEFVSPQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
QY 121 VMPPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGQIAPSSHILIREGNSHAQ 180
DB 121 VMPPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGQIAPSSHILIREGNSHAQ 180
QY 181 YVEDPITGRQSVLPYEPPOVGTETTVLYNFMCNSSCVGAMNRPILLITVLETRDGOV 240
DB 181 YVEDPITGRQSVLPYEPPOVGTETTVLYNFMCNSSCVGAMNRPILLITVLETRDGOV 240
QY 241 LGRRCFARICACGDRKKADEDSIRKQOYSDSTKNGDGTKRPRRONTGHIQMTSIKRR 300
DB 241 LGRRCFARICACGDRKKADEDSIRKQOYSDSTKNGDGTKRPRRONTGHIQMTSIKRR 300
QY 301 SPDELLYLVRGRTYEMLKIKESLELMQYLPQHTIEYRQOQOQHLLQKQTSIQ 360
DB 301 SPDELLYLVRGRTYEMLKIKESLELMQYLPQHTIEYRQOQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLKMNKMLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLKMNKMLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456

RESULT 8
US-09-850-716A-152
; Sequence 152, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850.716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PR
; ORGANISM: Homo sapien
; US-09-850-716A-152

Query Match      97.8%; Score 2397; DB 10; Length 586;
Best Local Similarity 99.1%; Pred. No. 1e-192;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNGILNSMDQIQIONGSSSTSPYNTDHAQNSVTAAPSPYAPQSS 60
DB 1 MLYENNAQTOFSEPOYTNGILNSMDQIQIONGSSSTSPYNTDHAQNSVTAAPSPYAPQSS 60
QY 61 TFDALSPSPAIPSTNDYPGHSEFVSPQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSTNDYPGHSEFVSPQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
```

Db 61 TFDALSPSPALPSNTDYPGPHSFDSVFSQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNASHAQ 180
Db 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNASHAQ 180
QY 181 YVEDPITGRQSVLVPEPPVGTETFTVLYNFMCNSSCVGMMNRPLILIVTLETBRGOV 240
Db 181 YVEDPITGRQSVLVPEPPVGTETFTVLYNFMCNSSCVGMMNRPLILIVTLETBRGOV 240
QY 241 LGRCFEARIACACGDRKADEDSIRKQVSDSTKNGDGTRKPRRONTGHIOMTSIKRR 300
Db 241 LGRCFEARIACACGDRKADEDSIRKQVSDSTKNGDGTRKPRRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPRRGRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLLQKQTSIQ 360
Db 301 SPDELLYLPRRGRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLLQKQTSIQ 360
QY 301 SPDELLYLPRRGRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLLQKQTSIQ 360
Db 301 SPDELLYLPRRGRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLKMNKSNKLPVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKMNKSNKLPVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456

RESULT 9
US-09-897-778-152
; Sequence 152, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-152

Query Match 97.8%; Score 2397; DB 10; Length 586;
Best Local Similarity 99.1%; Pred. No. 1e-192;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNAGTQFSEPOYTNGILNSMDQIQIONGSSSTSPYNTDHAQNSVTAAPSYAPSS 60
Db 1 MYLENNAGTQFSEPOYTNGILNSMDQIQIONGSSSTSPYNTDHAQNSVTAAPSYAPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDSVFSQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNTDYPGPHSFDSVFSQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNASHAQ 180
Db 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNASHAQ 180
QY 181 YVEDPITGRQSVLVPEPPVGTETFTVLYNFMCNSSCVGMMNRPLILIVTLETBRGOV 240
Db 181 YVEDPITGRQSVLVPEPPVGTETFTVLYNFMCNSSCVGMMNRPLILIVTLETBRGOV 240

QY 241 LGRCFEARIACACGDRKADEDSIRKQVSDSTKNGDGTRKPRRONTGHIOMTSIKRR 300
Db 241 LGRCFEARIACACGDRKADEDSIRKQVSDSTKNGDGTRKPRRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPRRGRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLLQKQTSIQ 360
Db 301 SPDELLYLPRRGRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLLQKQTSIQ 360
QY 301 SPDELLYLPRRGRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLLQKQTSIQ 360
Db 301 SPDELLYLPRRGRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLKMNKSNKLPVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKMNKSNKLPVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456

RESULT 10
US-09-466-396A-152
; Sequence 152, Application US/09466396A
; Publication No. US20030119763A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.455C4
; CURRENT APPLICATION NUMBER: US/09/466,396A
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-466-396A-152

Query Match 97.8%; Score 2397; DB 11; Length 586;
Best Local Similarity 99.1%; Pred. No. 1e-192;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNAGTQFSEPOYTNGILNSMDQIQIONGSSSTSPYNTDHAQNSVTAAPSYAPSS 60
Db 1 MYLENNAGTQFSEPOYTNGILNSMDQIQIONGSSSTSPYNTDHAQNSVTAAPSYAPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDSVFSQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNTDYPGPHSFDSVFSQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNASHAQ 180
Db 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNASHAQ 180
QY 181 YVEDPITGRQSVLVPEPPVGTETFTVLYNFMCNSSCVGMMNRPLILIVTLETBRGOV 240
Db 181 YVEDPITGRQSVLVPEPPVGTETFTVLYNFMCNSSCVGMMNRPLILIVTLETBRGOV 240
QY 241 LGRCFEARIACACGDRKADEDSIRKQVSDSTKNGDGTRKPRRONTGHIOMTSIKRR 300
Db 241 LGRCFEARIACACGDRKADEDSIRKQVSDSTKNGDGTRKPRRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPRRGRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLLQKQTSIQ 360
Db 301 SPDELLYLPRRGRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLLQKQTSIQ 360
QY 301 SPDELLYLPRRGRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLLQKQTSIQ 360
Db 301 SPDELLYLPRRGRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLKMNKSNKLPVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKMNKSNKLPVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMSTSHCTPPPPYPTDCSIV 456

```
RESULT 11
US-09-735-705-344
: Sequence 344, Application US/09735705
: Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C14
: CURRENT APPLICATION NUMBER: US/09/735,705
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 344
: LENGTH: 516
: TYPE: PR
: ORGANISM: Homo sapiens
US-09-735-705-344

Query Match      97.1%; Score 2379; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 2,7e-191;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PÖYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDALSPSPALPSN 74
DB 70 PÖYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDALSPSPALPSN 129
QY 75 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQCAVIRAM 134
DB 130 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQCAVIRAM 189
QY 135 PVYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
DB 190 PVYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQOVIGRRCFEARICACP 254
DB 250 PYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQOVIGRRCFEARICACP 309
QY 255 GRDRKADEDSIRKQOVSDSTKNGDGTKRPRFRONTGHIOMTSIKRRSPDDELLYLPVGR 314
DB 310 GRDRKADEDSIRKQOVSDSTKNGDGTKRPRFRONTGHIOMTSIKRRSPDDELLYLPVGR 369
QY 315 ETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHHLLKQTSIOSPSSYGNSSPPLNK 374
DB 370 ETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHHLLKQTSIOSPSSYGNSSPPLNK 429
QY 375 MNSMNLKLPVSQILNPOORNALPPTTIPDGKANIPMGTHMPAGDMNGLSPTQALPPP 434
DB 430 MNSMNLKLPVSQILNPOORNALPPTTIPDGKANIPMGTHMPAGDMNGLSPTQALPPP 489
QY 435 LSPSTSHCTPPPPYPTDCSIVRIWQY 461
DB 490 LSPSTSHCTPPPPYPTDCSIVRIWQY 516

RESULT 12
US-09-850-716A-344
: Sequence 344, Application US/09650716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
```

```
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Better, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716A
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 344
: LENGTH: 516
: TYPE: PR
: ORGANISM: Homo sapiens
US-09-850-716A-344

Query Match      97.1%; Score 2379; DB 10; Length 516;
Best Local Similarity 100.0%; Pred. No. 2,7e-191;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PÖYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDALSPSPALPSN 74
DB 70 PÖYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDALSPSPALPSN 129
QY 75 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQCAVIRAM 134
DB 130 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQCAVIRAM 189
QY 135 PVYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
DB 190 PVYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQOVIGRRCFEARICACP 254
DB 250 PYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQOVIGRRCFEARICACP 309
QY 255 GRDRKADEDSIRKQOVSDSTKNGDGTKRPRFRONTGHIOMTSIKRRSPDDELLYLPVGR 314
DB 310 GRDRKADEDSIRKQOVSDSTKNGDGTKRPRFRONTGHIOMTSIKRRSPDDELLYLPVGR 369
QY 315 ETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHHLLKQTSIOSPSSYGNSSPPLNK 374
DB 370 ETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHHLLKQTSIOSPSSYGNSSPPLNK 429
QY 375 MNSMNLKLPVSQILNPOORNALPPTTIPDGKANIPMGTHMPAGDMNGLSPTQALPPP 434
DB 430 MNSMNLKLPVSQILNPOORNALPPTTIPDGKANIPMGTHMPAGDMNGLSPTQALPPP 489
QY 435 LSPSTSHCTPPPPYPTDCSIVRIWQY 461
DB 490 LSPSTSHCTPPPPYPTDCSIVRIWQY 516

RESULT 13
US-09-897-778-344
: Sequence 344, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
```

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 344
LENGTH: 516
TYPE: PRF
ORGANISM: Homo sapiens
US-09-897-778-344

Query Match 97.1%; Score 2379; DB 10; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.7e-191;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 POYTMGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDALSPSPAIPSN 74
DB POYTMGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDALSPSPAIPSN 129
QY 75 TDYGPSPHSDVDFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPPPQGAIVIRAM 134
DB 130 TDYGPSPHSDVDFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPPPQGAIVIRAM 189
QY 135 PYYKKAHEVTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 194
DB 190 PYYKKAHEVTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 249
QY 195 PYEPPOVGTEFTTVLYNFMCNSSCVGMMNRRLIIVTLETRDGVLGRCFEARICACP 254
DB 250 PYEPPOVGTEFTTVLYNFMCNSSCVGMMNRRLIIVTLETRDGVLGRCFEARICACP 309
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIKRRSPDDELLYLPVGR 314
DB 310 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIKRRSPDDELLYLPVGR 369
QY 315 EYEMMLIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
DB 370 EYEMMLIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 429
QY 375 NMSMKKLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
DB 430 NMSMKKLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
QY 435 LSMSTSHCTPPPPYPTDCSIVIRIMOV 461
DB 490 LSMSTSHCTPPPPYPTDCSIVIRIMOV 516

RESULT 14

US-09-735-705-339
Sequence 339, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRF
ORGANISM: Homo sapiens
US-09-735-705-339

Query Match 95.9%; Score 2350; DB 9; Length 641;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 POYTMGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDALSPSPAIPSN 74
DB POYTMGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDALSPSPAIPSN 129
QY 75 TDYGPSPHSDVDFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPPPQGAIVIRAM 134
DB 130 TDYGPSPHSDVDFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPPPQGAIVIRAM 189
QY 135 PYYKKAHEVTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 194
DB 190 PYYKKAHEVTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 249
QY 195 PYEPPOVGTEFTTVLYNFMCNSSCVGMMNRRLIIVTLETRDGVLGRCFEARICACP 254
DB 250 PYEPPOVGTEFTTVLYNFMCNSSCVGMMNRRLIIVTLETRDGVLGRCFEARICACP 309
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIKRRSPDDELLYLPVGR 314
DB 310 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIKRRSPDDELLYLPVGR 369
QY 315 EYEMMLIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
DB 370 EYEMMLIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 429
QY 375 NMSMKKLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
DB 430 NMSMKKLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
QY 435 LSMSTSHCTPPPPYPTDCSIV 456
DB 490 LSMSTSHCTPPPPYPTDCSIV 511

RESULT 15

US-09-850-716A-339
Sequence 339, Application US/09850716A
Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRF
ORGANISM: Homo sapiens
US-09-850-716A-339

Query Match 95.9%; Score 2350; DB 10; Length 641;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 POYTMGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDALSPSPAIPSN 74
DB 70 POYTMGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDALSPSPAIPSN 129
QY 75 TDYGPSPHSDVDFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPPPQGAIVIRAM 134
DB 130 TDYGPSPHSDVDFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWTPPPQGAIVIRAM 189
QY 135 PYYKKAHEVTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 194

```

Db      190 PYKKAHEVTEVYKRCPNHEL$RE$FNEGQIAP$SHLIRVEGNSHAQYVEDPITGRQSYLV 249
QY      195 PYEPPOYGETEETVLYNFMGNS$CVGGMNRRPILITVLETRDQVIGRRCFEARICACP 254
Db      250 PYEPPOYGETEETVLYNFMGNS$CVGGMNRRPILITVLETRDQVIGRRCFEARICACP 309
QY      255 GRDRKADED$IRKQOVSD$TKNGD$GTRKPRFRONT$HGIOMT$SIKRRSPDDEL$LYLPVGR 314
Db      310 GRDRKADED$IRKQOVSD$TKNGD$GTRKPRFRONT$HGIOMT$SIKRRSPDDEL$LYLPVGR 369
QY      315 ETYEMLKIKESLELMQYLPQHTIETYROOQOQOHOHLQKOTSIO$PSSYGNS$PPLNK 374
Db      370 ETYEMLKIKESLELMQYLPQHTIETYROOQOQOHOHLQKOTSIO$PSSYGNS$PPLNK 429
QY      375 MNSMNL$PSV$QOLINPOORNAL$PTTIPDGMGANIPM$GTHM$PMAGDMNGLSPTQALPP 434
Db      430 MNSMNL$PSV$QOLINPOORNAL$PTTIPDGMGANIPM$GTHM$PMAGDMNGLSPTQALPP 489
QY      435 LSM$P$T$H$C$T$P$P$P$Y$P$T$D$C$S$IV 456
Db      490 LSM$P$T$H$C$T$P$P$P$Y$P$T$D$C$S$IV 511

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Search completed: August 7, 2003, 09:57:11
 Job time : 21.6814 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: August 7, 2003, 09:42:03 ; Search time 14.534 Seconds

(without alignments)
3050.350 Million cell updates/sec

Title: US-09-538-106-17

Perfect score: 2450

Sequence: 1 MYLENNAGTQFSEPDYTNL.....HCTPPPPYPTDCSIVRIWQV 461

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_76:.*
2: PIR1:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	839.5	34.3	396	1 JH0631	cellular tumor ant
2	762	31.1	363	1 A29376	cellular tumor ant
3	758.5	31.0	367	1 S02193	cellular tumor ant
4	744	30.4	386	1 S51648	cellular tumor ant
5	723	29.5	391	1 S02192	cellular tumor ant
6	712	29.1	396	1 JH0633	cellular tumor ant
7	707.5	28.9	393	1 DNH053	cellular tumor ant
8	703	28.7	393	1 S06594	cellular tumor ant
9	702	28.7	390	1 DMS553	cellular tumor ant
10	700	28.6	391	1 JC6193	tumor suppressor p
11	697.5	28.5	393	2 JC6176	tumor suppressor p
12	688.5	28.1	381	2 S38824	cellular tumor ant
13	259.5	10.6	77	2 T146226	cellular tumor ant
14	138	5.6	925	2 T19361	hypothetical prote
15	135	5.5	1520	1 TVPFA	protein-tyrosine k
16	133.5	5.4	2578	2 A56922	transcription fact
17	129	5.3	963	2 T40290	hypothetical prote
18	129	5.3	964	2 T41547	hypothetical prote
19	129	5.3	1051	2 G59436	KIAA1304 protein f
20	129	5.3	1621	2 T15264	hypothetical prote
21	128.5	5.2	628	2 S19150	hypothetical prote
22	127	5.2	1081	2 S66736	transcription acti
23	126.5	5.2	628	2 JQ0110	hypothetical 69k p
24	126	5.1	590	2 A44068	cell pattern forma
25	126	5.1	2529	2 A56923	transcription fact
26	126	5.1	2897	2 B48666	cell proliferation
27	126	5.1	3256	2 A48666	cell proliferation
28	125.5	5.1	628	2 S01955	hypothetical prote
29	125	5.1	724	2 T47149	hypothetical prote

30	123	5.0	969	2 T15446	hypothetical prote
31	123	5.0	1572	2 S45251	SNF2alpha protein
32	121.5	5.0	947	2 T23107	hypothetical prote
33	120.5	4.9	901	2 JC6093	dead ringer nuclea
34	120	4.9	864	2 H85335	hypothetical prote
35	120	4.9	864	2 T04518	hypothetical prote
36	119	4.9	1145	2 T18235	transcription acti
37	119	4.9	1819	2 T32008	hypothetical prote
38	118.5	4.8	513	2 T41011	hypothetical prote
39	118.5	4.8	1062	2 G86325	hypothetical prote
40	118	4.8	792	2 T26050	hypothetical prote
41	118	4.8	1586	2 S39580	HBW protein - hum
42	117.5	4.8	596	2 T03908	hypothetical prote
43	117	4.8	533	2 JS0304	developmental cont
44	117	4.8	2715	2 T13049	eyelid - fruit fly
45	116.5	4.8	578	2 T22888	hypothetical prote

ALIGNMENTS

RESULT 1

JH0631
cellular tumor antigen p53 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0631
R:de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Sousa, T.
Gene 112, 241-245, 1992
A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A:Reference number: JH0631; MUID:92210006; PMID:1339362
A:Accession: JH0631
A:Molecule type: mRNA
A:Residues: 1-396 <DEF>
A:Cross-references: GB:W5145; NID:g213828; PID:AAA49605.1; PID:g213829
A:Experimental source: liver
A:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; p53
F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match	34.3%	Score 839.5;	DB 1;	Length 396;
Best Local Similarity	55.2%	Pred. No. 9,4e-53;		
Matches 165;	Conservative 47;	Mismatches 79;	Indels 11;	Gaps 6;
QY	49	VTAPSPYAQPS-STFDALS-PSPAIDBSNDYDPPGHSFDVSFQGSSTAKSATWTYTELRK	106	
DB	61	VSATEPAPQPSISTLDTGSPPTSTVPTSDYPGAIGFQLRFLQSSSTAKSVTCYSPDLNK	120	
QY	107	LYCOIAKTCPTQIKVMTPPGAGAVIRAMPVYKKAHEVTEVKKCPNHELSREFNEGOIAP	166	
DB	121	LFQOLAKTCPTQIVQVLDHPPPGAGAVIRALATYKRLSDVADAVKRCPHQOSTSENNEG-AP	179	
QY	167	PSHLIRVGNSSHAQVEDPTTGROSVLVPEPPQVGETFTTVLVNFCNSSCGVGNRRP	226	
DB	180	RGLVLRVGNQREYEDGNTLRHSVLVPEPPQVSECTTVLVNFCNSSCGVGNRRP	239	
QY	227	ILIIIVTLRETDGVLGRCEPARICAPGDRKADEDSIRKQO---VSDTKMGDGTGRP	263	
DB	240	ILIIIVTLRETDGVLGRCEPARICAPGDRKADEDSIRKQO---VSDTKMGDGTGRP	263	
QY	284	FRQ-NTHGIOMTSIKRRS---PDDELLYLPVGRGRTYMLKIKESLLELMYLOPHIT	338	
DB	300	MKEASLPAPQPGASKTKSSPAVSDBETVLTQIRGKEKEMLRKFNDSLELSELVPAADA	359	
QY	339	ETTRQO 344		
DB	360	DKYRQK 365		
RESULT 2	A29376			

cellular tumor antigen p53 - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A29376; S61531; S72313; I51639
 R:Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.
 Oncogene 1, 71-78, 1987
 A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein
 A:Reference number: A29376; MUID:88143684; PMID:2830576
 A:Accession: A29376
 A:Molecule type: mRNA
 A:Residues: 1-363 <SOU>
 A:Cross-references: EMBL:X05191; NID:964961; PIDN:CAA28821.1; PID:964962
 R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knochel, W.
 Oncogene 9, 109-120, 1994
 A:Title: Overexpression of wild-type p53 interferes with normal development in Xenopus 1
 A:Reference number: I51639; MUID:941134403; PMID:8302570
 A:Accession: S61531
 A:Molecule type: mRNA
 A:Residues: 1-293,295-363 <HOE>
 A:Cross-references: EMBL:X7546; NID:9468513; PIDN:CAA54672.1; PID:9468514
 R:Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knochel, W.
 submitted to the EMBL Data Library, March 1994
 A:Reference number: S72313
 A:Accession: S72313
 A:Molecule type: mRNA
 A:Residues: 1-51, S', 53-70, 72-293, 295-363 <HOW>
 A:Cross-references: EMBL:X7546; NID:9468513; PIDN:CAA54672.1; PID:9468514
 A:Gene: p53
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; nucleus; phosph
 F;150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F;362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 31.1%; Score 762; DB 1; Length 363;
 Best Local Similarity 54.5%; Pred. No. 3e-47;
 Matches 151; Conservative 42; Mismatches 68; Indels 16; Gaps 5;

Qy 68 SPAIPSTNDYRPHSPFVSFOQSSSTAKSATWTSTELKLYCOLAKTCPIQIKWTTPPQ 127
 Db 68 SCAVPSTDDYDQKGLQDFQNGTAKSVCTCTSPENLKLFCOLAKTCPLVAVRESPPR 127
 Qy 128 GAVIRAMPYVYKKAHYEVYKRCNHNELSRFNEGQIARPSHLIRVENSNAQVDEPIT 187
 Db 128 GSILRAVAAYKSSHVAEYKRCNHNELSRFNEGQIARPSHLIRVENSNAQVDEPIT 186
 Qy 188 GROSIVLYEPYQGTETTYLYNFMNCSSCVGGMNRRPILITLYLETRDGOVGRGCFE 247
 Db 187 GRHVCVYEPYQGTETTYLYNFMNCSSCVGGMNRRPILITLYLETRDGOVGRGCFE 246
 Qy 248 ARICACPGDRKADSDS-IRKQOVSSTKNGDGTKRPFQNTH--GIQMTSIRKRR--S 301
 Db 247 VRVACACPGDRRREDDNTYKRGKLPKSGK-----RELAKHPPSSSEPLPKRRLVVD 297
 Qy 302 PDDELTYLVGRGTYEMLIKIKESLELMQYLPQHTI 338
 Db 298 DDEETFLIRKRSRYEMIKLMDALELQESLDDQKV 334

RESULT 3
 S02193
 cellular tumor antigen p53 - chicken
 N:Alternate names: nuclear oncoprotein p53
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S02193
 R:Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P.
 Nucleic Acids Res. 16, 11383, 1988
 A:Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.
 A:Reference number: S02193; MUID:89083584; PMID:3060861
 A:Accession: S02193
 A:Molecule type: mRNA
 A:Residues: 1-367 <SOU>

A:Cross-references: EMBL:X13057; NID:963740; PIDN:CAA31456.1; PID:963741
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; nucleus; pho
 F;161,164,224,228/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 31.0%; Score 758.5; DB 1; Length 367;
 Best Local Similarity 52.8%; Pred. No. 5.5e-47;
 Matches 151; Conservative 42; Mismatches 80; Indels 13; Gaps 5;

Qy 48 SVTAPSPYAPSSSTFDALSPDIPSTNDYRPHSPFVSFOQSSSTAKSATWTSTELKL 107
 Db 61 AAAAPSPPLNMP--TPPRAAPSPVYPTEDYGGDDDFRGFEAGCTAKSVCTSPVLNKV 118
 Qy 108 YCOIAKTCPIQIKWTTPPOGAVIRAMPYVYKKAHYEVYKRCNHNELSRFNEGQIARP 167
 Db 119 YCRIAKRCPPYVRGAVAPPPSSILRAVAVYKSEHVAEYKRCNHNELSRFNEGQIARP 177
 Qy 168 SHLIRVENSNAQVDEPITGRQSVLYPEEPYQGTETTYLYNFMNCSSCVGGMNRRPI 227
 Db 178 QHLIRVENSNAQVDEPITGRQSVLYPEEPYQGTETTYLYNFMNCSSCVGGMNRRPI 237
 Qy 228 LIYTLERDGOVGRGCFEARIACPGDRKADSDSIRKQOVSSTKNGDGT--TKRPR 285
 Db 238 LTITLESPPGQILGRGCFEVRVACPGDRKADSDSIRKQOVSSTKNGDGT--TKRPR 290
 Qy 286 QNTGIGQMTSIRKRRSPDELLYLVGRGTYEMLIKIKESLELMQ 331
 Db 291 PPTAPPEPRK-KRYLNPDPNEIFYLVGRGTYEMLIKIKESLELMQ 335

RESULT 4
 S51648
 cellular tumor antigen p53 - bovine
 N:Alternate names: tumor-suppressor protein p53
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
 R:Dequiedt, F.; Williams, L.; Burny, A.; Kettmann, R.
 submitted to the EMBL Data Library, September 1994
 A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and 1t
 A:Reference number: S51648
 A:Accession: S51648
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-386 <DEQ>
 A:Cross-references: EMBL:X81704; NID:9602332; PIDN:CAA57348.1; PID:9602333
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; phosphoprote
 F;168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F;385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 30.4%; Score 744; DB 1; Length 386;
 Best Local Similarity 41.5%; Pred. No. 6.5e-46;
 Matches 164; Conservative 65; Mismatches 120; Indels 46; Gaps 12;

Qy 5 ENNAQTFSEPOYTNLGLL---NSMDQIQNGSSSTSPYN---TDHAQNSYAP-- 52
 Db 7 ELNVEPPLSQETFDLWNLPENNILSELAPVDDLLPYDVAWTWLDCEPNE--ADQMP 64
 Qy 53 ---SPYADPSSTFPALSPSPA-----IPSNIDYRPHSPFVSFOQSSSTAKSATWTYS 101
 Db 65 EPSAPAPPPAT-----PAPATSWPLSSFPVSQKTYGNGFRIQSGTAKSVCTYS 119
 Qy 102 TELKLYCOLAKTCPIQIKWTTPPOGAVIRAMPYVYKKAHYEVYKRCNHNELSRFNE 161
 Db 120 PSLKLYCOLAKTCPIQIKWTTPPOGAVIRAMPYVYKKAHYEVYKRCNHNELSRFNE 179
 Qy 162 GOIAPPSHLIRVENSNAQVDEPITGRQSVLYPEEPYQGTETTYLYNFMNCSSCVG 221
 Db 180 G-LAPPPHLIRVENSNAQVDEPITGRQSVLYPEEPYQGTETTYLYNFMNCSSCVG 238
 Qy 222 MNRPPILITLYLETRDGOVGRGCFEARIACPGDRKADSDSIRKQOVSSTKNGDGT 281


```

Db      ||||||| :||| :||| || :||||||| :||| :||| :|||
239  MNRRPILITILEDSCGMLLGRNSFEVYVCACPGPRDRTEENLRKKQCSQSPPEPPSTK 298
Oy      282  RPRONTHGIOMTSIKRRSP-DDELLYLPVGRREYEMLLKIKESLELMQYLPQHTIET 340
Db      299  RALPTNT-----SSSPQPKKKPLDGEYFTLIQRGRKREMFRELNDALDEL-----KDALDG 349
Oy      341  YRQOQOQOQH-QLLQKQTSIOSPSSYGNSSPPLK 374
Db      350  REPESRAHSHLSKSK---KRSPSCHKKPMKR 380

RESULT 5
S02192
C:cellular tumor antigen p53 - rat
N:Alternate names: gene p53 protein; nuclear oncoprotein p53
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02192; S41149
R:Soussi, T., de Fromental, C.C., Breugnot, C., May, E.
Nucleic Acids Res. 16, 11384, 1988
A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A:Reference number: S02192; MUID:89083585; PMID:3060862
A:Accession: S02192
A:Molecule type: mRNA
A:Residues: 1-391 <SOUT>
A:Cross-references: EMBL:X13058; NID:956828; PIDN:CA31457.1; PID:956829
R:Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A:Title: Structure of the rat p53 tumor suppressor gene.
A:Reference number: S41149; MUID:93181268; PMID:8441680
A:Accession: S41149
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173, 'w', 175-391 <HUL>
A:Cross-references: EMBL:L07909
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:
A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F:174,177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:390/Binding site: phospho-tyr-RNA (Ser) (covalent) #status predicted

Query Match      29.5%  Score 723;  DB 1;  Length 391;
Best Local Similarity  41.1%  Pred. No. 2.1e-44;
Matches 158;  Conservative  64;  Mismatches 116;  Indels  46;  Gaps  9;

Oy      18  TNLGLLMSNO-----QIQNSSSTSPYNTDHAQNSVT-ASPPAQPSTSDALSPS 68
Db      35  TATSPNSMEDLFLPDVAELLEGPEALQVSAQADEPGETAPAPAPASNPWPPLSS 94
Oy      69  PAISNDIDYPPHAFDVSFOOSTAKSATWYSTRELKKYQLQAIKTCPIQIKVTPPG 128
Db      95  --VSQRTQGNCTFHLGFLDQSGTAKSYMCTYSLSLKKLFQIAKTCPPVQLMWTSTPPG 152
Oy      129  AVIRAMPYKKAHVTEVYKRCPNHELRSRENEGQ-IAPSHLIRVGNSHAQYVEDPIT 187
Db      153  TRVRAAMATYKSKQMTVEVRCRNHE--RCSDDGGLAPQHLIRVGNAPYAEVLDLROT 209
Oy      188  GRSVLYPYEPPOVGTETTYLYINFGNCSVGVGAMRRPILIIYLETROQVLYGRCFE 247
Db      210  FRHSVVVYEPPEVGSDDYTIHYKMYCNSSCMGMNRRPILITITLEDSSGNLLGRDSFE 269
Oy      248  ARIACAGRGDKAEDSIRKQVSDSTKNGDGTGRPRONTHGIOMTSIKRRSP-DDEL 306
Db      270  VRVACAGGRDRKTEENFRKKEHCPELPESGARALPTST---SSSPQKKKPLDGEY 325
Oy      307  LYLVGRREYEMLLKIKESLELMQYLPQHTIETVROOQOQOQHLLQKQTSIOSPSSYG 366
Db      326  FTLAIREREREMRELNEALELK-----DAAAEHSGDSRA 362
Oy      367  NSPPLNK--MNSMNLPSVSOL 387

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[illegible]

A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-925 <M1>
 C:Cross-references: EMBL:Z78415; PIDN:CAB01670.1; GSPDB:GND00028; CESP:CI7G1.4
 A:Experimental source: clone CI7G1
 C:Genetics:
 A:Gene: CESP:CI7G1.4
 A:Map position: X
 A:Introns: 40/3; 98/2; 295/1; 443/3; 590/3; 619/3; 691/1; 810/1; 868/3
 C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

Query Match 5.6%; Score 138; DB 2; Length 925;
 Best Local Similarity 23.0%; Pred. No. 0.067;
 Matches 124; Conservative 53; Mismatches 182; Indels 180; Gaps 28;

```

OY 3 YLENN-----AQTF-SEPQYTNGLN-----SMDQIQNGSSST----- 37
DB 407 YNNNNLSPNHGASSLSGQKHGSSPMGSSLMPLNGQYPSMTQNNQSPASISMEPTKEP 466
OY 38 -----SPYNTDHAQNSVTAPSPYAQPSSTPDALSPSPALPSNDYPCGPHSFDVSFOQSS 91
DB 467 AVPIRHSFQPMPTLQSPVHSPSPGAPPA-YNAPSSSKT-PDPTQOQRPHS--PTFAVPT 522
OY 92 TAKSATWYSTEKKLYQIAKTCPIQK-----VMTPT-----PGCAVIR-----AMPYK 138
DB 523 LPAATTLAQAESANQISTK-PKTSQKKHEDGVPEPTADPTPTTYHYELPAMTFIR 581
OY 139 KAENV-----TEVVKRCRNHELSEFNEGOIAPPSHLIRVEG-NSHAQYVEDPTGROSVALY 194
DB 582 DTLHVGRMDKHYHPQEKHYFRKKQQLRVPR-----EGINSHTPTTEPTNTGTFMGNG 635
OY 195 PYEPQVGTETTYLYNPMCNSSCGVGNRRPILITYLETRDGOVLGRCEFEARICACP 254
DB 636 PYEPDK-----YNNM-----VPSQTSHPGLLSR----- 659
OY 255 GRDRKADEDSIRKQOVSDSTKNGDGTAKPRFRONTGIMTSIKRRSPDDEL-----LYL 309
DB 660 -----SQSMHTWPISTNFNAS-----QPTSGRO-PAKARKASDSSEPPENVPH 703
OY 310 PVRGRETYEMLLKIKESLELMQYLPHQTIETTYROOQOQHLLQKQTSI---QSPSSYG 366
DB 704 PSSRGSMQROLOQOQLOMOQY-HQH---MOMQKQOQMAQOQSRMGSGSPSSAG 758
OY 367 N-----SSPPLKNKMSNMKLPVSQGLNPQQRNALPTTITPDGKANTIPMGCTHMPM 418
DB 759 PGSGQLPSLAPSLQRADSPMLPSQOQ-----PPMGG--PM 793
OY 419 AGDMNGLSPTQALP-----PPLSM-----PSTSHCTPPPPYPTDCS 454
DB 794 ANHMGMPMNGTPEGTANNIGLNSNNAAGLPPLSLRSQGPDSQNDPFGIPSTSS 852

```

RESULT 15

TVFPA

protein-tyrosine kinase (EC 2.7.1.112) abl - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C:Date: 15-Nov-1984 #sequence_revision 30-Sep-1989 #text_change 11-Jun-1999

C:Accession: A28128; A00628

R:Henkemeyer, M.J.; Bennett, R.L.; Gertler, F.B.; Hoffmann, F.M.

Mol. Cell. Biol. 8, 843-853, 1988

A:Title: DNA sequence, structure, and tyrosine kinase activity of the *Drosophila melanogaster*

A:Reference number: A28128; MUID:86174728; PMID:2832740

A:Accession: A28128

A:Molecule type: DNA

A:Residues: 1-1520 <HEN>

A:Cross-references: GB:M19692; GB:M18402; NID:g158598; PIDN:AAA28934.1; PID:g158600

R:Hoffmann, F.M.; Fresco, L.D.; Hoffmann-Falk, H.; Shilo, B.Z.

Cell 35, 393-401, 1983

A:Title: Nucleotide sequences of the *Drosophila* src and abl homologs: conservation and v

A:Reference number: A00628; MUID:84082064; PMID:6317185

A:Accession: A00628

A:Molecule type: DNA

A:Residues: 'A', '375', 'AQ', '378-644', 'VGDV' <HOF>

A:Cross-references: GB:K01042; NID:g157175; PIDN:AAA28443.1; PID:g157176
 C:Genetics:
 A:Gene: abl
 A:Introns: 112/1; 130/1; 310/2; 449/1; 644/3; 735/1; 775/2; 805/1; 1350/1
 C:Superfamily: *Drosophila* protein-tyrosine kinase abl; protein kinase homology; SH2 h
 C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transformin
 F:211-260/Domain: SH3 homology <SH3>
 F:271-363/Domain: SH2 homology <SH2>
 F:386-646/Domain: protein kinase homology <KIN>
 F:394-402/Region: protein kinase ATP-binding motif
 F:417/Active site: Lys #status predicted

Query Match 5.5%; Score 135; DB 1; Length 1520;
 Best Local Similarity 21.7%; Pred. No. 0.22;
 Matches 110; Conservative 61; Mismatches 209; Indels 128; Gaps 21;

```

OY 23 LNSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTPDALSPSP-----AI 71
DB 656 LNAATSAASSAPSTSGVATGGATTTTAAAGCASSSAPATASLTLQMYKKGLPGQAL 715
OY 72 PSNTDYCGPHSFDVSFOQSSSTAKSATWTYSTEK-----KLYQIAKTCPIQIKVMTTP 125
DB 716 TPNAHNDPHQ-----QQASTPMSETGSTKLTSTSSQKGNVQMRRTNKKQKQAPAP 770
OY 126 PQGAVIRAM--PYKKAENVTEVVKRC-----PNHELSEFNEGOIAPPSHLIRVEGN 176
DB 771 PKRTSLSSRDSSTYREEDPAN--ARCNFTDLSTNGLARDINS-----LTQRYD 818
OY 177 SHAQYVEDPTGROSVALYVPRPOV-GTEFTTYLYNPMCNSSCGVGNRRPILITYLET 235
DB 819 SETPDAPDPTDATGDSLEQSLQVIAAPYNNKQHSLHSGGGGGGIPSSQOQSSFKR 878
OY 236 RDG-QVIGRCFEARICACPRDRKADEDSIRKQOVSDSTKNGDGTAKPRFRON-----T 288
DB 879 PTGTPVGNRLELR-----QSKRQGLHQAQGRGPRSPRHGNNGVYTS 925
OY 289 HGIMTSIKRRSPDDEL--LPVGRRETYEMLLKIKESLELMQYLPHQTIETTYROOQ 346
DB 926 HPITVGLDVNNKQVNNRGTLP-KGARIGAYLDSLEDSSEAPALP----- 972
OY 347 QQHQLQKQTSISQSPSSYGNSSPPLKNKMSNMKLPVSQGLNPQQRNALPTTITPD 403
DB 973 -----ATAPSLPRANGHATPAPARLN-----PAASP-TPQQAIRNSSSGGYTMQN 1017
OY 404 GCGANIPM-----GTHNPM-----AGDMNGLSPTQA--LPPL 435
DB 1018 NAAASLNKLGQHRRTTGTMTTFSSFRAGSSSPKRSASGAVAGVPALANLEFPPL 1077
OY 436 SM--PSTSHCTPPPPYPTDCSYIRIQ 460
DB 1078 DLPPPEFEFGPPPPPPAPESAVQAIQ 1105

```

Search completed: August 7, 2003, 09:53:29
 Job time : 15.534 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: August 7, 2003, 09:32:13 ; Search time 8.17537 Seconds

(without alignments)
2651.784 Million cell updates/sec

Title: US-09-538-106-17

Perfect score: 2450
Sequence: 1 MLYENNAQTFSEPPYTNL.....HCTPPPYPTDCSIVIMQV 461

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1415.5	57.8	636	P73_HUMAN	O15350 homo sapien
2	1408.5	57.5	637	P73_CERAE	O9X8K8 cercopithec
3	839.5	34.3	396	P53_ONCMY	P25035 oncorhynchu
4	819.5	33.4	369	P53_BARBU	O9W678 barbatus barb
5	806.5	32.9	373	P53_BARBU	P79734 brachydanio
6	795	32.4	376	P53_ICTPU	O93379 ictalurus p
7	762	31.1	363	P53_XENLA	P07193 xenopus lae
8	761.5	31.1	366	P53_PIG	O9tub2 sus scrofa
9	758.5	31.0	367	P53_CHICK	P10360 gallus gall
10	753.5	30.8	386	P53_FELCA	P41685 felis silve
11	745	30.4	367	P53_TEMMU	O9W679 tetraodon m
12	744	30.4	381	P53_CANFA	O29537 canis famill
13	744	30.4	386	P53_BOVIN	O29628 bos taurus
14	738.5	30.1	391	P53_MARMO	O36006 marmota mon
15	737.5	30.1	352	P53_ORYLA	P79620 oryzias lat
16	727	29.7	382	P53_SHEEP	P51664 ovis aries
17	723	29.5	391	P53_RAT	P10361 rattus norv
18	721	29.4	391	P53_CAVPO	O9W676 cavia porce
19	719.5	29.4	393	P53_TUGB	O9tub1 tupia glis
20	717.5	29.3	366	P53_PLAIF	O12246 platichthys
21	712	29.1	396	P53_MESAU	O00066 mesocricetu
22	707.5	28.9	393	P53_HUMAN	P04637 homo sapien
23	703	28.7	314	P53_SPEBE	O64662 spermophilu
24	703	28.7	393	P53_CERAE	P13481 cercopithec
25	703	28.7	393	P53_CERAE	P56423 macaca fasc
26	703	28.7	393	P53_MACMU	P56424 macaca mula
27	702.5	28.7	342	P53_XIPHE	O57338 xiphophorus
28	702.5	28.7	342	P53_XIPMA	O92143 xiphophorus
29	702	28.7	390	P53_MOUSE	P02340 mus musculu
30	701.5	28.6	393	P53_CRIGR	O09185 cricetulus
31	700	28.6	391	P53_RABIT	O95380 oryctolagus
32	689.5	28.1	280	P53_HORSE	P79892 equus cabal
33	591.5	24.1	207	P53_EQUAS	O29480 equus asinu

34	135	5.5	1520	1	ABL_DROME	P00522 drosophila
35	134.5	5.5	1386	1	ZAP3_MOUSE	O9r017 mus musculu
36	129.5	5.3	766	1	TLR4_MOUSE	O62441 mus musculu
37	129	5.3	964	1	YOKA_SCHPO	O74522 schizosacch
38	128.5	5.2	628	1	V70K_TYMC	P28478 turnip yell
39	128.5	5.2	766	1	TLR4_HUMAN	O04727 homo sapien
40	128.5	5.2	1544	1	TUSP_HUMAN	O9nr14 homo sapien
41	127	5.2	1081	1	GALY_YEAST	P19659 saccharomyc
42	126.5	5.2	628	1	V70K_TYMA	P20131 turnip yell
43	126	5.1	590	1	STUA_EMENT	P36011 emeritella
44	126	5.1	356	1	K167_HUMAN	P46013 homo sapien
45	125.5	5.1	628	1	V70K_TYMV	P10357 turnip yell

ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	636 AA.
P73_HUMAN	O15350	O15351	O9WTK8		
AC	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Tumor protein p73 (p53-like transcription factor) (p53-related protein).				
GN	TP73 OR P73.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid-9606;				
XP	SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).				
RC	TISSUE=Colon;				
RC	MEDLINE=97433090; PubMed=9288759;				
RA	Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A.,				
RA	Miny A., Chalton P., Lelias J.-M., Dumont X., Ferrara P., McKeon F.,				
RA	Caput D.;				
RT	*Monoclonally expressed gene related to p53 at 1p36, a region				
RT	frequently deleted in neuroblastoma and other human cancers.;				
RL	Cell 90:809-819(1997).				
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).				
RP	MEDLINE=99289209; PubMed=10362363;				
RA	Yoshikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagihara K.,				
RA	Harris C.C.;				
RT	*Mutational analysis of p73 and p53 in human cancer cell lines.;				
RL	Oncogene 18:3415-3421(1999).				
RP	SEQUENCE FROM N.A. (ISOFORM GAMMA AND DELTA).				
RP	MEDLINE=98389621; PubMed=9721206;				
RA	Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B.,				
RA	Jenkins R., Smith D.I., Liu W.;				
RT	*Genomic organization and mutation analysis of p73 in				
RT	oligodendrogliomas with chromosome 1 p-arm deletions.;				
RL	Genomics 51:359-363(1998).				
RP	SEQUENCE FROM N.A. (ISOFORM GAMMA AND DELTA).				
RP	TISSUE=Neuroblastoma;				
RC	MEDLINE=99021697; PubMed=9802988;				
RA	De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,				
RA	Annunziarico-Petruzzelli M., Levero M., Melino G.;				
RT	*Two new p73 splice variants, gamma and delta, with different				
RT	transcriptional activity.;				
RL	J. Exp. Med. 188:1763-1768(1998).				
RP	SEQUENCE FROM N.A. (ISOFORM EPSILON AND ZETA).				
RP	TISSUE=Breast cancer, Hepatoma, Lymphocytes, and Skin;				
RC	MEDLINE=99310938; PubMed=10381648;				
RA	Costanzo A., Catani M.V., Terrinoni A., Corazzari M., Melino G.,				
RA	De Laurenzi V., Knight R.A.;				
RT	*Additional complexity in p73: induction by mitogens in lymphoid cells				
RT	and identification of two new splicing variants epsilon and zeta.;				

RL Cell Death Differ. 6:389-390(1999).
 RL [6]
 RP SEQUENCE FROM N.A. (ISOFORM KAPPA).
 RA Thomas D.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
 RA MEDLINE=99318135; PubMed=10391251;
 RP MEDLINE=99217940; PubMed=10203277;
 RA Kaelin W.G. Jr.;
 RL "The emerging p53 gene family";
 RL J. Natl. Cancer Inst. 91:594-598(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 439-506.
 RA MEDLINE=99380160; PubMed=10449409;
 RL Chi S.W., Ayed A., Arrowsmith C.H.;
 RL "Solution structure of a conserved C-terminal domain of p73 with
 structural homology to the SAM domain.";
 RL EMBO J. 18:4438-4445(1999).
 RL -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
 CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
 CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
 CC PROTEIN.
 CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
 CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
 CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
 CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
 CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing: Named isoforms=7;
 CC Name=Alpha:
 CC IsoId=O15350-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=O15350-2; Sequence=VSP_006539;
 CC Name=Gamma;
 CC IsoId=O15350-3; Sequence=VSP_006540, VSP_006541;
 CC Note=The splicing of exon 11 results in a frameshift from the
 CC original reading frame.
 CC Name=Delta;
 CC IsoId=O15350-4; Sequence=VSP_006542, VSP_006543;
 CC Name=Epsilon;
 CC IsoId=O15350-5; Sequence=VSP_006544, VSP_006545;
 CC Note=The splicing of exon 11 results in a frameshift from the
 CC original reading frame. The splicing of exon 13 reverts the
 CC reading frame to the sequence of isoform Alpha;
 CC Name=Zeta;
 CC IsoId=O15350-6; Sequence=VSP_006546;
 CC Name=Kappa;
 CC IsoId=O15350-7; Sequence=VSP_006538;
 CC -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
 CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
 CC -1- INDUCTION: NOT INDUCED BY DNA DAMAGE.
 CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
 CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
 CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
 CC -1- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE
 CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
 CC IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
 CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

CC				This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).
CC				-----
DR	EMBL	Y11416; CAA72220.1; -;		
DR	EMBL	Y11416; CAA72221.1; -;		
DR	EMBL	Y11416; CAA72219.1; -;		
DR	EMBL	AF077628; AAC61887.1; -;		
DR	EMBL	AF077616; AAC61887.1; JOINED.		
DR	EMBL	AF077617; AAC61887.1; JOINED.		
DR	EMBL	AF077618; AAC61887.1; JOINED.		
DR	EMBL	AF077619; AAC61887.1; JOINED.		
DR	EMBL	AF077620; AAC61887.1; JOINED.		
DR	EMBL	AF077621; AAC61887.1; JOINED.		
DR	EMBL	AF077624; AAC61887.1; JOINED.		
DR	EMBL	AF077625; AAC61887.1; JOINED.		
DR	EMBL	AF077626; AAC61887.1; JOINED.		
DR	EMBL	AF077627; AAC61887.1; JOINED.		
DR	EMBL	AF079094; AAD39696.1; -;		
DR	EMBL	AF079082; AAD39696.1; JOINED.		
DR	EMBL	AF079083; AAD39696.1; JOINED.		
DR	EMBL	AF079084; AAD39696.1; JOINED.		
DR	EMBL	AF079085; AAD39696.1; JOINED.		
DR	EMBL	AF079086; AAD39696.1; JOINED.		
DR	EMBL	AF079087; AAD39696.1; JOINED.		
DR	EMBL	AF079088; AAD39696.1; JOINED.		
DR	EMBL	AF079089; AAD39696.1; JOINED.		
DR	EMBL	AF079090; AAD39696.1; JOINED.		
DR	EMBL	AF079091; AAD39696.1; JOINED.		
DR	EMBL	AF079092; AAD39696.1; JOINED.		
DR	EMBL	AF079093; AAD39696.1; JOINED.		
DR	EMBL	AL136528; CAB82742.1; -;		
DR	PDB	1COK; I7-AUG-99.		
DR	PDB	1DXS; 08-AUG-01.		
DR	TRANSFAC	T04931; -;		
DR	Genew	HGNC:12003; TP73.		
DR	MIM	601990; -;		
DR	GO	GO:0003700; F:transcription factor activity; TAS.		
DR	GO	GO:0008630; P:induction of apoptosis by DNA damage; TAS.		
DR	GO	GO:0006298; P:mismatch repair; TAS.		
DR	InterPro	IPR002117; PS3.		
DR	InterPro	IPR001607; SAM.		
DR	Pfam	PF00870; P53; 1.		
DR	Pfam	PF00536; SAM; 1.		
DR	PRINTS	PR00386; P53SUPPRESSOR.		
DR	ProDom	PD002681; P53; 1.		
DR	SMART	SM00454; SAM; 1.		
DR	PROSITE	PS00348; P53; 1.		
KW	Transcription regulation; Activator; DNA-binding; Anti-oncogene; Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing; 3d-structure.			
FT	DOMAIN	1 46 TRANSACTIVATION (BY SIMILARITY).		
FT	DOMAIN	1 55 ASP/GLU-RICH (ACIDIC).		
FT	DOMAIN	287 304 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).		
FT	DOMAIN	346 435 MEDIATES OLIGOMERIZATION (POTENTIAL).		
FT	DOMAIN	168 171 POLY-PRO.		
FT	DOMAIN	391 394 POLY-GLN.		
FT	DOMAIN	483 486 POLY-PRO.		
FT	DOMAIN	131 310 DNA-BINDING (POTENTIAL).		
FT	MOD_RES	99 PHOSPHORYLATION (BY ABL) (IN ISOFORM BETA).		
FT	VARSPLIC	282 282 g -> GMRCHRWVLCGRGLSRPVLCGPSG (in isoform kappa).		
FT	VARSPLIC	495 636 /FTID-VSP_006538		
FT		SFLWTGCLQPCNCTETFTSQGLSTIHLONLTIEDLGALKIRE QYRTITNGLODLKQGHDSYAQDLLSSNNATISIGSSE LQRQWEAVEHFRVRHTITTPNRGGPGCGDEWDVFDFDP DCKRAKVEEKEFEAEIH -> RTMCP (in isoform DCKRAKVEEKEFEAEIH)		


```

Query Match          57.8%; Score 1415.5; DB 1; Length 636;
Best Local Similarity 53.6%; Pred. No. 1.7e-89;
Matches 283; Conservative 50; Mismatches 85; Indels 27; Gaps 10

QY 22 LNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSVAQSPSTEDALSPSPALPSNTDYPGPH 81
DB 67 LLSSTMDQMSRAASAPSYTPEHAA-SVPTHSAPYQSPSTFDMSAPAPYIPNTDYPGPH 125
QY 82 SFVDSFQOSSAKFASATWYTSLETKLKYQIAKTCIGTQIKVMTPPQGAIVAMPYKKA 141
DB 126 HFEVTFQOSSAKFASATWYTSLETKLKYQIAKTCIGTQIKVSTPPPGTAIRAMPYKKA 185
QY 142 HVEVYVRCRPHNELSREFNEGOIAPPSHLIRFGSHQVYEDPTTGOSYLVVEPEPOY 201
DB 186 HVTQVYRCRPHNELGRDNEQASAPSHLIRFGSHNSQYVDDPTGROSVPVPEPEPOY 245
QY 202 GTEFTTVLYNPMCNSSCGVGNRRRILITVLETGQVLGRRCFEARICACPGDRKAD 261
DB 246 GTEFTTVLYNPMCNSSCGVGNRRRILITVLETMRDQVLGRRSPEGRICACPGDRKAD 305
QY 262 EDSIRKQOV--SDSTKNDGDKRKPRRQTHQIM--TSIKRRSPDDELITVYVGRETY 317
DB 306 EDHREQOALNESSAKNGAASKRAFKOSPAPVAPALGAVYKKRRHDEFTYTLQVYGRERF 365
QY 318 EMLIKRESLEIMQYLPOHTEYTRQOQOQOHOHLQKOTSISQSPSSYGNSSPUNKMN- 376
DB 366 EILMKIKRESLEIMELVYRQPLVDSTRQOQ-----LLQRPSHIQ-PPSIGPVLSPMKKHG 419
QY 377 SMNKLPSYSQILN--PQQRNALTPPTTIDPGMCAINPMKGTN--MPMAGDNMGLSPQAL 431
DB 420 GMNKLPSYNQVLVGP RPSSASATPYMGVPGG---MLNNHGHAVPANGEMSSSHAO-- 473
QY 432 PPLSPMSTSHCTPPPPYTCQSY 456
DB 474 ---SMVSGSHCTPPPHADPSLV 494

RESULT 2
P73-CERAE
ID P73-CERAE STANDARD: PRT: 637 AA.
AC 09XSK8; 09TSQ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor protein p73 (p53-like transcription factor) (p53-related protein).
DE TP73 OR P73.
GN Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RP TISSUE=Kidney;
RA Caput D.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN
CC (BY SIMILARITY).
CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named Isoforms=2;
CC Name=Alpha;
CC IsoId=Q9XSK8-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=Q9XSK8-2; Sequence=VSP_006537;
CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSCATION DOMAIN, A CENTRAL DNA

```

```
CC BLINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
-----
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CC -----
DR EMBL; Y11419; CAAT2224.1; -.
DR DR EMBL; Y11419; CAAT2225.1; -.
DR HSSP; O13350; ICOK.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00386; P53SUPPRESSOR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Transcription regulation; Activator; DNA-binding; Anti-oncogene;
KW Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing;
FT VASPLIC 495 637
FT FT
FT FT
FT FT
SO SEQUENCE 637 AA; 69630 MW; 7CB200B919C9C70A CRC64;
Query Match 57.5%; Score 1408.5; DB 1; Length 637;
Best Local Similarity 63.1%; Pred. No. 5.1e-89;
Matches 281; Conservative 51; Mismatches 86; Indels 27; Gaps 10;
QY 22 LNSMDQOIQNGSSSTSPYNTDHAQNSVTABSPYAOPDSSTFDALSPSDAIPSNMIDYRGP 81
DB 67 LLSTMDQMSSRAASAPYPTEHNA-SVPTSPYAOPSSTEDTMSPAIVPSNMDYRGPH 125
QY 82 SFVYSFOOSSAKKATWTYSLELKLLKLCQAIAKTPIQIKWTPPPQCAVIRAMVYKKAE 141
DB 126 HEFETFOOSSFAKSATWTYSPLEKLKLCQAIAKTPIQIKVASAPPFGAIRAMPVYKKA 185
QY 142 HVTEVAVRCRPHETSRENEGOIAPPSHLIRVEGNSHAOVVEDITGRSVLYVEPEPV 201
DB 186 HYVDIVARCENHEIGRPNEGQSAPASHLIRVENNNISQYDDVYTGRQSVVYVERPY 245
QY 202 GTETTYLVNFMNCSSCVGGNNRRRLIIYLLETTRDGQVLGRFCFEARICACPGRRDKAD 261
DB 246 GTEETTYLVNMCSSCVGGNNRRRLIIILTLETTRDGQVLGRSGEGRICACPGRRDKAD 305
QY 262 EDSTRKQGV--SDSKNGDGTKRPFRRONTGIQW--TSIKRSPPDEDLAYLPVRGETY 317
DB 306 EDHYREQOALNESSAKNGASKRAFQKSPPAVPLGLGVKKRRRDDEDTYYLQVRGENE 365
QY 318 EMLIKIKESLELMQYLPOHTIETYRQQOQHQLLKQTSIQSPSSYGNSSPFLNMKN- 376
DB 366 ELIMKLKESLEMLQVLPOLVDSTRQOO----LLQRPShLO-PSTGYPLSPMNKHVG 419
QY 377 SMMKLFPVSQILIN--POQRNALPFTTTPIDKGANIPMKGT---MPNAGDMNGSLPTQAL 431
DB 420 GVNKLPLSVNQLDVGGPRPHSAAPRNPLGPRVSG---MLNNHGVAVPANSENSETSHGNO-- 473
QY 432 PPPLSMPSHCHCPPPPYPPTDCSLV 456
DB 474 ----SNVSGSCHCTPPPYHADPSLV 494
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AC p25035;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9221006; PubMed=1339362;
RA de Fromental C.C.; Padkel F.; Chapus A.; Baney C.; May P.; Soussi T.;
RT "Rainbow trout p53: cDNA cloning and biochemical characterization.";
RL Gene 112:241-245(1992).

-1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
Bax and Fas antigen expression, or by repression of Bcl-2
expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC -----
DR EMBL; M75145; AAA49605.1; -.
DR PIR; JH0631; JH0631.
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DNASIS 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNASIS 90 281 BY SIMILARITY.
FT DNASIS 325 356 OLIGOMERIZATION.
FT DNASIS 369 392 BASIC (REPRESSION OF DNA-BINDING).
FT DNASIS 303 318 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 396 AA; 43966 MW; 8422250765545A1C CRC64;

Query Match 34.3%; Score 839.5; DB 1; Length 396;
Best Local Similarity 55.2%; Pred. No. 2.2e-50;
Matches 169; Conservative 47; Mismatches 79; Indels 11; Gaps 6;

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DB 240 ILTIETLEDEGQLGRSEFVRVACPGDRKTEELINLKQDSTTETKPAQGIKRA 299
OY 284 FRO-NTGIGIOMTSIKRRS-----PDDELLVPVGREYTELKIKESLEIMQYLPQHTI 338
DB 300 MKEASLAPQPGASKTKRSSPAVSDETYLTQINGKEKYEKLFKFNDSLSELVPAADA 359
OY 339 ETVRQO 344
DB 360 DKYRQK 365

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RESULT 4

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P53_BARBU STANDARD; PRT; 369 AA.
ID P53_BARBU
AC 09W678;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Barbus barbus (Barbel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Barbus.
OX NCBI_TaxID=40830;
RN [1]
RP SEQUENCE FROM N.A.
RA Bhaskaran A.; May D.; Rand-Weaver M.; Tyler C.R.;
RT "Evolutionary conservancy of p53 gene sequences in fish.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
Bax and Fas antigen expression, or by repression of Bcl-2
expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

-----
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CC -----
DR EMBL; AF071570; AAD34212.1; -.
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DNASIS 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNASIS 66 256 BY SIMILARITY.
FT DNASIS 298 329 OLIGOMERIZATION.
FT DNASIS 342 365 BASIC (REPRESSION OF DNA-BINDING).
FT DNASIS 276 292 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 368 368 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 369 AA; 41233 MW; 0BE2CF2CEA74C304 CRC64;

Query Match 33.4%; Score 819.5; DB 1; Length 369;
Best Local Similarity 51.2%; Pred. No. 4.6e-49;
Matches 167; Conservative 49; Mismatches 87; Indels 23; Gaps 8;

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CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL: AF074967; AAC26824.1; -.
DR HSSP: P04637; ITUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DNAS_BIND 1 36 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNAS_BIND 77 268 BY SIMILARITY.
FT DOMAIN 303 334 OLIGOMERIZATION.
FT DOMAIN 347 372 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 285 298 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 375 375 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 376 AA; 41989 MW; 1B89CD98DB3289F2 CRC64;

Query Match 32.4%; Score 795; DB 1; Length 376;
Best Local Similarity 53.4%; Pred. No. 2.2e-47;
Matches 156; Conservative 44; Mismatches 88; Indels 4; Gaps 3;

QY 53 SPVQPSSTPDALSPSPAIPTNTDYPGPHSDVSPFOOSSTAKSATWYSTEKLKLYCOIA 112
DB 56 SDMLQPOSS--SSPPTSTVPTSDYPIGLNFTLHFOESSGKSYCTCTSPDLNKLFCOLA 113
QY 113 KTCPIQIKVMTPPROGAVIRAMPYKKAHEVTEVVKRCPNELHREFNEGSIAPSHIR 172
DB 114 KTCVYLAIVASSPPGSLVLRATVAYKSEHAIVVRRCPHERNSDSDGP-APPGHILR 172
QY 173 VEGNSHAQYVEDPITGROSVLVPEPQVGTETFTVLYNFCNSSCYGAMRRPILITVT 232
DB 173 VEGNSRAVYQEDGMTQAHSVVPEPQVGSQSTVLVLYNFCNSSCYGAMRRPILITVT 232
QY 232 LETFDGQVLRGRCEARICACPGDRKADSDSIRKQVSDSTKNGDGTFRPFRONTGIG 292
DB 233 LETDGHILGRTRFEVRVACPGDRKTEESNFKQQ-EPKTSKTLTKRSMKDPSPSHE 291
QY 293 MTSIKRRSPDELLYLVGRGRTYEMLKIKESLELMQVYPOHTIETRYRO 344
DB 292 ASKSKSSSDDELYTLQVGRKEREFLKTKINDGLESIDVVPADQEKYRK 343

RESULT 7
P53_XENIA
ID P53_XENIA STANDARD: PRT: 363 AA.
AC P07193;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE-98143684; PubMed-2830576;
RA Soussi T., de Fromental C.C., Mechali M., May P., Kress M.;
RT "Cloning and characterization of a cDNA from Xenopus laevis coding
RT for a protein homologous to human and murine p53.";
RL Oncogene 1:71-78(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-94134403; PubMed-8302570;
RA Hoevers M., Clement J.H., Medlich D., Montenarh M., Knoechel W.;
RT "Overexpression of wild-type p53 interferes with normal development
RT in Xenopus laevis embryos.";
RL Oncogene 9:109-120(1994).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL: M36962; AAA49923.1; -.
DR EMBL: X05191; CA28821.1; -.
DR EMBL: X77546; CA54672.1; -.
DR EMBL: S68353; AAC60746.1; -.
DR PIR: A29376; A29376.
DR HSSP: P04637; ITUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DNAS_BIND 1 29 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNAS_BIND 76 267 BY SIMILARITY.
FT DOMAIN 300 331 OLIGOMERIZATION.
FT DOMAIN 344 356 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 281 293 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 362 362 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 52 52 T->S (IN REF. 2).
FT CONFLICT 71 71 MISSING (IN REF. 2).
FT CONFLICT 296 296 MISSING (IN REF. 2).
SQ SEQUENCE 363 AA; 40692 MW; CE1F3E58F020D74D CRC64;

Query Match 31.1%; Score 762; DB 1; Length 363;
Best Local Similarity 54.5%; Pred. No. 3.9e-45;
Matches 151; Conservative 42; Mismatches 68; Indels 16; Gaps 5;

QY 68 SPAIPSTWDYGPSPFVSFQOSSTAKSATWYSTEKLKLYCQIAKTCPIQIKVMTPPQ 127
DB 68 SCAVPSYDDYAGKGLQDPQNGTAKSVCTYSPELNKLFCQIAKTCPIVLRSPSPR 127
QY 128 GAVIRAMPYKKAHEVTEVVKRCPNELHREFNEGSIAPSHIRVGENSHAQYVEDPIT 187
DB 128 GSILRAVAVYKKSHEVAVVVKRCPHERNSVPEGE-DAAPSHILRVGENSHQAYMEVNS 186
QY 188 GROSVLVPEPQVGTETFTVLYNFCNSSCYGAMRRPILITVTLEPFGQVLRGRCE 247

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CC EMBL: X13057; CAA31456.1;
DR PIR: S02193; S02193.
DR HSSP: P04637; 1TUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KM Anti-oncogene: DNA-binding: Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 30 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNABIND 87 278 BY SIMILARITY.
FT DOMAIN 308 339 OLIGOMERIZATION.
FT DOMAIN 347 364 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 292 306 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 367 AA; 40169 MW; FC37D0FCDF9195B6 CRC64;

Query Match 31.0%; Score 758.5; DB 1; Length 367;
Best Local Similarity 52.8%; Pred. No. 6.8e-45;
Matches 151; Conservative 42; Mismatches 80; Indels 13; Gaps 5;

QY 48 SVTAPSPYAPSSFTDALSPPALPSTNDYGPSPFVSFOQSSSTAKSATWTYTELKL 107
DB 61 AAAAPPLNMP--TPPRAAPSPVSTEDYCGDFRFGVEAGTAKSVTCTYSPVLNKV 118
QY 108 YCOLAKTCPIQIKYMPPOGAVIRAMPYKKAHTEVYKRCNHLSRFNGGOTAP 167
DB 119 YCRALKPCPVQKGVAPPPSSLRVAAYKSSHVAEYKRCNHEGCGGTG-LAPA 177
QY 168 SHLRVESHQAQYVEDPITGRQSVLYPEPQVTEFTVLYVFMSCSCVGMNRRPI 227
DB 178 QHLRVESNPGARHDEETTKRHSVVVYPEPEVGSODCTVLYVFMSCSCGMGNRRPI 237
QY 228 LIYVLETRQGVYGRCFEAKRICACGRRKADSDSTRKQVSDSTRKNGC--TKRPR 285
DB 238 LTITLLEPGQGLGRCFEVRVACACGRRKRIEENR-----RGAGGVAKRRMS 290
QY 286 QNTGCIQMTSIRKRRSPDELLYPVGRRETYEMLKIKESLEMO 331
DB 291 PPTAPPEPR-KRYLNPDEIFLYQVGRRRREMLKEINELQALAE 335

RESULT 10
P53_FELCA STANDARD; PRT; 386 AA.
ID P53_FELCA AC P41685;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR TRP53.
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCB1;taxid=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Lymph node;
RX MEDLINE-94333960; PubMed-8056458;
RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y.,
RA Watarai T., Gotsuka R., Tsujimoto H., Hasegawa A.;
RT "Cloning of feline p53 tumor-suppressor gene and its aberration in
hematopoietic tumors."
RL Int. J. Cancer 58:602-607(1994).
RN [2]
RP SEQUENCE OF 34-354 FROM N.A.
RX MEDLINE-94114699; PubMed-8286534;
RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watarai T., Gotsuka R.,
RA O'Brien S.J., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning and chromosomal mapping of feline p53 tumor
suppressor gene."

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RL J. Vet. Med. Sci. 55:801-805(1993).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotetramer (by similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
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CC -----
DR EMBL: D26608; BAA05653.1; -.
DR EMBL: D16460; BAA03927.1; -.
DR HSSP: P04637; 10LG.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KM Anti-oncogene: DNA-binding: Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNABIND 94 285 BY SIMILARITY.
FT DOMAIN 318 349 OLIGOMERIZATION.
FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRK) (BY
FT SIMILARITY).
FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 285 285 K -> R (IN REF. 2).
SQ SEQUENCE 386 AA; 42692 MW; D08B43BA1BC8E78 CRC64;

Query Match 30.8%; Score 753.5; DB 1; Length 386;
Best Local Similarity 49.8%; Pred. No. 1.6e-44;
Matches 147; Conservative 49; Mismatches 82; Indels 17; Gaps 4;

QY 43 DHAQNSTAPSPYAPSSFTDALSPPALPSTNDYGPSPFVSFOQSSSTAK 94
DB 58 DDASGMSAVPAPAPAPAT-----PAPALSWPLSSFPQKTYGAVGFLGDSGTAK 112
QY 95 SATWTYTELKLKYQIAKTCPIQIKYMPPOGAVIRAMPYKKAHTEVYKRCNHE 154
DB 113 SVTCTYSPPLNKLFQQLAKTCPVQWVRSPPEPCTCVRAAIYKSSFEVYVRCPHNE 172
QY 155 LSREFNGOIALPESHLIRVESHQAQYVEDPITGRQSVLYPEPQVTEFTVLYVFM 214
DB 173 RCPDSSDG-LAPPOHLIRVESHNLAKTLDNRNFRHSVVVYPEPEVGSODCTVHYVFC 231
QY 215 NSSCVGMNRRPIIYVLETRQGVYGRCFEAKRICACGRRKADSDSTRKQVSDST 274
DB 232 NSSCGMGNRRPIITITLDSNKLGRSFVRVACACGRRRRIEENFRKKGECP 291
QY 275 KNGDTRPRFRONTGQIMTSIKKRRSPDELLYPVGRRETYEMLKIKESLEL 329
DB 292 PPTPSTRALPPST--STPPQKKKPLDVEYFTLQIRGRERFERMELNEALEL 343

RESULT 11
P53_METMO

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ID      P53_TETMU      STANDARD:      PRT:      367 AA.
AC      Q9W679;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DE      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Cellular tumor antigen p53 (Tumor suppressor p53).
GN      TP53 OR P53.
OS      Tetraodon murtus (Congo puffer).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC      Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
OC      Tetraodontidae; Tetraodontidae; Tetraodon.
OX      NCBI_TaxID=94908;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-Ovary;
RA      Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
RT      "Evolutionary conservancy of p53 gene sequences in fish.";
RL      Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
CC      -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC      growth arrest or apoptosis depending on the physiological
CC      circumstances and cell type. Involved in cell cycle regulation as
CC      a trans-activator that acts to negatively regulate cell division
CC      by controlling a set of genes required for this process. One of
CC      the activated genes is an inhibitor of cyclin-dependent kinases.
CC      Apoptosis induction seems to be mediated either by stimulation of
CC      BAX and FAS antigen expression, or by repression of Bcl-2
CC      expression (By similarity).
CC      -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AF071571; AAD34213.1; -
DR      HSSP: P04637; 1TUP.
DR      InterPro: IPR002117; P53.
DR      Pfam: PF00870; P53; 1.
DR      PRINTS: PR00386; P53SUPERSSR.
DR      PRODOM: PD002681; P53; 1.
DR      PROSITE: PS00348; P53; 1.
KM      Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KM      Nuclear protein; Phosphorylation; Apoptosis.
FT      DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
FT      DNA_BIND 86 273 BY SIMILARITY.
FT      DOMAIN 308 337 OLIGOMERIZATION.
FT      DOMAIN 342 363 BASIC (REPRESSION OF DNA-BINDING).
FT      DOMAIN 288 301 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT      MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
SQ      SEQUENCE 367 AA; 41266 MW; ACC10EE2F5F9CFD CRC64;
Query Match 30.4%; Score 745; DB 1; Length 367;
Best Local Similarity 51.9%; Pred. No. 5.7e-44;
Matches 148; Conservative 43; Mismatches 76; Indels 18; Gaps 3;
QY      57 QPSSTFDALSPSPALNTDTPGPHSPVDFQSSSTAKSATWTSTELKLYCQIAKCP 116
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      67 EPPSRDGNSSSPVPTVTDYDGEKFLRKQKSTASTSVSTSEILNKLYCQIAKSL 126
QY      117 IQIKMTPPPGAVIRAMPVYKKAHVYKRCNHEHLSRFNQCQIAPSHLRVBN 176
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      127 VEVLLGKDPGAVIRATYIKTEHVAEYVVRCPHQ-----NEDSAEHRSHLRIMGS 181
QY      177 SHAGVEDPITGRGSLVPEYPPGVTEFTTLYVFMCNSSCVGGMNRRLIITLFR 236
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      182 ERAQTFEHPHTRKOSVYTPYEPDQIGSEFTTLLSFMCNSSCGMGMRNRRPILITLLETO 241

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QY      237 DGVILGRRCFEARICACRGDRKADEDSIRKQVSDSTKNGDTRRPPRONTHGIOMTSI 296
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      242 EGVILGRRCFEVRVACACRGDRKTRKETNTKNG-----DNAKAKRKRKSPPTDSTTI 294
QY      297 KRRRS-----PDDELTLVPVGRRETYEMLKIKESLEIMQYLPQ 335
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      295 KSKTASASAEEDNNEVYTLQIRGRKRYEMLKIKINDGLDLEKPK 339
RESULT 12
ID      P53_CANFA      STANDARD:      PRT:      381 AA.
AC      Q29537; Q9TV78;
DT      01-NOV-1997 (Rel. 35, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Cellular tumor antigen p53 (Tumor suppressor p53).
GN      TP53 OR P53.
OS      Canis familiaris (Dog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX      NCBI_TaxID=9615;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Leukocyte;
RX      MEDLINE=98178696; PubMed=9519801;
RT      Veldhoen N., Milner J.;
RT      "Isolation of canine p53 cDNA and detailed characterization of the
RT      full length canine p53 protein.";
RT      Oncogene 16:1077-1084(1998).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Spleen;
RA      Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
RA      Watarai T., Hasagawa A., Tsujimoto H.;
RT      "Aberrations of p53 tumor suppressor gene in various spontaneous
RT      tumors in the dog.";
RT      submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
RN      [3]
RP      SEQUENCE OF 25-300 FROM N.A.
RC      STRAIN=Beagle;
RX      MEDLINE=95323915; PubMed=7600529;
RA      Kraegel S.A., Pazzi K.A., Madewell B.R.;
RT      "Sequence analysis of canine p53 in the region of exons 3-8.";
RT      Cancer Lett. 92:181-186(1995).
CC      -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC      growth arrest or apoptosis depending on the physiological
CC      circumstances and cell type. Involved in cell cycle regulation as
CC      a trans-activator that acts to negatively regulate cell division
CC      by controlling a set of genes required for this process. One of
CC      the activated genes is an inhibitor of cyclin-dependent kinases.
CC      Apoptosis induction seems to be mediated either by stimulation of
CC      BAX and FAS antigen expression, or by repression of Bcl-2
CC      expression.
CC      -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- DISEASE: p53 is found in increased amounts in a wide variety
CC      of transformed cells. p53 is frequently mutated or inactivated
CC      in many types of cancer.
CC      -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AF060514; AAC16909.1; -
DR      EMBL: AB020761; BAA78379.1; -
DR      EMBL: S77819; AAB42022.1; -
DR      HSSP: P04637; 1OLG.

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DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 89 280 OLIGOMERIZATION.
FT DOMAIN 313 344 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 356 375 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 299 311 PHOSPHORYLATION (BY PRK) (BY
FT MOD_RES 15 SIMILARITY).
FT MOD_RES 380 380 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 1 4 MEES -> MOEP (IN REF. 2).
FT CONFLICT 378 378 L -> P (IN REF. 2).
SQ SEQUENCE 381 AA: 42486 MW: 761A718FDC93DA59 CRC64:

Query Match 30.4%; Score 744; DB 1; Length 381;
Best Local Similarity 42.9%; Pred. No. 7e-44;
Matches 159; Conservative 61; Mismatches 119; Indels 32; Gaps 9;

QY 5 ENNAQTQFSFQPYNTL----GLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 28 ENNVLSSELCPAVDLLPESVNWIDE---DSDAAPRMP--ATSAPAPAGP--APSW 78
QY 61 TFDALSSPAIPSTDPGPHSFVDFVFSQSSSTAKATWTSTELKTKLYCQIAKTCPIQIK 120
DB 79 PL-----SSVPSKRTPTGRTGFLGLHSGTAKSVMTYTPPLINKLFCQIAKTCPIQLW 133
QY 121 VMPPPGAVIRAMPYTKAKAHTEVYVRCNPHELSPREFNGQIAPSPHLIRVEGNSHAQ 180
DB 134 VSSPPNPTCVRAMATYKSEFEVYVRCNPHELSPREFNGQIAPSPHLIRVEGNSHAQ 192
QY 181 YVEPPITGROSLVAPRPPQVGTETVLYVFMGNSGVGMNRPRLITLTLETRGOV 240
DB 193 YLDRNTRFRHSVVPYEPPEQSDYTIHVMKNSGGMNRPRLITLTLEDSQNV 252
QY 241 LGRRCFEARICACGRDRKADSDSIRKQVSDSTKNGDTRPRPFRONTGICMTSIRKR 300
DB 253 LGRNSFEVRCACGRDRTEENFMHKGECPPRPGSTRALPSP--SSSPQKKK 309
QY 301 SPDELLLYPRGKETEMLIKESLEMOYLP-----QHT--LETRYQQQOQOQ 350
DB 310 PLDEYFTLQIRGERYEMFENLEALDKDAQSGKEPGSGRAHSHLKAKGOSTSRK 369
QY 351 HLLQKOTSIO 361
DB 370 KLMFKREGIDS 380

RESULT 13
P53_BOVIN STANDARD: PRT: 386 AA.
AC 028628:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Bos taurus (Bovine), and
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913; 9915;
RN [1]
RP SEQUENCE FROM N. A.
RC SPECIES=Bovine; TISSUE=Liver;
RA MEDLINE=95352829; PubMed=7626789;
RA Deguidt F., Kettmann R., Bury A., Willems L.;
RT "Nucleotide sequence of the bovine p53 tumor-suppressor cDNA.";
```

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RL DNA Seq. 5:261-264(1995).
RN [2]
RP SEQUENCE OF 13-386 FROM N.A.
RC SPECIES=Bovine; STRAIN=Holstein; TISSUE=Thymus;
RX MEDLINE=96401400; PubMed=8807776;
RA Komori H., Ishiguro N., Horinchi M., Shingawa M., Aida Y.;
RT "Predominant p53 mutations in enzootic bovine leukemic cell lines.";
RL Vet. Immunol. Immunopathol. 52:53-63(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B. indicus; STRAIN=Boran; TISSUE=Blood;
RL Bishop R.R.P., Goblright E.E.I.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC Bax and Fas antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X81704; CAAS7348.1; -.
DR EMBL: D49825; BAA08629.1; -.
DR EMBL: U74486; AAB51214.1; -.
DR PIR: S51648; S51648.
DR HSSP: P04637; ITUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 94 285 OLIGOMERIZATION.
FT DOMAIN 318 349 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 361 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 304 316 PHOSPHORYLATION (BY PRK) (BY
FT MOD_RES 15 SIMILARITY).
FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 380 380 MEES -> T (IN REF. 2).
FT CONFLICT 386 380 R -> T (IN REF. 2).
SQ SEQUENCE 386 AA: 43255 MW: 222473F28C548F31 CRC64:

Query Match 30.4%; Score 744; DB 1; Length 386;
Best Local Similarity 41.5%; Pred. No. 7.1e-44;
Matches 164; Conservative 65; Mismatches 120; Indels 46; Gaps 12;

QY 5 ENNAQTQFSFQPYNTLCL----NSMDQIQNGSSSTSPYN----TDHAQNSVTAP--- 52
DB 7 ELNVEPLSQETFTDNLNLPENNLSSLSAPVDLLPTTDVATWIDECBPNE--AQMP 64
QY 53 ---SPYAPSTFDALSPSPA-----IPSNTPGPHSFVDFVFSQSSSTAKATWTYS 101
DB 65 EPSAPAPAPPAT-----PAPATSWPLSSFVPSQRTYGVNGYFLGFLQSGTAKSVTCTYS 119
QY 102 TELKKLYCQIAKTCPIQIKWTTPPGAVIRAMPYTKAKAHTEVYVRCNPHELSPREFNE 161
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Db      120  PSINKLFCOLAKTCVQLWVDSPPPGTRVRAMATYKKLEHTEVVRCPHHERSSDYS 179
      162  GQIAPPSHLIRVEGSHAOYVEDPTTGQSVLVPYEPPOVGEFTVLVNFMCNCSGCG 221
      180  G-LAPQHLIRVEGSLRAEYLDNRTPFRSHVVPYEPSEIDSECTTHYNFMCNCSGCG 238
      222  MNRRLITLITLFTFDGVLGRCEPFIACPGDRADEDSIRKQGVSDTKNGDGT 281
      239  MNRRLITLITLFTEDSCGLGRNFEVYACPGDRKTEENLKKQSCPEPPRSTK 298
      282  RPFQNTGIGMTSIRKRRSP-DELLLYLVPGRETYEMLKIKESLEIMQYLPOHTTET 340
      299  RALPNT-----SSSPQPKKKPLDGEYFTLQIRGFKRYEMFRELNDALDEL-----KDALDG 349
      341  YRQOQOQOH-QHLQKQTSIQSSPSSTYGNSSPPLNK 374
      350  REPGESRAHSHLSK-----KRPPSCHKKPKMLKR 380

```

RESULT 14

P53_MARMO STANDARD: PRT; 391 AA.

```

AC      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Cellular tumor antigen p53 (Tumor suppressor p53).
TP53.

```

Marmota monax (Woodchuck).

OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.

NCBI_TaxID=9995;

SEQUENCE FROM N.A.

RA MEDLINE-97376996; PubMed-9233767;

RA Feltelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;

RT "Partial characterization of the woodchuck tumor suppressor, p53, and
its interaction with woodchuck hepatitis virus X antigen in
hepatocarcinogenesis.";

RL Oncogene 15:327-336(1997).

CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.

CC Apoptosis induction seems to be mediated either by stimulation of
BAX and FAS antigen expression, or by repression of Bcl-2
expression.

CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- DISEASE: p53 is found in increased amounts in a wide variety
of transformed cells. p53 is frequently mutated or inactivated
in many types of cancer.

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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or send an email to license@sdb-sdb.ch).

CC -----

CC EMBL; AJ001022; CA04478.1; -

CC HSSP; P04637; ITUP.

CC InterPro: IPR002117: P53.

CC Pfam: PF00870: P53.1.

CC PRINTS; PR00386; P53SUPPRESSR.

CC PRODOM; PD002681; P53; 1.

CC PROSITE; PS00348; P53; 1.

```

KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 100 290 BY SIMILARITY.
FT DOMAIN 323 354 OLIGOMERIZATION.
FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
SIMILARITY).
FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 391 AA; 43468 MW; ELDE5DB84BA40182 CRC64;

```

Query Match 30.1%; Score 738.5; DB 1; Length 391;
Best local similarity 41.3%; Pred. No. 1,7e+43;
Matches 158; Conservative 65; Mismatches 117; Indels 43; Gaps 9;

```

      5  ENNAQTFSEPOYTNLGLNSMDQIONGSSSTSPYNTDHAQNSVTAPSPAQPSSTDA 64
      28  ENNVLSPLVLSPPMDL-LLSSED--VENWFDK-----GPDEALQMSAABAPKAPTAASTL 80
      65  LSPSPA-----IPSTNDYRPHSPFVSPOQSSATATWYSTEIKLYCOLAKTCP 116
      81  AAPSPATSWPLSSSVSONTYPGVYGFRLGHSQASVTCYSPSLNKLFQOLAKTCP 140
      117  IQIKVTPPOGAVTRAPVYKKAETVEVYRCRNHLSREFNGQIAPSHLIRVGN 176
      141  VQLWVDSITPPETRTARRAAIYKSKHTEVYARCKHNE--KCSDDGLAPQHLIRVEGN 198
      177  SHAQYVEDPTTGQSVLVPYEPPOVGEFTVLVNFMCNCSGCGMNRPIIIVLETR 236
      199  LRAEYLDNRTPFRSHVVPYEPPEVGESECTTHYNKNCNSGCGMNRPIIITLIGS 258
      237  DGQVGRRCFEARICACPGDRKKADEDSIRKQGVSDTKNGDGTAPRPPRNT-----IGI 291
      259  SGNLLGRNSSFYRVACPGDRKTEENFRK-----GPCEPPRSTKRALPMGT 310
      292  QMTSIRKRRSPDELLLYLVPGRETYEMLKIKESLEIMQYLPOHT-----IFETV 341
      311  SSSPPKPKKPLDGEYFTLIKIRGARFEMQELNALTELKDAQAEKPEPSRHPSTLASK 370
      342  RQOQOQOHOHLQKQTSIQSSPS 364
      371  KGQSTSRHKITIFKR---EGPDS 390

```

RESULT 15

P53_ORYLA STANDARD: PRT; 352 AA.

AC P79820; Q9PSU7; Q9PSU8;

DT 01-NOV-1997 (Rel. 35, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor p53).

GN TP53 OR P53.

OS Oryzias latipes (Medaka fish) (Japanese ricefish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

OC Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.

NCBI_TaxID=8090;

SEQUENCE FROM N.A.

TISSUE: Liver.

MEDLINE-97305153; PubMed-9161419;

Krause M.K., Rhodes L.D., van Beneden R.J.;

"Cloning of the p53 tumor suppressor gene from the Japanese medaka
(Oryzias latipes) and evaluation of mutational hotspots in MNNG-
exposed fish.";

Gene 189:101-106(1997).

SEQUENCE FROM N.A., AND VARIANT THR-91.

STRAIN-Himedaka;

Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:41:09 ; Search time 37.092 Seconds
(without alignments)
3207.225 Million cell updates/sec

Title: US-09-538-106-17

Perfect score: 2450

Sequence: 1 MYLENNMQTQSFEPQYTNL.....HCTPPPPPTDGSIVRMQV 461

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organellar:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-rylirus:*
- 16: sp-bacteriap:*
- 17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2450	100.0	461	4 Q9UP26	Q9UP26 homo sapien
2	2443	99.7	461	4 Q9P1B5	Q9P1B5 homo sapien
3	2427	99.1	461	11 Q9QWY9	Q9QWY9 mus musculu
4	2421	98.8	586	4 Q9UBV9	Q9UBV9 homo sapien
5	2421	98.8	586	4 Q9P1B4	Q9P1B4 mus musculu
6	2418	98.7	461	11 Q9QWY9	Q9QWY9 mus musculu
7	2404	98.1	586	4 Q9P1B5	Q9P1B5 homo sapien
8	2398	97.9	586	4 Q9P1B5	Q9P1B5 mus musculu
9	2389	97.5	586	11 Q9QWY9	Q9QWY9 mus musculu
10	2379	97.1	555	4 Q9H3D3	Q9H3D3 mus musculu
11	2372	96.8	516	4 Q9P1B7	Q9P1B7 mus musculu
12	2356	96.2	555	11 Q9QWY9	Q9QWY9 mus musculu
13	2352	96.0	538	11 Q9QWY9	Q9QWY9 mus musculu
14	2352	96.0	535	11 Q9QWY9	Q9QWY9 mus musculu
15	2350	95.9	641	4 Q9H3D3	Q9H3D3 mus musculu
16	2350	95.9	680	4 Q9H3D4	Q9H3D4 mus musculu

17	2342	95.6	680	4 Q9UE10	Q9UE10 mus musculu
18	2327	95.0	680	11 Q9H3D3	Q9H3D3 mus musculu
19	2323	94.8	663	11 Q9QWY9	Q9QWY9 mus musculu
20	2323	94.8	680	11 Q9QWY9	Q9QWY9 mus musculu
21	2303	94.0	582	13 Q9DEC7	Q9DEC7 mus musculu
22	2148	87.7	416	4 Q9P1B6	Q9P1B6 mus musculu
23	2077	84.8	471	4 Q9H3D3	Q9H3D3 mus musculu
24	1918.5	78.3	501	4 Q9H3D3	Q9H3D3 mus musculu
25	1884	76.9	333	4 Q9H3D3	Q9H3D3 mus musculu
26	1872	76.4	336	4 Q9H3D3	Q9H3D3 mus musculu
27	1868	76.2	333	11 Q9QWY9	Q9QWY9 mus musculu
28	1837	75.0	389	11 Q9H3D3	Q9H3D3 mus musculu
29	1826	74.5	457	13 Q9H3D3	Q9H3D3 mus musculu
30	1818	74.2	576	13 Q9H3D3	Q9H3D3 mus musculu
31	1816	74.1	568	13 Q9H3D3	Q9H3D3 mus musculu
32	1813	74.0	487	4 Q9H3D3	Q9H3D3 mus musculu
33	1802	73.6	487	11 Q9QWY9	Q9QWY9 mus musculu
34	1802	73.6	487	11 Q9QWY9	Q9QWY9 mus musculu
35	1766	72.1	483	11 Q9H3D3	Q9H3D3 mus musculu
36	1730.5	70.6	365	13 Q9H3D3	Q9H3D3 mus musculu
37	1489	60.8	284	11 Q9H3D3	Q9H3D3 mus musculu
38	1461.5	59.7	641	13 Q9H3D3	Q9H3D3 mus musculu
39	1442.5	58.9	590	11 Q9QWY9	Q9QWY9 mus musculu
40	1438.5	58.7	631	11 Q9QWY9	Q9QWY9 mus musculu
41	1435.5	58.6	450	4 Q9H3D3	Q9H3D3 mus musculu
42	1420.5	58.0	587	4 Q9H3D3	Q9H3D3 mus musculu
43	1256	51.3	426	4 Q9H3D3	Q9H3D3 mus musculu
44	1256	51.3	514	11 Q9H3D3	Q9H3D3 mus musculu
45	1217	49.7	232	4 Q9H3D3	Q9H3D3 mus musculu

ALIGNMENTS

RESULT 1

Q9UP26 PRELIMINARY; PRT; 461 AA.

AC Q9UP26; 01-MAY-2000 (TREMBL) 13, Created

DT 01-MAY-2000 (TREMBL) 13, Last sequence update

DT 01-OCT-2002 (TREMBL) 22, Last annotation update

DE DN P63 beta.

GN P63.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP MEDLINE=98448095; PubMed=9774969;

RX Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKone F.;

RT "P63, a p53 homolog at 3q27-29, encodes multiple products with

RT transactivating, death-inducing, and dominant-negative activities."

RL MOL. Cell 2:305-316(1998).

RN [2]

RP SEQUENCE FROM N.A.

RA Haglwa K., McMenamin M.G., Harris C.C.;

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL: AF075433; AAC62638.1; -

DR EMBL: AF124539; AAG45611.1; -

DR EMBL: AF124530; AAG45611.1; JOINED.

DR EMBL: AF124531; AAG45611.1; JOINED.

DR EMBL: AF124532; AAG45611.1; JOINED.

DR EMBL: AF124533; AAG45611.1; JOINED.

DR EMBL: AF124534; AAG45611.1; JOINED.

DR EMBL: AF124535; AAG45611.1; JOINED.

DR EMBL: AF124536; AAG45611.1; JOINED.

DR EMBL: AF124537; AAG45611.1; JOINED.

DR HSSP: P04637; 1YCS.

DR InterPro: IPR002117; P53.

DR	PF008070: p53; 1.	DR	PF00386: p53SUPPRESSR.
DR <td>Prodrom; P0002681; p53; 1.</td> <td>DR<td>Prodrom; P0002681; p53; 1.</td></td>	Prodrom; P0002681; p53; 1.	DR <td>Prodrom; P0002681; p53; 1.</td>	Prodrom; P0002681; p53; 1.
DR <td>ProSite; P500348; p53; 1.</td> <td>DR<td>ProSite; P500348; p53; 1.</td></td>	ProSite; P500348; p53; 1.	DR <td>ProSite; P500348; p53; 1.</td>	ProSite; P500348; p53; 1.
DR <td>Nucleic protein.</td> <td>DR<td>Nucleic protein.</td></td>	Nucleic protein.	DR <td>Nucleic protein.</td>	Nucleic protein.
DR <td>SEQUENCE 461 AA; 51404 MW; 68B63547A46C1B05 CRC64;</td> <td>DR<td>SEQUENCE 461 AA; 51404 MW; 68B63547A46C1B05 CRC64;</td></td>	SEQUENCE 461 AA; 51404 MW; 68B63547A46C1B05 CRC64;	DR <td>SEQUENCE 461 AA; 51404 MW; 68B63547A46C1B05 CRC64;</td>	SEQUENCE 461 AA; 51404 MW; 68B63547A46C1B05 CRC64;
DR <td>Query Match</td> <td>DR<td>Query Match</td></td>	Query Match	DR <td>Query Match</td>	Query Match
DR <td>Best Local Similarity 100.0%; Score 2450; DB 4; Length 461;</td> <td>DR<td>Best Local Similarity 100.0%; Score 2450; DB 4; Length 461;</td></td>	Best Local Similarity 100.0%; Score 2450; DB 4; Length 461;	DR <td>Best Local Similarity 100.0%; Score 2450; DB 4; Length 461;</td>	Best Local Similarity 100.0%; Score 2450; DB 4; Length 461;
DR <td>Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</td> <td>DR<td>Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</td></td>	Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR <td>Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</td>	Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR <td>OY 1 MLYENNAQOTFSEPOYNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60</td> <td>DR<td>OY 1 MLYENNAQOTFSEPOYNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60</td></td>	OY 1 MLYENNAQOTFSEPOYNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60	DR <td>OY 1 MLYENNAQOTFSEPOYNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60</td>	OY 1 MLYENNAQOTFSEPOYNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DR <td>Db 1 MLYENNAQOTFSEPOYNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60</td> <td>DR<td>Db 1 MLYENNAQOTFSEPOYNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60</td></td>	Db 1 MLYENNAQOTFSEPOYNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60	DR <td>Db 1 MLYENNAQOTFSEPOYNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60</td>	Db 1 MLYENNAQOTFSEPOYNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DR <td>OY 61 TFDALSPSPALPSNMDYGPSPSPDPSPOSSSTAKSATMTYSTELKKLYCOLAKTCPIQIK 120</td> <td>DR<td>OY 61 TFDALSPSPALPSNMDYGPSPSPDPSPOSSSTAKSATMTYSTELKKLYCOLAKTCPIQIK 120</td></td>	OY 61 TFDALSPSPALPSNMDYGPSPSPDPSPOSSSTAKSATMTYSTELKKLYCOLAKTCPIQIK 120	DR <td>OY 61 TFDALSPSPALPSNMDYGPSPSPDPSPOSSSTAKSATMTYSTELKKLYCOLAKTCPIQIK 120</td>	OY 61 TFDALSPSPALPSNMDYGPSPSPDPSPOSSSTAKSATMTYSTELKKLYCOLAKTCPIQIK 120
DR <td>Db 61 TFDALSPSPALPSNMDYGPSPSPDPSPOSSSTAKSATMTYSTELKKLYCOLAKTCPIQIK 120</td> <td>DR<td>Db 61 TFDALSPSPALPSNMDYGPSPSPDPSPOSSSTAKSATMTYSTELKKLYCOLAKTCPIQIK 120</td></td>	Db 61 TFDALSPSPALPSNMDYGPSPSPDPSPOSSSTAKSATMTYSTELKKLYCOLAKTCPIQIK 120	DR <td>Db 61 TFDALSPSPALPSNMDYGPSPSPDPSPOSSSTAKSATMTYSTELKKLYCOLAKTCPIQIK 120</td>	Db 61 TFDALSPSPALPSNMDYGPSPSPDPSPOSSSTAKSATMTYSTELKKLYCOLAKTCPIQIK 120
DR <td>OY 121 VMTPPPGAVIRAMPVYKKAETHVEYKRCPNHELSPENEGQIAPSHLIRVEGNSHAQ 180</td> <td>DR<td>OY 121 VMTPPPGAVIRAMPVYKKAETHVEYKRCPNHELSPENEGQIAPSHLIRVEGNSHAQ 180</td></td>	OY 121 VMTPPPGAVIRAMPVYKKAETHVEYKRCPNHELSPENEGQIAPSHLIRVEGNSHAQ 180	DR <td>OY 121 VMTPPPGAVIRAMPVYKKAETHVEYKRCPNHELSPENEGQIAPSHLIRVEGNSHAQ 180</td>	OY 121 VMTPPPGAVIRAMPVYKKAETHVEYKRCPNHELSPENEGQIAPSHLIRVEGNSHAQ 180
DR <td>Db 121 VMTPPPGAVIRAMPVYKKAETHVEYKRCPNHELSPENEGQIAPSHLIRVEGNSHAQ 180</td> <td>DR<td>Db 121 VMTPPPGAVIRAMPVYKKAETHVEYKRCPNHELSPENEGQIAPSHLIRVEGNSHAQ 180</td></td>	Db 121 VMTPPPGAVIRAMPVYKKAETHVEYKRCPNHELSPENEGQIAPSHLIRVEGNSHAQ 180	DR <td>Db 121 VMTPPPGAVIRAMPVYKKAETHVEYKRCPNHELSPENEGQIAPSHLIRVEGNSHAQ 180</td>	Db 121 VMTPPPGAVIRAMPVYKKAETHVEYKRCPNHELSPENEGQIAPSHLIRVEGNSHAQ 180
DR <td>OY 181 YVEDPITGRQSVLYPPEPPQGETETTYLYNPMCMSSCVGGMNRPRILITYLETRDQY 240</td> <td>DR<td>OY 181 YVEDPITGRQSVLYPPEPPQGETETTYLYNPMCMSSCVGGMNRPRILITYLETRDQY 240</td></td>	OY 181 YVEDPITGRQSVLYPPEPPQGETETTYLYNPMCMSSCVGGMNRPRILITYLETRDQY 240	DR <td>OY 181 YVEDPITGRQSVLYPPEPPQGETETTYLYNPMCMSSCVGGMNRPRILITYLETRDQY 240</td>	OY 181 YVEDPITGRQSVLYPPEPPQGETETTYLYNPMCMSSCVGGMNRPRILITYLETRDQY 240
DR <td>Db 181 YVEDPITGRQSVLYPPEPPQGETETTYLYNPMCMSSCVGGMNRPRILITYLETRDQY 240</td> <td>DR<td>Db 181 YVEDPITGRQSVLYPPEPPQGETETTYLYNPMCMSSCVGGMNRPRILITYLETRDQY 240</td></td>	Db 181 YVEDPITGRQSVLYPPEPPQGETETTYLYNPMCMSSCVGGMNRPRILITYLETRDQY 240	DR <td>Db 181 YVEDPITGRQSVLYPPEPPQGETETTYLYNPMCMSSCVGGMNRPRILITYLETRDQY 240</td>	Db 181 YVEDPITGRQSVLYPPEPPQGETETTYLYNPMCMSSCVGGMNRPRILITYLETRDQY 240
DR <td>OY 241 LGRRCFEARICACPGRRKKADEDSIRKQVSDSTKNGGCTRKPRPQNTHGIDMTSIRKR 300</td> <td>DR<td>OY 241 LGRRCFEARICACPGRRKKADEDSIRKQVSDSTKNGGCTRKPRPQNTHGIDMTSIRKR 300</td></td>	OY 241 LGRRCFEARICACPGRRKKADEDSIRKQVSDSTKNGGCTRKPRPQNTHGIDMTSIRKR 300	DR <td>OY 241 LGRRCFEARICACPGRRKKADEDSIRKQVSDSTKNGGCTRKPRPQNTHGIDMTSIRKR 300</td>	OY 241 LGRRCFEARICACPGRRKKADEDSIRKQVSDSTKNGGCTRKPRPQNTHGIDMTSIRKR 300
DR <td>Db 241 LGRRCFEARICACPGRRKKADEDSIRKQVSDSTKNGGCTRKPRPQNTHGIDMTSIRKR 300</td> <td>DR<td>Db 241 LGRRCFEARICACPGRRKKADEDSIRKQVSDSTKNGGCTRKPRPQNTHGIDMTSIRKR 300</td></td>	Db 241 LGRRCFEARICACPGRRKKADEDSIRKQVSDSTKNGGCTRKPRPQNTHGIDMTSIRKR 300	DR <td>Db 241 LGRRCFEARICACPGRRKKADEDSIRKQVSDSTKNGGCTRKPRPQNTHGIDMTSIRKR 300</td>	Db 241 LGRRCFEARICACPGRRKKADEDSIRKQVSDSTKNGGCTRKPRPQNTHGIDMTSIRKR 300
DR <td>OY 301 SPDELLLYPGRRETYEMLLIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQ 360</td> <td>DR<td>OY 301 SPDELLLYPGRRETYEMLLIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQ 360</td></td>	OY 301 SPDELLLYPGRRETYEMLLIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQ 360	DR <td>OY 301 SPDELLLYPGRRETYEMLLIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQ 360</td>	OY 301 SPDELLLYPGRRETYEMLLIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQ 360
DR <td>Db 301 SPDELLLYPGRRETYEMLLIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQ 360</td> <td>DR<td>Db 301 SPDELLLYPGRRETYEMLLIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQ 360</td></td>	Db 301 SPDELLLYPGRRETYEMLLIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQ 360	DR <td>Db 301 SPDELLLYPGRRETYEMLLIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQ 360</td>	Db 301 SPDELLLYPGRRETYEMLLIKESLELMQYLPQHTIETRYRQOQOQHLLKQTSIQ 360
DR <td>OY 361 SPSSGNSPPLNKNKSNKPLPSYQSLNPOORNALPFTTIPDGGANINPMGTMPMAG 420</td> <td>DR<td>OY 361 SPSSGNSPPLNKNKSNKPLPSYQSLNPOORNALPFTTIPDGGANINPMGTMPMAG 420</td></td>	OY 361 SPSSGNSPPLNKNKSNKPLPSYQSLNPOORNALPFTTIPDGGANINPMGTMPMAG 420	DR <td>OY 361 SPSSGNSPPLNKNKSNKPLPSYQSLNPOORNALPFTTIPDGGANINPMGTMPMAG 420</td>	OY 361 SPSSGNSPPLNKNKSNKPLPSYQSLNPOORNALPFTTIPDGGANINPMGTMPMAG 420
DR <td>Db 361 SPSSGNSPPLNKNKSNKPLPSYQSLNPOORNALPFTTIPDGGANINPMGTMPMAG 420</td> <td>DR<td>Db 361 SPSSGNSPPLNKNKSNKPLPSYQSLNPOORNALPFTTIPDGGANINPMGTMPMAG 420</td></td>	Db 361 SPSSGNSPPLNKNKSNKPLPSYQSLNPOORNALPFTTIPDGGANINPMGTMPMAG 420	DR <td>Db 361 SPSSGNSPPLNKNKSNKPLPSYQSLNPOORNALPFTTIPDGGANINPMGTMPMAG 420</td>	Db 361 SPSSGNSPPLNKNKSNKPLPSYQSLNPOORNALPFTTIPDGGANINPMGTMPMAG 420
DR <td>OY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDSCIVRIQY 461</td> <td>DR<td>OY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDSCIVRIQY 461</td></td>	OY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDSCIVRIQY 461	DR <td>OY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDSCIVRIQY 461</td>	OY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDSCIVRIQY 461
DR <td>Db 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDSCIVRIQY 461</td> <td>DR<td>Db 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDSCIVRIQY 461</td></td>	Db 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDSCIVRIQY 461	DR <td>Db 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDSCIVRIQY 461</td>	Db 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDSCIVRIQY 461
DR <td>RESULT 2</td> <td>DR<td>RESULT 2</td></td>	RESULT 2	DR <td>RESULT 2</td>	RESULT 2
DR <td>Q9P1B5</td> <td>DR<td>Q9P1B5</td></td>	Q9P1B5	DR <td>Q9P1B5</td>	Q9P1B5
DR <td>Q9P1B5 PRELIMINARY; PRT; 461 AA.</td> <td>DR<td>Q9P1B5 PRELIMINARY; PRT; 461 AA.</td></td>	Q9P1B5 PRELIMINARY; PRT; 461 AA.	DR <td>Q9P1B5 PRELIMINARY; PRT; 461 AA.</td>	Q9P1B5 PRELIMINARY; PRT; 461 AA.
DR <td>AC Q9P1B5;</td> <td>DR<td>AC Q9P1B5;</td></td>	AC Q9P1B5;	DR <td>AC Q9P1B5;</td>	AC Q9P1B5;
DR <td>DT 01-OCT-2000 (TREMBLrel. 15, Created)</td> <td>DR<td>DT 01-OCT-2000 (TREMBLrel. 15, Created)</td></td>	DT 01-OCT-2000 (TREMBLrel. 15, Created)	DR <td>DT 01-OCT-2000 (TREMBLrel. 15, Created)</td>	DT 01-OCT-2000 (TREMBLrel. 15, Created)
DR <td>DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)</td> <td>DR<td>DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)</td></td>	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DR <td>DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)</td>	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DR <td>DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)</td> <td>DR<td>DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)</td></td>	DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)	DR <td>DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)</td>	DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DR <td>DE p51 isoform delNbeta.</td> <td>DR<td>DE p51 isoform delNbeta.</td></td>	DE p51 isoform delNbeta.	DR <td>DE p51 isoform delNbeta.</td>	DE p51 isoform delNbeta.
DR <td>OS Homo sapiens (Human).</td> <td>DR<td>OS Homo sapiens (Human).</td></td>	OS Homo sapiens (Human).	DR <td>OS Homo sapiens (Human).</td>	OS Homo sapiens (Human).
DR <td>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</td> <td>DR<td>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</td></td>	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DR <td>OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</td>	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR <td>OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.</td> <td>DR<td>OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.</td></td>	OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	DR <td>OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.</td>	OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
DR <td>OX NCBI_TaxID=9606;</td> <td>DR<td>OX NCBI_TaxID=9606;</td></td>	OX NCBI_TaxID=9606;	DR <td>OX NCBI_TaxID=9606;</td>	OX NCBI_TaxID=9606;
DR <td>RP [1]</td> <td>DR<td>RP [1]</td></td>	RP [1]	DR <td>RP [1]</td>	RP [1]
DR <td>RP SEQUENCE FROM N.A.</td> <td>DR<td>RP SEQUENCE FROM N.A.</td></td>	RP SEQUENCE FROM N.A.	DR <td>RP SEQUENCE FROM N.A.</td>	RP SEQUENCE FROM N.A.
DR <td>RX MEDLINE=20388515; PubMed=10935472;</td> <td>DR<td>RX MEDLINE=20388515; PubMed=10935472;</td></td>	RX MEDLINE=20388515; PubMed=10935472;	DR <td>RX MEDLINE=20388515; PubMed=10935472;</td>	RX MEDLINE=20388515; PubMed=10935472;
DR <td>RA Yokota J.;</td> <td>DR<td>RA Yokota J.;</td></td>	RA Yokota J.;	DR <td>RA Yokota J.;</td>	RA Yokota J.;
DR <td>RA Tan M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,</td> <td>DR<td>RA Tan M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,</td></td>	RA Tan M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,	DR <td>RA Tan M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,</td>	RA Tan M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
DR <td>RT "Mutation and expression of the p51 gene in human lung cancer.";</td> <td>DR<td>RT "Mutation and expression of the p51 gene in human lung cancer.";</td></td>	RT "Mutation and expression of the p51 gene in human lung cancer.";	DR <td>RT "Mutation and expression of the p51 gene in human lung cancer.";</td>	RT "Mutation and expression of the p51 gene in human lung cancer.";
DR <td>RL Neoplasia 1:71-79(1999).</td> <td>DR<td>RL Neoplasia 1:71-79(1999).</td></td>	RL Neoplasia 1:71-79(1999).	DR <td>RL Neoplasia 1:71-79(1999).</td>	RL Neoplasia 1:71-79(1999).
DR <td>CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).</td> <td>DR<td>CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).</td></td>	CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).	DR <td>CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).</td>	CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR <td>CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.</td> <td>DR<td>CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.</td></td>	CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.	DR <td>CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.</td>	CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR <td>DR EMBL; AF116769; AAF3492.1; -</td> <td>DR<td>DR EMBL; AF116769; AAF3492.1; -</td></td>	DR EMBL; AF116769; AAF3492.1; -	DR <td>DR EMBL; AF116769; AAF3492.1; -</td>	DR EMBL; AF116769; AAF3492.1; -
DR <td>DR EMBL; AF116758; AAF3492.1; JOINED.</td> <td>DR<td>DR EMBL; AF116758; AAF3492.1; JOINED.</td></td>	DR EMBL; AF116758; AAF3492.1; JOINED.	DR <td>DR EMBL; AF116758; AAF3492.1; JOINED.</td>	DR EMBL; AF116758; AAF3492.1; JOINED.
DR <td>DR EMBL; AF116759; AAF3492.1; JOINED.</td> <td>DR<td>DR EMBL; AF116759; AAF3492.1; JOINED.</td></td>	DR EMBL; AF116759; AAF3492.1; JOINED.	DR <td>DR EMBL; AF116759; AAF3492.1; JOINED.</td>	DR EMBL; AF116759; AAF3492.1; JOINED.
DR <td>DR EMBL; AF116760; AAF3492.1; JOINED.</td> <td>DR<td>DR EMBL; AF116760; AAF3492.1; JOINED.</td></td>	DR EMBL; AF116760; AAF3492.1; JOINED.	DR <td>DR EMBL; AF116760; AAF3492.1; JOINED.</td>	DR EMBL; AF116760; AAF3492.1; JOINED.
DR <td>DR EMBL; AF116761; AAF3492.1; JOINED.</td> <td>DR<td>DR EMBL; AF116761; AAF3492.1; JOINED.</td></td>	DR EMBL; AF116761; AAF3492.1; JOINED.	DR <td>DR EMBL; AF116761; AAF3492.1; JOINED.</td>	DR EMBL; AF116761; AAF3492.1; JOINED.
DR <td>DR EMBL; AF116762; AAF3492.1; JOINED.</td> <td>DR<td>DR EMBL; AF116762; AAF3492.1; JOINED.</td></td>	DR EMBL; AF116762; AAF3492.1; JOINED.	DR <td>DR EMBL; AF116762; AAF3492.1; JOINED.</td>	DR EMBL; AF116762; AAF3492.1; JOINED.
DR <td>DR EMBL; AF116763; AAF3492.1; JOINED.</td> <td>DR<td>DR EMBL; AF116763; AAF3492.1; JOINED.</td></td>	DR EMBL; AF116763; AAF3492.1; JOINED.	DR <td>DR EMBL; AF116763; AAF3492.1; JOINED.</td>	DR EMBL; AF116763; AAF3492.1; JOINED.
DR <td>DR EMBL; AF116764; AAF3492.1; JOINED.</td> <td>DR<td>DR EMBL; AF116764; AAF3492.1; JOINED.</td></td>	DR EMBL; AF116764; AAF3492.1; JOINED.	DR <td>DR EMBL; AF116764; AAF3492.1; JOINED.</td>	DR EMBL; AF116764; AAF3492.1; JOINED.

Query Match	Best Local Similarity	99.7%	Score 2443	DB 4	Length 461
Matches 460	Conservative	0	Mismatches 1	Indels 0	Gaps 0
DR EMBL: AF116765; AAF43492.1; JOINED.					
DR EMBL: AF116766; AAF43492.1; JOINED.					
DR EMBL: AF116767; AAF43492.1; JOINED.					
DR HSSP: P04637; 1YCS.					
DR InterPro: IPR002117; P53.					
DR Pfam: PF00870; P53; 1.					
DR PRINTS: PR00386; P53SUPPRESSOR.					
DR PROSITE: PS002681; P53; 1.					
DR PROSITE: PS00348; P53; 1.					
KW Nuclear protein.					
SW SEQUENCE 461 AA: 51305 MW: 686354781C1B05 CRC64;					
QY 1 MLYLENNQOTQFSEFYQNTNLGLNSMDQIQNGSSSTSPYNTDHNQNSVTAPSPYAQSS 60					
DB 1 MLYLENNQOTQFSEFYQNTNLGLNSMDQIQNGSSSTSPYNTDHNQNSVTAPSPYAQSS 60					
QY 61 TFDALSPSPALPSPNDYDGPSPSFDVSFOQSSSTAKSATWTYSTELKKLYCOLAKTQPIQIK 120					
DB 61 TFDALSPSPALPSPNDYDGPSPSFDVSFOQSSSTAKSATWTYSTELKKLYCOLAKTQPIQIK 120					
QY 121 VMTPEPGAVIRAMPYVYKKAHEVTEVYKRCPNHELSREFNEQIAPPSHLIVEGNSHQ 180					
DB 121 VMTPEPGAVIRAMPYVYKKAHEVTEVYKRCPNHELSREFNEQIAPPSHLIVEGNSHQ 180					
QY 181 YVEDPITGRQSLVYEPPEQVTEETLYLVNMCNNSCGGNGRRPILITVLETRDQV 240					
DB 181 YVEDPITGRQSLVYEPPEQVTEETLYLVNMCNNSCGGNGRRPILITVLETRDQV 240					
QY 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTYKNGDKTKRPFRONTNGIOMTSIKRR 300					
DB 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTYKNGDKTKRPFRONTNGIOMTSIKRR 300					
QY 301 SPDDDELILPVRGRRTYEMLKIKESLELMQVLPQHTLETYRQOQOQOHLLQKOTSIO 360					
DB 301 SPDDDELILPVRGRRTYEMLKIKESLELMQVLPQHTLETYRQOQOQOHLLQKOTSIO 360					
QY 361 SPSSYGNSSPPLKNKNSMKNKLPSVSQILNPQQRNALPTPTIPDGAGANIPMGTHMPAG 420					
DB 361 SPSSYGNSSPPLKNKNSMKNKLPSVSQILNPQQRNALPTPTIPDGAGANIPMGTHMPAG 420					
QY 421 DMNGLSPTQALPPLPMSMSTSHCTPPRYPDCCSYVRIMQV 461					
DB 421 DMNGLSPTQALPPLPMSMSTSHCTPPRYPDCCSYVRIMQV 461					
RESULT 3					
Q9QWY9	PRELIMINARY:	PRT:	461 AA.		
AC Q9QWY9:					
DT 01-MAY-2000 (TREMBLrel. 13, Created)					
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)					
DE DN p63 beta.					
CN TRp63.					
OS Mus musculus (Mouse).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.					
OX NCBI_Taxid=10090;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=98448095; PubMed=9774969;					
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,					
RA Caput D., McKeon F.;					
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with					
RT transcriptional, death-inducing, and dominant-negative activities.";					
RL Mol. Cell 2:305-316(1998).					
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).					
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.					
DR EMBL: AF075438; AAC62645.1; -.					

DR HSP: P04637; 1YCS.
 DR MGD: MGI:1330810; Trp63.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR ProDom: PD002681; P53; 1.
 DR PROSITE: PS00348; P53; 1.
 DR Nuclear protein.
 SO SEQUENCE 461 AA; 51455 MW; 76132962F85DBC8 CRC64;

Query Match 99.1%; Score 2427; DB 11; Length 461;
 Best Local Similarity 98.9%; Pred. No. 3, 8e-197;
 Matches 456; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNAOTQSEPOYTINGLINSMDOQIQNGSSSTSPYNDHAONSTAPSPYQPS 60
 DB 1 MYLENNAOTQSEPOYTINGLINSMDOQIQNGSSSTSPYNDHAONSTAPSPYQPS 60
 QY 61 TEDALSPSPALPSNDYDPPHSPDVSFQOOSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
 DB 61 TEDALSPSPALPSNDYDPPHSPDVSFQOOSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
 QY 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELSTREFNEGOIAPSHLIRVEGNSHAQ 180
 DB 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELSTREFNEGOIAPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLYPEPPQVGTETTVLYNFMCNSSCVGMMRRPILIIIVLETNDGOV 240
 DB 181 YVEDPITGRQSVLYPEPPQVGTETTVLYNFMCNSSCVGMMRRPILIIIVLETNDGOV 240
 QY 241 LGRCFEARIACPGDRKRADEDSIRKQOVSDSTKNGDGTKRFRONTGIGIOMTSIKRR 300
 DB 241 LGRCFEARIACPGDRKRADEDSIRKQOVSDSTKNGDGTKRFRONTGIGIOMTSIKRR 300
 QY 301 SPDELLYLPVGRREYEMLIKESLELMQYLPQHTIETTRQOOQOHLLQKOTSIO 360
 DB 301 SPDELLYLPVGRREYEMLIKESLELMQYLPQHTIETTRQOOQOHLLQKOTSIO 360
 QY 361 SPSSYGNSSPPLKNNKSNKLPVSQOLINPOORNALPTTIPDGMGANIPMGTHMPAG 420
 DB 361 SPSSYGNSSPPLKNNKSNKLPVSQOLINPOORNALPTTIPDGMGANIPMGTHMPAG 420
 QY 421 DMNGLSPTQALPPPLSPMSTSHCTPPPYPTDCSIV 461
 DB 421 DMNGLSPTQALPPPLSPMSTSHCTPPPYPTDCSIV 461

RESULT 4

Q9UBV9 PRELIMINARY; PRT; 586 AA.

AC Q9UBV9;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE DN P53 alpha.
 GN P53.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kaghad M., Wang Y., Gallet E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKoon F.,
 RA "P53, a p53 homolog at 3q27-29, encodes multiple products with
 RA transactivating, death-inducing, and dominant-negative activities.";
 RL Mol. Cell 2:305-316(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lee L.A., Walsh P., Prater C.A., Su L., Marchbank A., Egbert T.B.,
 RA Delavalle R.P., Targoff I.N., Kaufman K.M., Chorzeiski T.P.,
 RA Jablonska S.;

RT "Characterization of an autoantigen associated with chronic ulcerative
 stomatitis. The CUSP autoantigen is a member of the p53 family.";
 RL J. Invest. Dermatol. 0:0-0(1999).

RA SEQUENCE FROM N.A.
 RA Haglwaara K., McMenamin M.G., Harris C.C.;
 RA Submitted (JAN-1999) to the EMBL/Genbank/DDJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL: AF075431; AAC62636.1; -;
 DR EMBL: AF091627; AAC43038.1; -;
 DR EMBL: AF124539; AAG45610.1; JOINED.
 DR EMBL: AF124530; AAG45610.1; JOINED.
 DR EMBL: AF124531; AAG45610.1; JOINED.
 DR EMBL: AF124532; AAG45610.1; JOINED.
 DR EMBL: AF124533; AAG45610.1; JOINED.
 DR EMBL: AF124534; AAG45610.1; JOINED.
 DR EMBL: AF124535; AAG45610.1; JOINED.
 DR EMBL: AF124536; AAG45610.1; JOINED.
 DR EMBL: AF124537; AAG45610.1; JOINED.
 DR EMBL: AF124538; AAG45610.1; JOINED.
 DR HSP: P04637; 1YCS.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR ProDom: PD002681; P53; 1.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 DR Nuclear protein.
 SO SEQUENCE 586 AA; 65756 MW; 2E2P92ABF1AF8629 CRC64;

Query Match 98.8%; Score 2421; DB 4; Length 586;
 Best Local Similarity 100.0%; Pred. No. 1, 7e-196;
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLENNAOTQSEPOYTINGLINSMDOQIQNGSSSTSPYNDHAONSTAPSPYQPS 60
 DB 1 MYLENNAOTQSEPOYTINGLINSMDOQIQNGSSSTSPYNDHAONSTAPSPYQPS 60
 QY 61 TEDALSPSPALPSNDYDPPHSPDVSFQOOSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
 DB 61 TEDALSPSPALPSNDYDPPHSPDVSFQOOSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
 QY 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELSTREFNEGOIAPSHLIRVEGNSHAQ 180
 DB 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELSTREFNEGOIAPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLYPEPPQVGTETTVLYNFMCNSSCVGMMRRPILIIIVLETNDGOV 240
 DB 181 YVEDPITGRQSVLYPEPPQVGTETTVLYNFMCNSSCVGMMRRPILIIIVLETNDGOV 240
 QY 241 LGRCFEARIACPGDRKRADEDSIRKQOVSDSTKNGDGTKRFRONTGIGIOMTSIKRR 300
 DB 241 LGRCFEARIACPGDRKRADEDSIRKQOVSDSTKNGDGTKRFRONTGIGIOMTSIKRR 300
 QY 301 SPDELLYLPVGRREYEMLIKESLELMQYLPQHTIETTRQOOQOHLLQKOTSIO 360
 DB 301 SPDELLYLPVGRREYEMLIKESLELMQYLPQHTIETTRQOOQOHLLQKOTSIO 360
 QY 361 SPSSYGNSSPPLKNNKSNKLPVSQOLINPOORNALPTTIPDGMGANIPMGTHMPAG 420
 DB 361 SPSSYGNSSPPLKNNKSNKLPVSQOLINPOORNALPTTIPDGMGANIPMGTHMPAG 420
 QY 421 DMNGLSPTQALPPPLSPMSTSHCTPPPYPTDCSIV 456
 DB 421 DMNGLSPTQALPPPLSPMSTSHCTPPPYPTDCSIV 456

RESULT 5

Q9P1B4 PRELIMINARY; PRT; 586 AA.

AC Q9P1B4;
 AC Q9P1B4;

DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE p51 isoform delNalpa.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RT Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF116769; AAF3491.1; JOINED.
DR EMBL; AF116758; AAF3491.1; JOINED.
DR EMBL; AF116759; AAF3491.1; JOINED.
DR EMBL; AF116760; AAF3491.1; JOINED.
DR EMBL; AF116761; AAF3491.1; JOINED.
DR EMBL; AF116762; AAF3491.1; JOINED.
DR EMBL; AF116763; AAF3491.1; JOINED.
DR EMBL; AF116764; AAF3491.1; JOINED.
DR EMBL; AF116765; AAF3491.1; JOINED.
DR EMBL; AF116766; AAF3491.1; JOINED.
DR EMBL; AF116767; AAF3491.1; JOINED.
DR EMBL; AF116768; AAF3491.1; JOINED.
DR HSSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 586 AA; 65726 MW; 9A2316B631AF8634 CRC64;

Query Match 98.8%; Score 2421; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.7e-196;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQTFSEPOYTNIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAQTFSEPOYTNIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSTWDYPGPHSPFVSFOQSTAKSATWTSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSTWDYPGPHSPFVSFOQSTAKSATWTSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHELSPREFNEGQIAPPSHLIRVGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHELSPREFNEGQIAPPSHLIRVGNSHAQ 180
QY 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHELSPREFNEGQIAPPSHLIRVGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHELSPREFNEGQIAPPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLYPYEPPOVGEFTTVLYNFMKNSSCVGGMNRPLIIVTLETRDGOV 240
DB 181 YVEDPITGRQSVLYPYEPPOVGEFTTVLYNFMKNSSCVGGMNRPLIIVTLETRDGOV 240
QY 181 YVEDPITGRQSVLYPYEPPOVGEFTTVLYNFMKNSSCVGGMNRPLIIVTLETRDGOV 240
DB 181 YVEDPITGRQSVLYPYEPPOVGEFTTVLYNFMKNSSCVGGMNRPLIIVTLETRDGOV 240
QY 241 LGRRCFEARICACGRDRKADESIRKQOYSDSTKNGDGTGRPRONTHTGIOMTSIKRR 300
DB 241 LGRRCFEARICACGRDRKADESIRKQOYSDSTKNGDGTGRPRONTHTGIOMTSIKRR 300
QY 301 SPDELLLYLPVREGRETEMLKIKESLELMQYLPQHTIETRYRQOQOOHLLQKOTSIQ 360
DB 301 SPDELLLYLPVREGRETEMLKIKESLELMQYLPQHTIETRYRQOQOOHLLQKOTSIQ 360
QY 361 SPSSYGNSPPLNKMNSMNLPSVSQLINPOQRNALPPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSPPLNKMNSMNLPSVSQLINPOQRNALPPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSPSTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSPSTSHCTPPPPYPTDCSIV 456

DB 421 DMNGLSPTQALPPLSPSTSHCTPPPPYPTDCSIV 456
|||||
RESULT 6
ID 099J06 PRELIMINARY; PRT; 461 AA.
AC 099J06;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE DN KET beta protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
RT variants.";
RT FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AJ277453; CAC37105.1; JOINED.
DR HSSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51398 MW; B5F898EBE7E4F97A CRC64;

Query Match 98.7%; Score 2418; DB 11; Length 461;
Best Local Similarity 98.5%; Pred. No. 2.2e-196;
Matches 454; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLYENNAQTFSEPOYTNIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAQTFSEPOYTNIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSTWDYPGPHSPFVSFOQSTAKSATWTSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSTWDYPGPHSPFVSFOQSTAKSATWTSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHELSPREFNEGQIAPPSHLIRVGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHELSPREFNEGQIAPPSHLIRVGNSHAQ 180
QY 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHELSPREFNEGQIAPPSHLIRVGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHELSPREFNEGQIAPPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLYPYEPPOVGEFTTVLYNFMKNSSCVGGMNRPLIIVTLETRDGOV 240
DB 181 YVEDPITGRQSVLYPYEPPOVGEFTTVLYNFMKNSSCVGGMNRPLIIVTLETRDGOV 240
QY 181 YVEDPITGRQSVLYPYEPPOVGEFTTVLYNFMKNSSCVGGMNRPLIIVTLETRDGOV 240
DB 181 YVEDPITGRQSVLYPYEPPOVGEFTTVLYNFMKNSSCVGGMNRPLIIVTLETRDGOV 240
QY 241 LGRRCFEARICACGRDRKADESIRKQOYSDSTKNGDGTGRPRONTHTGIOMTSIKRR 300
DB 241 LGRRCFEARICACGRDRKADESIRKQOYSDSTKNGDGTGRPRONTHTGIOMTSIKRR 300
QY 301 SPDELLLYLPVREGRETEMLKIKESLELMQYLPQHTIETRYRQOQOOHLLQKOTSIQ 360
DB 301 SPDELLLYLPVREGRETEMLKIKESLELMQYLPQHTIETRYRQOQOOHLLQKOTSIQ 360
QY 361 SPSSYGNSPPLNKMNSMNLPSVSQLINPOQRNALPPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSPPLNKMNSMNLPSVSQLINPOQRNALPPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSPSTSHCTPPPPYPTDCSIV 461
DB 421 DMNGLSPTQALPPLSPSTSHCTPPPPYPTDCSIV 461

RESULT 7			
ID	075080	PRELIMINARY:	PRT: 586 AA.
AC	075080;		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)		
DE	p73H.		
GN	p73H.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE:98369596; PubMed-9703973;		
RA	Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,		
RA	Tanaka T., Shindai Y., Kato H.;		
RT	"A second p53-related protein, p73L, with high homology to p73.";		
RL	Biochem. Biophys. Res. Commun. 248:603-607(1998).		
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE p53 FAMILY.		
DR	EMBL: AB010153; BAAs2433.1; ..		
DR	HSSP: P04637; IYCS.		
DR	InterPro: IPR002117; P53.		
DR	InterPro: IPR001660; SAM.		
DR	Pfam: PF00870; P53; 1.		
DR	PRINTS: PR00386; P53SUPPRESSR.		
DR	ProDom: PD002681; P53; 1.		
DR	SMART: SM00454; SAM; 1.		
DR	PROSITE: PS00348; P53; 1.		
DR	NUCLEAR protein.		
SQ	SEQUENCE 586 AA; 65734 MW; 9DC102AB57120C0F CRC64;		

Query Match	98.1%	Score 2404	DB 4	Length 586
Best Local Similarity	99.3%	Pred. No. 4,66-195		
Matches 455	Conservative 1	Mismatches 2	Indels 0	Gaps 0
QY	1	MLYENNAQOTFSEPOYTNIGLNSMDQOIOMGSSSTSPYNTDHAQNSVTAPSPYAQDPS	60	
Db	1	MLYENNAQAOTFSEPOYTNIGLNSMDQOIQINSSSTSPYNTDHAQNSVTAPSPYAQSP	60	
QY	61	TFDALSPPALPSMTDYPGHSFPIVSPQSSSTASTATWTYSTELKKLYCOIAKTCPIQIK	120	
Db	61	TFDALSPPALPSMTDYPGHSFPIVSPQSSSTASTATWTYSTELKKLYCOIAKTCPIQIK	120	
QY	121	VMTPPQGAIVRAMPVYKKAHEVTEYVKRCNHNHLSREFNFGQIAPSHLIRVEGNSHAQ	180	
Db	121	VMTPPQGAIVRAMPVYKKAHEVTEYVKRCNHNHLSREFNFGQIAPSHLIRVEGNSHAQ	180	
QY	181	YVEDPITGROSVLYPEPPQVTEFTTVLYNFMCNSSCVGAMNRRPILIIVLTETRDGV	240	
Db	181	YVEDPITGROSVLYPEPPQVTEFTTVLYNFMCNSSCVGAMNRRPILIIVLTETRDGV	240	
QY	241	IGRRCFARICACGGRKADDEDSIRKQOVSdstKNGGTRPRPRONTHGIOMTSIKRR	300	
Db	241	IGRRCFARICACGGRKADDEDSIRKQOVSdstKNGGTRPRPRONTHGIOMTSIKRR	300	
QY	301	SPDELLLYPVGRHETYEMLKIKESLELMQYLPHQHTIETVYRQOQOQHHLQKQTSIQ	360	
Db	301	SPDELLLYPVGRHETYEMLKIKESLELMQYLPHQHTIETVYRQOQOQHHLQKQTSIQ	360	
QY	361	SPSSYGSSPPPLNMNSMKNKLPSVQLINPOQRAHALPTTIPDGMGANIPMGCTHMPAG	420	
Db	361	SPSSYGSSPPPLNMNSMKNKLPSVQLINPOQRAHALPTTIPDGMGANIPMGCTHMPAG	420	
QY	421	DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV	456	
Db	421	DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV	456	

ID	089097	PRELIMINARY;	prt;	586 AA.
AC	089097;			
DT	01-NOV-1998 (TREMBLrel. 08, Created)			
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	DN P63 alpha.			
GN	TRP63 OR P73H.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
PN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98448095; PubMed=9774969;			
RA	Yang A., Kaiguan M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,			
RA	Caput D., McKeon F.;			
RT	"p63, a p53 homolog at 3q27-29, encodes multiple products with			
RT	transactivating, death-inducing, and dominant-negative activities.";			
RL	Mol. Cell 2:305-316(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Thymus;			
RX	MEDLINE=98369596; PubMed=9703973;			
RA	Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,			
RA	Tanaka T., Shinkai Y., Kato H.;			
RT	"A second p53-related protein, p73L, with high homology to p73.";			
RL	Biochem. Biophys. Res. Commun. 248:603-607(1998).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE P53 FAMILY.			
DR	EMBL; AF075439; AAC62644.1; -;			
DR	HSSP; AB010152; BAA32432.1; -;			
DR	HSSP; P04637; 1YCS.			
DR	MGD; MGI:1330810; Trp63.			
DR	InterPro: IPR002117; P53.			
DR	InterPro: IPR001660; SAM.			
DR	Pfam; PF00870; P53; 1.			
DR	PRINTS; PR00386; P53SUPPRESSR.			
DR	PRODOM; PD002681; P53; 1.			
DR	SMART; SMO0454; SAM; 1.			
DR	PROSITE; PS00348; P53; 1.			
KW	Nuclear protein.			
QJ	SEQUENCE 586 AA; 65789 MW; 622E24085BBDBCH7 CRC64;			

Query Match	97.9%;	Score 2398;	DB 11;	Length 586;
Best Local Similarity	96.9%;	Pred. No. 15e-194;		
Matches 451;	Conservative	3;	Mismatches 2;	Indels 0;
			Gaps	0;
QY	1	MLYLENNAQOTOFSEPOYTNLGLNLSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS	60	
Db	1	MLYLENNAQIQOFSEPOYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS	60	
QY	61	TFPDALSSPAIPSTDTDPGHSPVSVSQOOSTAKSATWYTSYTELKKLYCQIAKCPQIQK	120	
Db	61	TFPALSSPAIPSTWDYDPGHSPVSVSQOOSTAKSATWYTSYTELKKLYCQIAKCPQIQK	120	
QY	121	VMPPPPGAVIRAMPVYKKAHEVTEYVKKRCPNHELSREFNEGQIAPPSHLIRVGNSHAQ	180	
Db	121	VMPPPPGAVIRAMPVYKKAHEVTEYVKKRCPNHELSREFNEGQIAPPSHLIRVGNSHAQ	180	
QY	181	YVEDPPIINGROSVLYPEPPOVGTETFTVLYNFMCNSSCVGAMNRPILLIIVTLETRDGOV	240	
Db	181	YVEDPPIINGROSVLYPEPPOVGTETFTVLYNFMCNSSCVGAMNRPILLIIVTLETRDGOV	240	
QY	241	LGRRCFEARICACGRRKADDEDSIRKQOVS DSTKNDGTRKRPQNTHTGIOMTSIKRR	300	
Db	241	LGRRCFEARICACGRRKADDEDSIRKQOVS DSTKNDGTRKRPQNTHTGIOMTSIKRR	300	
QY	301	SPDDELLLYLVYGRRETEYEMTLKTESLELMQOYLPOHTIEITYRQOOQOQHLLQOKOSTIQ	360	
Db	301	SPDDELLLYLVYGRRETEYEMTLKTESLELMQOYLPOHTIEITYRQOOQOQHLLQOKOSTIQ	360	
QY	361	SPSSYGNSSBPLNKMNSMNLPSVSQLINDQORNALPTPTIPDGMGANIDPMGTIMPMAG	420	

Db 361 SSSYGNSSPPLNKMNSNKLPSVSQILNPOORNALPTPTMEGKANIPMGTHMPAG 420
 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456
 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456

RESULT 9

099UE2 PRELIMINARY: PRT: 586 AA.
 ID 099UE2
 AC 099UE2
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE DN KET alpha protein.
 GN P63.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Jistat; TISSUE=Tongue;
 RX MEDLINE=21363378; PubMed=11470269;
 RA Bamberg C., Schmale H.;
 RT "Identification and tissue distribution of novel KET/p63 splice
 variants";
 RL FEBS Lett. 501:121-126(2001).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL: AJ277447; CAC37099.1; -.
 DR HSSP: P04637; 1YCS.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 586 AA: 65732 MW: 76AB8C4F52BA743 CRC64;

Query Match 97.5%; Score 2389; DB 11; Length 586;
 Best Local Similarity 98.5%; Pred. No. 8.6e-194;
 Matches 449; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLXYENNAQTQFSEPOYTNGLINSMDOQIQNGSSSTSPYNTDHAQNSVTAPSPAOPSS 60
 DB 1 MLXYENNAQTQFSEPOYTNGLINSMDOQIQNGSSSTSPYNTDHAQNSVTAPSPAOPSS 60
 QY 61 TFDALSPSPALPSTWDYGPSPFVSPFOSSSTAKSATWTYSELKLYCOJAKTCPTIOIK 120
 DB 61 TFDALSPSPALPSTWDYGPSPFVSPFOSSSTAKSATWTYSELKLYCOJAKTCPTIOIK 120
 QY 121 VMTPEPGAVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQ 180
 DB 121 VMTPEPGAVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQ 180
 QY 121 VMTPEPGAVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQ 180
 DB 121 VMTPEPGAVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQ 180
 QY 181 YVEBPITGRQSVLYPYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILIIYTLERDQOV 240
 DB 181 YVEBPITGRQSVLYPYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILIIYTLERDQOV 240
 QY 241 LGRRCFEARICACGRDKKADSDIRKQOVSDSTKNGDGTGRPRFRONTNGIOMTSIKRR 300
 DB 241 LGRRCFEARICACGRDKKADSDIRKQOVSDSTKNGDGTGRPRFRONTNGIOMTSIKRR 300
 QY 301 SPDELLYLTPVGRGTEYEMLIKESLELMQYLPQHTIETRYRQOOQOHQLKQTSIQ 360
 DB 301 SPDELLYLTPVGRGTEYEMLIKESLELMQYLPQHTIETRYRQOOQOHQLKQTSIQ 360
 QY 361 SPSSYGNSSPPLNKMNSNKLPSVSQILNPOORNALPTPTIPDGANIPMGTHMPAG 420
 DB 361 SPSSYGNSSPPLNKMNSNKLPSVSQILNPOORNALPTPTIPDGANIPMGTHMPAG 420

Db 361 SSSYGNSSPPLNKMNSNKLPSVSQILNPOORNALPTPTMEGKANIPMGTHMPAG 420
 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456
 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456

RESULT 10

09H3D3 PRELIMINARY: PRT: 555 AA.
 ID 09H3D3
 AC 09H3D3; Q9UP27;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE TA p63 beta.
 GN P63.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kagnad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKeon F.;
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities";
 RL Mol. Cell 2:305-316(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hagihara K., McMenamin M.G., Harris C.C.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL: AF124539; AAG45608.1; -.
 DR EMBL: AF124528; AAG45608.1; JOINED.
 DR EMBL: AF124529; AAG45608.1; JOINED.
 DR EMBL: AF124531; AAG45608.1; JOINED.
 DR EMBL: AF124532; AAG45608.1; JOINED.
 DR EMBL: AF124533; AAG45608.1; JOINED.
 DR EMBL: AF124534; AAG45608.1; JOINED.
 DR EMBL: AF124535; AAG45608.1; JOINED.
 DR EMBL: AF124536; AAG45608.1; JOINED.
 DR EMBL: AF124537; AAG45608.1; JOINED.
 DR EMBL: AF075432; AAC62637.1; -.
 DR HSSP: P04637; 1YCS.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 555 AA: 62433 MW: E22874BE7DBACBE CRC64;

Query Match 97.1%; Score 2379; DB 4; Length 555;
 Best Local Similarity 100.0%; Pred. No. 5.6e-193;
 Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLINSMDOQIQNGSSSTSPYNTDHAQNSVTAPSPAOPSSFTDALSPSPALPSN 74
 DB 15 PQTNLGLINSMDOQIQNGSSSTSPYNTDHAQNSVTAPSPAOPSSFTDALSPSPALPSN 74
 QY 109 PQTNLGLINSMDOQIQNGSSSTSPYNTDHAQNSVTAPSPAOPSSFTDALSPSPALPSN 168
 DB 109 PQTNLGLINSMDOQIQNGSSSTSPYNTDHAQNSVTAPSPAOPSSFTDALSPSPALPSN 168
 QY 75 TDYGPSPFVSPFOSSSTAKSATWTYSELKLYCOJAKTCPTIOIKWTPPGQAVIRAM 134
 DB 75 TDYGPSPFVSPFOSSSTAKSATWTYSELKLYCOJAKTCPTIOIKWTPPGQAVIRAM 134
 QY 169 TDYGPSPFVSPFOSSSTAKSATWTYSELKLYCOJAKTCPTIOIKWTPPGQAVIRAM 228
 DB 169 TDYGPSPFVSPFOSSSTAKSATWTYSELKLYCOJAKTCPTIOIKWTPPGQAVIRAM 228
 QY 135 PVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQYVEBPITGRQSVLY 194
 DB 135 PVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQYVEBPITGRQSVLY 194
 QY 229 PVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQYVEBPITGRQSVLY 288
 DB 229 PVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQYVEBPITGRQSVLY 288
 QY 195 PYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILIIYTLERDQOVLGRRCFEARICACP 254
 DB 195 PYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILIIYTLERDQOVLGRRCFEARICACP 254
 QY 289 PYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILIIYTLERDQOVLGRRCFEARICACP 348
 DB 289 PYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILIIYTLERDQOVLGRRCFEARICACP 348


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QY 255 GDRKADEDSTKRGDGTGRPFONTHTGIDMTSTKRRSPDELLYLVRGR 314
DB 349 GDRKADEDSTKRGDGTGRPFONTHTGIDMTSTKRRSPDELLYLVRGR 408
QY 315 EYEMLLKIKESLELMQYLPQHTIETRYRQOOQHLLQKOTSISPSYSGNSPPLNK 374
DB 409 EYEMLLKIKESLELMQYLPQHTIETRYRQOOQHLLQKOTSISPSYSGNSPPLNK 468
QY 375 MNSMKNLPSVSQLINPOQRNALTPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPPP 434
DB 469 MNSMKNLPSVSQLINPOQRNALTPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPPP 528
QY 435 LSMPSHCTPPPPYPTDCSIVIMOV 461
DB 529 LSMPSHCTPPPPYPTDCSIVIMOV 555

RESULT 11
QY 09P1B7 PRELIMINARY: PRT: 516 AA.
AC 09P1B7:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE P51 isoform TAP63beta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tanj M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF116766; AAF43488.1; JOINED.
DR EMBL: AF116756; AAF43488.1; JOINED.
DR EMBL: AF116757; AAF43488.1; JOINED.
DR EMBL: AF116759; AAF43488.1; JOINED.
DR EMBL: AF116760; AAF43488.1; JOINED.
DR EMBL: AF116761; AAF43488.1; JOINED.
DR EMBL: AF116762; AAF43488.1; JOINED.
DR EMBL: AF116763; AAF43488.1; JOINED.
DR EMBL: AF116764; AAF43488.1; JOINED.
DR EMBL: AF116765; AAF43488.1; JOINED.
DR EMBL: AF116766; AAF43488.1; JOINED.
DR EMBL: AF116767; AAF43488.1; JOINED.
DR HSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 516 AA; 57598 MW; 07553781103738B1 CRC64;

Query Match 96.8%; Score 2372; DB 4; Length 516;
Best Local Similarity 99.8%; Pred. No. 2e-192;
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 POUTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSPSTFDALSPSPAIPSN 74
DB 109 POUTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSPSTFDALSPSPAIPSN 129
QY 75 TDYPGHSDVYFQOOSTAKSATWTYSTELKLYCOIATCTPQIKVMPPRPOGAVIRAM 134
DB 130 TDYPGHSDVYFQOOSTAKSATWTYSTELKLYCOIATCTPQIKVMPPRPOGAVIRAM 189
QY 135 PYYKRAEHTEYVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
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DB 190 PYYKRAEHTEYVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGETFTVLYNEMCNSSCVGAMNRRPILITVLETRDGOVLGRCEARICAP 254
DB 250 PYEPPOVGETFTVLYNEMCNSSCVGAMNRRPILITVLETRDGOVLGRCEARICAP 309
QY 255 GDRKADEDSTKRGDGTGRPFONTHTGIDMTSTKRRSPDELLYLVRGR 314
DB 310 GDRKADEDSTKRGDGTGRPFONTHTGIDMTSTKRRSPDELLYLVRGR 369
QY 315 EYEMLLKIKESLELMQYLPQHTIETRYRQOOQHLLQKOTSISPSYSGNSPPLNK 374
DB 370 EYEMLLKIKESLELMQYLPQHTIETRYRQOOQHLLQKOTSISPSYSGNSPPLNK 429
QY 375 MNSMKNLPSVSQLINPOQRNALTPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPPP 434
DB 430 MNSMKNLPSVSQLINPOQRNALTPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPPP 489
QY 435 LSMPSHCTPPPPYPTDCSIVIMOV 461
DB 490 LSMPSHCTPPPPYPTDCSIVIMOV 516

RESULT 12
QY 09QWZ0 PRELIMINARY: PRT: 555 AA.
AC 09QWZ0:
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE TA*63 beta.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKee F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities."
RT Mol. Cell 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF075435; AAC62640.1; -.
DR HSP: P04637; 1YCS.
DR MGD: MGI:1330810; Trp63.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 555 AA; 62454 MW; 059E034046EB8887 CRC64;

Query Match 96.2%; Score 2356; DB 11; Length 555;
Best Local Similarity 98.9%; Pred. No. 5e-191;
Matches 442; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 15 POUTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSPSTFDALSPSPAIPSN 74
DB 109 POUTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSPSTFDALSPSPAIPSN 168
QY 75 TDYPGHSDVYFQOOSTAKSATWTYSTELKLYCOIATCTPQIKVMPPRPOGAVIRAM 134
DB 169 TDYPGHSDVYFQOOSTAKSATWTYSTELKLYCOIATCTPQIKVMPPRPOGAVIRAM 228
QY 135 PYYKRAEHTEYVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
DB 229 PYYKRAEHTEYVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 288
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QY 195 PYEPPOVGTETFTVLYNFMKNSSCVCGMNRRLIIVTLETRDGOVLGRRCFEARICACP 254
    |||||||
DB 289 PYEPPOVGTETFTVLYNFMKNSSCVCGMNRRLIIVTLETRDGOVLGRRCFEARICACP 348
QY 255 GROKKADEDSIRKQOVSdstkNGDGTkRPRONTNGIOMTSIKKRRSPDDELLYLPVGR 314
    |||||||
DB 349 GROKKADEDSIRKQOVSdstkNGDGTkRPRONTNGIOMTSIKKRRSPDDELLYLPVGR 408
QY 315 EYEMMLKIKESLELMQYLPQHTIETRYROOQOOHQHLLQKOTSIQSPSSYGNSSPPLNK 374
    |||||||
DB 409 EYEMMLKIKESLELMQYLPQHTIETRYROOQOOHQHLLQKOTSIQSPSSYGNSSPPLNK 468
QY 375 MNSMKNKLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 434
    |||||||
DB 469 MNSMKNKLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 528
QY 435 LSMPTSHCTPPPPYPTDCSIVRIWOY 461
    |||||||
DB 529 LSMPTSHCTPPPPYPTDCSIVRIWOY 555

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RESULT 13

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099JD7 ID 099JD7 PRELIMINARY: PRT: 538 AA.
AC 099JD7:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE TAI KET beta protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Missar; TISSUE= Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
RT variants.";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AJ277452; CAC37104.1; -.
DR HSSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 538 AA; 60326 MW; 66D0CA19786BF21B CRC64;

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Query Match 96.0%; Score 2352; DB 11; Length 538;
 Best Local Similarity 98.7%; Pred. No. 1e-190;
 Matches 441; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 15 PÖYNTNLGLNMQOQIONGSSSTSPYNTDHAONSVTAPSPYAPQSSSTFDALSPSPALPSN 74
    |||||||
DB 92 PÖYNTNLGLNMQOQIONGSSSTSPYNTDHAONSVTAPSPYAPQSSSTFDALSPSPALPSN 151
QY 75 TDYPGPHSFVSVFOQSSSTAKSATWTYSTELKLLYCOJAKTCPIQIKWMTPPPGAVIRAM 134
    |||||||
DB 152 TDYPGPHSFVSVFOQSSSTAKSATWTYSTELKLLYCOJAKTCPIQIKWMTPPPGAVIRAM 211
QY 135 PYAKKAHVTEVYAKRCNHELSPREFNGQIAPSHLIRVGNNSHAQYVEDPITGRÖSVLV 194
    |||||||
DB 212 PYAKKAHVTEVYAKRCNHELSPREFNGQIAPSHLIRVGNNSHAQYVEDPITGRÖSVLV 271
QY 195 PYEPPOVGTETFTVLYNFMKNSSCVCGMNRRLIIVTLETRDGOVLGRRCFEARICACP 254
    |||||||

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DB 272 PYEPPOVGTETFTVLYNFMKNSSCVCGMNRRLIIVTLETRDGOVLGRRCFEARICACP 331
QY 255 GROKKADEDSIRKQOVSdstkNGDGTkRPRONTNGIOMTSIKKRRSPDDELLYLPVGR 314
    |||||||
DB 332 GROKKADEDSIRKQOVSdstkNGDGTkRPRONTNGIOMTSIKKRRSPDDELLYLPVGR 391
QY 315 EYEMMLKIKESLELMQYLPQHTIETRYROOQOOHQHLLQKOTSIQSPSSYGNSSPPLNK 374
    |||||||
DB 392 EYEMMLKIKESLELMQYLPQHTIETRYROOQOOHQHLLQKOTSIQSPSSYGNSSPPLNK 451
QY 375 MNSMKNKLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 434
    |||||||
DB 452 MNSMKNKLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 511
QY 435 LSMPTSHCTPPPPYPTDCSIVRIWOY 461
    |||||||
DB 512 LSMPTSHCTPPPPYPTDCSIVRIWOY 538

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RESULT 14

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099JD8 ID 099JD8 PRELIMINARY: PRT: 555 AA.
AC 099JD8:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE TAI KET beta protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Missar; TISSUE= Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
RT variants.";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AJ277451; CAC37103.1; -.
DR HSSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 555 AA; 62426 MW; 65D8854E2387C74C CRC64;

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Query Match 96.0%; Score 2352; DB 11; Length 555;
 Best Local Similarity 98.7%; Pred. No. 1e-190;
 Matches 441; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 15 PÖYNTNLGLNMQOQIONGSSSTSPYNTDHAONSVTAPSPYAPQSSSTFDALSPSPALPSN 74
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DB 109 PÖYNTNLGLNMQOQIONGSSSTSPYNTDHAONSVTAPSPYAPQSSSTFDALSPSPALPSN 168
QY 75 TDYPGPHSFVSVFOQSSSTAKSATWTYSTELKLLYCOJAKTCPIQIKWMTPPPGAVIRAM 134
    |||||||
DB 169 TDYPGPHSFVSVFOQSSSTAKSATWTYSTELKLLYCOJAKTCPIQIKWMTPPPGAVIRAM 228
QY 135 PYAKKAHVTEVYAKRCNHELSPREFNGQIAPSHLIRVGNNSHAQYVEDPITGRÖSVLV 194
    |||||||
DB 229 PYAKKAHVTEVYAKRCNHELSPREFNGQIAPSHLIRVGNNSHAQYVEDPITGRÖSVLV 288
QY 195 PYEPPOVGTETFTVLYNFMKNSSCVCGMNRRLIIVTLETRDGOVLGRRCFEARICACP 254
    |||||||
DB 289 PYEPPOVGTETFTVLYNFMKNSSCVCGMNRRLIIVTLETRDGOVLGRRCFEARICACP 348
QY 255 GROKKADEDSIRKQOVSdstkNGDGTkRPRONTNGIOMTSIKKRRSPDDELLYLPVGR 314

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Db 349 GDRRADEDSIRKQVSDSAKNGDGTKRPFQNTGHIOMTSIKRRSPDDELLYLPVGR 408
QY 315 EYEMLLKIKESLEMOYLPOHTIETRYOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Db 409 EYEMLLKIKESLEMOYLPOHTIETRYOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 468
QY 375 MNSMNLKPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPPP 434
Db 469 MNSMNLKPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPPP 528
QY 435 LSMSTSHCTPPPPYPPTDCSIVRIWQV 461
Db 529 LSMSTSHCTPPPPYPPTDCSIVRIWQV 555

RESULT 15
075195 PRELIMINARY: PRT: 641 AA.
ID 075195
AC 075195
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE P51 Isoform TA63ALPHA (P51B protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98324755; PubMed=9662378;
RA Ikawa M., Ohba M., Kawahara C., IshioKa C., Kanamaru R., Katoh I.,
RA Ikawa Y., Nimura Y., Nakagawa A., Obinata M.
RT "Cloning and functional analysis of human p51, which structurally and
RT functionally resembles p53."
RL Nat. Med. 4:839-844(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20389515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.
RT "Mutation and expression of the p51 gene in human lung cancer."
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL, AB016073; BA82593.1; -.
DR EMBL, AF116769; AAF3487.1; -.
DR EMBL, AF116756; AAF3487.1; JOINED.
DR EMBL, AF116757; AAF3487.1; JOINED.
DR EMBL, AF116759; AAF3487.1; JOINED.
DR EMBL, AF116760; AAF3487.1; JOINED.
DR EMBL, AF116761; AAF3487.1; JOINED.
DR EMBL, AF116762; AAF3487.1; JOINED.
DR EMBL, AF116763; AAF3487.1; JOINED.
DR EMBL, AF116764; AAF3487.1; JOINED.
DR EMBL, AF116765; AAF3487.1; JOINED.
DR EMBL, AF116766; AAF3487.1; JOINED.
DR EMBL, AF116767; AAF3487.1; JOINED.
DR EMBL, AF116768; AAF3487.1; JOINED.
DR HSSP, P04637; IYCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KV Nuclear protein.
SQ SEQUENCE 641 AA: 72019 MW: 97AE61F66E63F618 CRC64;

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Query Match 95.9%; Score 2350; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 2e-190;

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Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 PQTNLGLNSMDQIQGSSSTSPYNTDHAONSTAPSPYQPSSTFDALSPPAISN 74
Db 70 PQTNLGLNSMDQIQGSSSTSPYNTDHAONSTAPSPYQPSSTFDALSPPAISN 129
QY 75 TDYCPHSPDVSFQOOSTAKSATWTYSTELKKLYQIAKTCPIQIKVMTPPQGAIVRAM 134
Db 130 TDYCPHSPDVSFQOOSTAKSATWTYSTELKKLYQIAKTCPIQIKVMTPPQGAIVRAM 189
QY 135 PYKKAHEVTEYVKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQYVEDPITGROSVLY 194
Db 190 PYKKAHEVTEYVKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQYVEDPITGROSVLY 249
QY 195 PYEPPOVGTEFTVLYNFCNSSCYGMMRRPILIIYVLETRDGOVLGRCEARICACP 254
Db 250 PYEPPOVGTEFTVLYNFCNSSCYGMMRRPILIIYVLETRDGOVLGRCEARICACP 309
QY 255 GDRRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIOMTSIKRRSPDDELLYLPVGR 314
Db 310 GDRRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIOMTSIKRRSPDDELLYLPVGR 369
QY 315 EYEMLLKIKESLEMOYLPOHTIETRYOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Db 370 EYEMLLKIKESLEMOYLPOHTIETRYOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
QY 375 MNSMNLKPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPPP 434
Db 430 MNSMNLKPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPPP 489
QY 435 LSMSTSHCTPPPPYPPTDCSIV 456
Db 490 LSMSTSHCTPPPPYPPTDCSIV 511

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Search completed: August 7, 2003, 09:51:43
Job time : 39.092 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 7, 2003, 09:31:28 ; Search time 27.1034 Seconds
(without alignments)
2301.535 Million cell updates/sec

Title: US-09-538-106-18

Perfect score: 2082
Sequence: 1 MLYLENNANQTFSEPOQYTNL.....PKQSDVFRHRSKPNRSYYP 393

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq.19Jun03.*

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20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2082	100.0	393	20	AAV05957
2	2082	100.0	393	23	ABG95133
3	2082	100.0	393	23	ABG95139
4	2011	96.6	448	20	AAV45246
5	2011	96.6	448	20	AAV05955
6	2011	96.6	448	21	ABAB1359
7	2011	96.6	448	22	ABAB82128
8	2011	96.6	448	23	ABG95127
9	2011	96.6	448	23	ABG95137

10	2011	96.6	448	23	ABG95143	Human oncogene p63
11	2011	96.6	448	23	ABP61911	Human p53 homolog
12	2011	96.6	448	23	ABP74991	Human p53 homolog
13	2011	96.6	448	24	ABU56418	Lung cancer-assoc
14	2009	96.5	389	20	AAV05964	Mouse cell regulat
15	1938	93.1	483	20	AAV05961	Mouse cell regulat
16	1884	90.5	416	23	ABG95130	Human oncogene p51
17	1884	90.5	461	21	ABAB1362	Human p63 protein
18	1884	90.5	461	23	ABG95131	Human oncogene p51
19	1884	90.5	461	23	ABG95138	Human oncogene p63
20	1884	90.5	461	23	ABP61914	Human p53 homolog
21	1884	90.5	461	23	ABP74994	Human p53 homolog
22	1884	90.5	586	20	AAV05956	Human cell regulat
23	1884	90.5	586	23	ABG95132	Human oncogene p51
24	1884	90.5	586	23	ABG95140	Human oncogene p63
25	1882	90.4	461	20	AAV05963	Mouse cell regulat
26	1882	90.4	586	20	AAV05962	Mouse cell regulat
27	1867	89.7	356	20	AAV43135	Human p40 protein
28	1867	89.7	356	21	ABAB1360	Human p63 protein
29	1867	89.7	356	23	ABP61912	Human lung cancer
30	1867	89.7	356	23	ABP74992	Human p53 homolog
31	1867	89.7	586	21	ABAB1357	Human p63 protein
32	1867	89.7	586	23	ABP61909	Human lung cancer
33	1867	89.7	586	23	ABP74989	Human p53 homolog
34	1860	89.3	586	20	AAV41032	Human lung tumor a
35	1860	89.3	586	21	ABAB1317	Human lung cancer-
36	1860	89.3	586	23	ABP61869	Human lung cancer
37	1860	89.3	586	23	ABP74949	Human lung tumor
38	1813	87.1	471	23	ABG95129	Human oncogene p51
39	1813	87.1	471	23	ABG95134	Human oncogene p51
40	1813	87.1	516	20	AAV05954	Human cell regulat
41	1813	87.1	516	21	ABAB1363	Human p63 protein
42	1813	87.1	516	23	ABG95135	Human oncogene p51
43	1813	87.1	516	23	ABG95141	Human oncogene p63
44	1813	87.1	516	23	ABP61915	Human lung cancer
45	1813	87.1	516	23	ABP74995	Human p53 homolog

ALIGNMENTS

```
RESULT 1
AAV05957
ID AAV05957 standard; Protein: 393 AA.
XX
AC AAV05957;
XX
16-AUG-1999 (first entry)
XX
DE Human cell regulatory protein p63, isoform delta p63 beta.
XX
KW Cell regulatory protein; p63; hu-delta p63 beta; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy.
XX
OS Homo sapiens.
XX
PN W09919357-A2.
XX
PD 22-APR-1999.
XX
PF 02-OCT-1998; 98WO-US21992.
XX
PR 29-MAY-1998; 98US-0087216.
PR 15-OCT-1997; 97US-0062076.
PA (HARD) HARVARD COLLEGE.
XX
PI McKeon F, Yang A;
XX WPI, 1999-277595/23.
DR N-PSDB; AAX58576.
XX
```

PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 XX
 PS Claim 23; Fig 13; 161pp; English.
 XX
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. It has been observed that the
 CC intron-exon organisation is conserved between p73 and p63, and from
 CC known exon and intron sizes for these 2 genes, it was possible to
 CC identify new members of this gene family using a PCR-based strategy
 CC of amplifying 2 exons in a conserved domain and their intervening
 CC intron. The human p53 gene was localised to chromosomal position
 CC 3q27-29. At least 6 different isoforms exist. Splice variants
 CC differing at the C-terminus have been designated as alpha, beta and
 CC gamma forms, while p63 members differing in the N-terminus are
 CC designated as deltaN and TA forms, where the deltaN form lacks the
 CC transactivation domain. The present sequence represents human
 CC p63 isoform hu-deltaNp63 beta. p63 was detected in a variety
 CC of human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and neuronal degenerative
 CC disorders. p63 polypeptides (see AY05953-64), polynucleotides (see
 CC AAX5872-83) and anti p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 CC
 XX
 SQ Sequence 393 AA;

Query Match 100.0%; Score 2082; DB 20; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.4e-182;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQGFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSS 60
 DB 1 MLYENNAQGFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSS 60
 QY 61 TFDALSPSPALPSTWDYPGHSEFDVSFQSSSTAKSATWTSTELKRLYQIACTCPQIK 120
 DB 61 TFDALSPSPALPSTWDYPGHSEFDVSFQSSSTAKSATWTSTELKRLYQIACTCPQIK 120
 QY 121 VMTPPGAVIRAMPYVKKAHTEVYKRCPNHLSFENEGQIAPPSHLIRVGNHQAQ 180
 DB 121 VMTPPGAVIRAMPYVKKAHTEVYKRCPNHLSFENEGQIAPPSHLIRVGNHQAQ 180
 QY 181 YVEDPTGROSVLYPPEPGVGFETTVLVNEMCNSSCGVMNRPLITVLTETRGQV 240
 DB 181 YVEDPTGROSVLYPPEPGVGFETTVLVNEMCNSSCGVMNRPLITVLTETRGQV 240
 QY 241 IGRKCFEARIACGPGRDRADEDSIRKQOYSDSTKNGDGTGRPRQTHGIGMTSIRKR 300
 DB 241 IGRKCFEARIACGPGRDRADEDSIRKQOYSDSTKNGDGTGRPRQTHGIGMTSIRKR 300
 QY 301 SPDELLLYLVGRREYEMLKIKESLELMQYLPORTIETRYRQOQOQHLLQKLLSA 360
 DB 301 SPDELLLYLVGRREYEMLKIKESLELMQYLPORTIETRYRQOQOQHLLQKLLSA 360
 QY 361 CFRRNEIVEPRRETPKQSDVFFRHSKPPNRSYTP 393
 DB 361 CFRRNEIVEPRRETPKQSDVFFRHSKPPNRSYTP 393

RESULT 2
 ABG95133
 ID ABG95133 standard; Protein: 393 AA.

AC ABG95133;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human oncogene p51 isoform delNgamma.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX
 OS Homo sapiens.
 XX
 PN W0200269900-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 01-MAR-2002; 2002WC-US06518.
 XX
 PR 01-MAR-2001; 2001US-272751P.
 XX
 PA (CONF-) CONFORMA THERAPEUTICS CORP.
 XX
 PI Filtz LC, Burrows FJ;
 XX
 DR WPI; 2002-698710/75.
 XX
 PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90
 PT
 XX
 XX Disclosure; Page 333-334; 389pp; English.
 XX
 CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock
 CC protein (HSP)-90, or selectively treating cells expressing (II)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.
 XX
 SQ Sequence 393 AA;

Query Match 100.0%; Score 2082; DB 23; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.4e-182;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQGFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSS 60
 DB 1 MLYENNAQGFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAPSS 60
 QY 61 TFDALSPSPALPSTWDYPGHSEFDVSFQSSSTAKSATWTSTELKRLYQIACTCPQIK 120
 DB 61 TFDALSPSPALPSTWDYPGHSEFDVSFQSSSTAKSATWTSTELKRLYQIACTCPQIK 120

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QY 121 VMTPPGAVIRAMPVYKKAHEVTVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQ 180
    |||
Db 121 VMTPPGAVIRAMPVYKKAHEVTVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQ 180
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    |||
Db 181 YVEDPITGRQSVLYPEPPQVGTETTYLYNFKMNCSSCVGGMNRRPILIIYTLERDQV 240
QY 241 LGRRCFEARICACGRDKADEDSIRKQVSDSTKNGDGTFRPFQNTNGHGIOMTSIKRR 300
    |||
Db 241 LGRRCFEARICACGRDKADEDSIRKQVSDSTKNGDGTFRPFQNTNGHGIOMTSIKRR 300
QY 301 SPDELILYLPVGRGRTYEMLIKESLELMQYLPQHTIETTYRQOQOQHLLQKHLISA 360
    |||
Db 301 SPDELILYLPVGRGRTYEMLIKESLELMQYLPQHTIETTYRQOQOQHLLQKHLISA 360
QY 361 CFRNELVPRRRTPKQSDVFFRHSKPPNRSYYP 393
    |||
Db 361 CFRNELVPRRRTPKQSDVFFRHSKPPNRSYYP 393

RESULT 3
ABG95139
ID ABG95139 standard; Protein: 393 AA.
AC ABG95139;
XX
XX 04-DEC-2002 (first entry)
DE
XX Human oncogene p63 isoform delta n p63 gamma.
XX
XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
XX Homo sapiens.
XX
XX WO200269900-A2.
XX
XX 12-SEP-2002.
XX
XX 01-MAR-2002; 2002WO-US06518.
XX
XX 01-MAR-2001; 2001US-272751P.
XX
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX
XX Fritz LC, Burrows FJ;
XX
XX WPI; 2002-698710/75.
XX
XX N-PSDB; ABS73331.
XX
XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins; e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90
XX
XX
XX Disclosure; Page 345-346; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock
XX protein (HSP)-90, or selectively treating cells expressing (II)
XX involving administering HSP90-inhibitor. The method is useful for
XX treating genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion

```

```

CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
XX
XX Sequence 393 AA:
XX
XX Query Match 100.0%; Score 2082; DB 23; Length 393;
XX Best Local Similarity 100.0%; Pred. No. 1,4e-182;
XX Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLYLENNMQTFSEEQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
    |||
Db 1 MLYLENNMQTFSEEQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
    |||
Db 61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPVYKKAHEVTVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQ 180
    |||
Db 121 VMTPPGAVIRAMPVYKKAHEVTVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYPEPPQVGTETTYLYNFKMNCSSCVGGMNRRPILIIYTLERDQV 240
    |||
Db 181 YVEDPITGRQSVLYPEPPQVGTETTYLYNFKMNCSSCVGGMNRRPILIIYTLERDQV 240
QY 241 LGRRCFEARICACGRDKADEDSIRKQVSDSTKNGDGTFRPFQNTNGHGIOMTSIKRR 300
    |||
Db 241 LGRRCFEARICACGRDKADEDSIRKQVSDSTKNGDGTFRPFQNTNGHGIOMTSIKRR 300
QY 301 SPDELILYLPVGRGRTYEMLIKESLELMQYLPQHTIETTYRQOQOQHLLQKHLISA 360
    |||
Db 301 SPDELILYLPVGRGRTYEMLIKESLELMQYLPQHTIETTYRQOQOQHLLQKHLISA 360
QY 361 CFRNELVPRRRTPKQSDVFFRHSKPPNRSYYP 393
    |||
Db 361 CFRNELVPRRRTPKQSDVFFRHSKPPNRSYYP 393

RESULT 4
AAY45246
ID AAY45246 standard; Protein: 448 AA.
AC AAY45246;
XX
XX 07-JAN-2000 (first entry)
DE
XX Human p51 protein A.
XX
XX Human; p51: p53 related gene; cell proliferation; regulation; cancer;
XX tumour suppression; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Domain 1..59
XX FT Domain /label= transactivation_domain
XX FT Domain 142..321
XX FT Domain /label= dna_binding_domain
XX FT Domain 353..397
XX FT Domain /label= oligomerisation_domain
XX PN WO9950412-A1.
XX PD 07-OCT-1999.

```

XX 24-MAR-1999; 99WO-JP01512.
 XX
 XX 27-MAR-1998; 98JP-0100467.
 XX
 XX (SAKA) OTSUKA PHARM CO LTD.
 XX (IKAWA) IKAWA Y.
 XX
 XX Ikawa Y, Ikawa S, Obinata M;
 XX
 XX WPI; 1999-591318/50.
 XX N-PSDB; AA225770.
 XX
 XX New p53 related human gene p51, useful for diagnosis, investigation and
 XX treatment of cancers and screening for potential cell proliferation and
 XX agents -
 XX
 XX Claim 1; Page 147-148; 163pp; Japanese.
 XX
 XX The present sequence represents a human p51 protein, which is related to
 XX p53 and has cell proliferation regulation and tumour suppression
 XX activity. The p51 gene can be used in the investigation, diagnosis and
 XX treatment of diseases such as cancer, with which the p53 family cell
 XX proliferation regulation is associated. The p51 protein may be used for
 XX screening potential agonists and antagonists of its regulatory function,
 XX for use as drugs,
 XX
 XX Sequence 448 AA;

Query Match 96.6%; Score 2011; DB 20; Length 448;
 Best Local Similarity 100.0%; Pred. No. 5.6e-176;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSSFDALSPSPALPSN 74
 DB 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSSFDALSPSPALPSN 129
 QY 75 TDYPPGHSFVSVFQSSSTAKSATWTSTELKLYCQIAKTCPIQIKVMPPPGAVIRAM 134
 DB 130 TDYPPGHSFVSVFQSSSTAKSATWTSTELKLYCQIAKTCPIQIKVMPPPGAVIRAM 189
 QY 135 PVYKKAHEVYVRCRNHLSREPNFGQIAPPSHLIRVGNNSHAQYVEDPITGRQSVLV 194
 DB 190 PVYKKAHEVYVRCRNHLSREPNFGQIAPPSHLIRVGNNSHAQYVEDPITGRQSVLV 249
 QY 195 PYRPPQVGEFTTVLYNFMCNSSCVGGMNRRPILIIYLET RDQGVYGRRCFEARICACP 254
 DB 250 PYRPPQVGEFTTVLYNFMCNSSCVGGMNRRPILIIYLET RDQGVYGRRCFEARICACP 309
 QY 255 GRRKKADEDSIRKQVSDSTKNGDGTRPRONTNGIQTMSIKKRSPDDELLYLPRGR 314
 DB 310 GRRKKADEDSIRKQVSDSTKNGDGTRPRONTNGIQTMSIKKRSPDDELLYLPRGR 369
 QY 315 ETEYMLIKIKESLEIMQYLPQHTIETPRQOQOQOHOHLQKHLSACFRNEIYPRRET 374
 DB 370 ETEYMLIKIKESLEIMQYLPQHTIETPRQOQOQOHOHLQKHLSACFRNEIYPRRET 429
 QY 375 KQSDVEFRHSKPPNRSYYP 393
 DB 430 KQSDVEFRHSKPPNRSYYP 448

RESULT 5
 ID AAY05955
 AAY05955 standard; Protein; 448 AA.

XX AAY05955;
 XX
 XX 16-AUG-1999 (first entry)
 XX
 XX Human cell regulatory protein p63, isoform hUTAP63 gamma.
 XX
 XX Cell regulatory protein; p63; hUTAP63 gamma; Tap63 gamma; human;

KW cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; therapy.

XX Homo sapiens.

XX W09919357-A2.

XX 22-APR-1999.

XX 02-OCT-1998; 98WO-US21992.

XX 29-MAY-1998; 98US-0087216.

XX 15-OCT-1997; 97US-0062076.

XX (HARD) HARVARD COLLEGE.

XX McKeon F, Yang A;

XX WPI; 1999-277595/23.

XX N-PSDB; AAX58574.

XX Claim 23; Fig 11; 161pp; English.

XX The present invention concerns the discovery of a new family of
 XX cell regulatory proteins (CRPs) termed the p63 family of proteins,
 XX which demonstrate certain sequence identity to known tumour
 XX suppressor proteins p53 and p73. It has been observed that the
 XX intron-exon organisation is conserved between p73 and p53, and from
 XX known exon and intron sizes for these 2 genes. It was possible to
 XX identify new members of this gene family using a PCR-based strategy
 XX of amplifying 2 exons in a conserved domain and their intervening
 XX intron. The human p53 gene was localised to chromosomal position
 XX 3q27-29. At least 6 different isoforms exist. Splice variants
 XX differing at the C-terminus have been designated as alpha, beta and
 XX gamma forms, while p63 members differing in the N-terminus are
 XX designated as delta and TA forms, where the delta form lacks the
 XX transactivation domain. The present sequence represents human
 XX p63 isoform Tap63 gamma. p63 was detected in a variety of
 XX human and mouse tissue. It demonstrates remarkably divergent
 XX activities, such as the ability to transactivate p53 reporter genes
 XX and induce apoptosis. Cessation or down-regulation of p63 expression
 XX may play a critical role in the process of cervical squamous
 XX differentiation, both benign and neoplastic. Delta isoforms of p63
 XX act as dominant negatives towards transactivation by p53 and p63.
 XX p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 XX cachexia) and neuronal differentiation and related degenerative
 XX disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 XX AAX58572-83) and anti-p63 antibodies of the invention can be used to
 XX identify compounds useful for treating disorders involving such
 XX processes, in detection and diagnosis, and in the production of
 XX transgenic animals.

XX Sequence 448 AA;

Query Match 96.6%; Score 2011; DB 20; Length 448;
 Best Local Similarity 100.0%; Pred. No. 5.6e-176;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSSFDALSPSPALPSN 74
 DB 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSSFDALSPSPALPSN 129
 QY 75 TDYPPGHSFVSVFQSSSTAKSATWTSTELKLYCQIAKTCPIQIKVMPPPGAVIRAM 134
 DB 130 TDYPPGHSFVSVFQSSSTAKSATWTSTELKLYCQIAKTCPIQIKVMPPPGAVIRAM 189
 QY 135 PVYKKAHEVYVRCRNHLSREPNFGQIAPPSHLIRVGNNSHAQYVEDPITGRQSVLV 194
 DB 190 PVYKKAHEVYVRCRNHLSREPNFGQIAPPSHLIRVGNNSHAQYVEDPITGRQSVLV 249

QY 195 PYEPVGTETFTVLYNFMNCSSCVGMMRRPILITVLETRDGOVLRRCFEARICACP 254
 DB 250 PYEPVGTETFTVLYNFMNCSSCVGMMRRPILITVLETRDGOVLRRCFEARICACP 309
 QY 255 GRDKRADEDSIRKQOVSDSTKNGDGTKRPFRONTGIGIOMTSIKRRSPDDELLYLPVGR 314
 DB 310 GRDKRADEDSIRKQOVSDSTKNGDGTKRPFRONTGIGIOMTSIKRRSPDDELLYLPVGR 369
 QY 315 ETYEMLLKIKESLELMOYLPOHTIETTYRQOOQOQHLLQKHLLSACFRNELVEBRRET 374
 DB 370 ETYEMLLKIKESLELMOYLPOHTIETTYRQOOQOQHLLQKHLLSACFRNELVEBRRET 429
 QY 375 KQSDVFFRHSKRPNRSVYP 393
 DB 430 KQSDVFFRHSKRPNRSVYP 448

RESULT 6
 AAB1359 standard; Protein: 448 AA.
 ID AAB1359 standard; Protein: 448 AA.
 AC AAB1359;
 XX 21-FEB-2001 (first entry)
 DT 21-FEB-2001 (first entry)
 DE Human p63 protein isoform #3.
 XX Human p63 protein isoform #3.
 KW Lung cancer; therapy: treatment; human; tumor; immunogenic; cytostatic;
 KM vaccine; detection.
 XX Homo sapiens.
 OS Homo sapiens.
 XX MO200061612-A2.
 PD 19-OCT-2000.
 XX 03-APR-2000; 2000MO-US08896.
 PF 03-APR-2000; 2000MO-US08896.
 XX 02-APR-1999; 99US-0285479.
 PR 17-DEC-1999; 99US-0466396.
 PR 30-DEC-1999; 99US-0476496.
 PR 10-JAN-2000; 2000US-0480884.
 PR 22-FEB-2000; 2000US-0510376.
 XX (CORI-) CORIXA CORP.
 PA (CORI-) CORIXA CORP.
 XX Wang T, Fan L;
 PI Wang T, Fan L;
 DR WPI: 2000-628399/60.
 DR N-PSDB; AAC66029.
 XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
 PT protein is used for detecting and monitoring progression of lung cancer
 PT in a patient -
 PS Disclosure: Page 247-249; 261pp; English.
 XX This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.
 XX Sequence 448 AA;
 SQ Query Match 96.6%; Score 2011; DB 21; Length 448;
 Best Local Similarity 100.0%; Pred. No. 5.6e-176;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PQTMLGLNSDDQIQNGSSSTSPYNTDHAQNSTAPSAQPSSTDALSPSAIPSN 74
 DB 70 PQTMLGLNSDDQIQNGSSSTSPYNTDHAQNSTAPSAQPSSTDALSPSAIPSN 129
 QY 75 TDYPPHSEFDSYFQSSSTAKSATWTYSTEELKLYCOIAKTCPIQIKVMTPPQGAIVIRAM 134
 DB 130 TDYPPHSEFDSYFQSSSTAKSATWTYSTEELKLYCOIAKTCPIQIKVMTPPQGAIVIRAM 189
 QY 135 PYVKAHEVTEYVKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDPITGQSVLV 194
 DB 190 PYVKAHEVTEYVKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDPITGQSVLV 249
 QY 195 PYEPVGTETFTVLYNFMNCSSCVGMMRRPILITVLETRDGOVLRRCFEARICACP 254
 DB 250 PYEPVGTETFTVLYNFMNCSSCVGMMRRPILITVLETRDGOVLRRCFEARICACP 309
 QY 255 GRDKRADEDSIRKQOVSDSTKNGDGTKRPFRONTGIGIOMTSIKRRSPDDELLYLPVGR 314
 DB 310 GRDKRADEDSIRKQOVSDSTKNGDGTKRPFRONTGIGIOMTSIKRRSPDDELLYLPVGR 369
 QY 315 ETYEMLLKIKESLELMOYLPOHTIETTYRQOOQOQHLLQKHLLSACFRNELVEBRRET 374
 DB 370 ETYEMLLKIKESLELMOYLPOHTIETTYRQOOQOQHLLQKHLLSACFRNELVEBRRET 429
 QY 375 KQSDVFFRHSKRPNRSVYP 393
 DB 430 KQSDVFFRHSKRPNRSVYP 448

RESULT 7
 AAB82128 standard; protein: 448 AA.
 ID AAB82128 standard; protein: 448 AA.
 AC AAB82128;
 XX 03-AUG-2001 (first entry)
 DT 03-AUG-2001 (first entry)
 DE Human protein #1 used to produce a chimeric p53 protein.
 XX Human protein #1 used to produce a chimeric p53 protein.
 KW Human; cytostatic; gene therapy; p53; human tumour.
 KM Human; cytostatic; gene therapy; p53; human tumour.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 1..59
 FT Domain /label= Transactivation_domain
 FT 142..321
 FT Domain /label= DNA_binding_domain
 FT 353..397
 FT Domain /label= Oligomerisation_domain
 PN JP2000354488-A.
 PD 26-DEC-2000.
 XX 09-APR-1999; 99JP-0139034.
 PF 09-APR-1999; 99JP-0139034.
 PR 09-APR-1999; 99JP-0139034.
 XX (IKAW/) IKAWA H.
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX WPI: 2001-268293/28.
 DR N-PSDB; AAF86588.
 XX Chimeric gene of the p53 family, useful for gene therapy, and treatment
 PT of cancer, comprises a transcription activating region and a DNA
 PT binding region -
 PS Example 1; Page 30-32; 57pp; Japanese.
 XX

CC The present invention relates to a chimera gene of p53 family encoding a
CC transcription activating region, a DNA binding region, and an oligomer
CC formation region of different p53 family proteins. The chimeric gene can
CC be used for gene therapy of p53 variant human tumors, and analysis of
CC the function of the p53 family gene. The present sequence was used in the
CC present invention.

XX Sequence 448 AA;

Query Match 96.6%; Score 2011; DB 22; Length 448;
Best Local Similarity 100.0%; Pred. No. 5,6e-176;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSTFDALSPSPALPSN 74
DB 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSTFDALSPSPALPSN 129
QY 75 TDYGPSPHSDVSPFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQGAIVRAM 134
DB 130 TDYGPSPHSDVSPFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQGAIVRAM 189
QY 135 PVYKKAHVTEVYKRCNHELSEFNEGQIAPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
DB 190 PVYKKAHVTEVYKRCNHELSEFNEGQIAPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGETFTTYLVYFMCNNSCVGGMNRRPILITVLETRDGOVLGRRCFEARICACP 254
DB 250 PYEPPOVGETFTTYLVYFMCNNSCVGGMNRRPILITVLETRDGOVLGRRCFEARICACP 309
QY 255 GRDKKADEDSIRKQOVSSTKNGDGTFRPRQNTHGIGOMTSIKRRSPDDELLYLPRGR 314
DB 310 GRDKKADEDSIRKQOVSSTKNGDGTFRPRQNTHGIGOMTSIKRRSPDDELLYLPRGR 369
QY 315 EYEMMLIKIKESLELMQYLPOHTIETRYRQOQOQHLLQKHLSACFRNELVEPRRETP 374
DB 370 EYEMMLIKIKESLELMQYLPOHTIETRYRQOQOQHLLQKHLSACFRNELVEPRRETP 429
QY 375 KQSDVFFRHSKPPNRSYYP 393
DB 430 KQSDVFFRHSKPPNRSYYP 448

RESULT 8

ABG95127 standard; Protein: 448 AA.

XX AC ABG95127;

DT 04-DEC-2002 (first entry)

XX Human oncogene p51A.

KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.

XX Homo sapiens.

XX NC200269900-A2.

XX 12-SEP-2002.

XX 01-MAR-2002; 2002MO-US06518.

XX 01-MAR-2001; 2001US-272751P.

XX (CONF-) CONFORMA THERAPEUTICS CORP.

PI Fritz LC, Burrows EJ;
XX WPI: 2002-698710/75.
DR N-PSDB; ABS73327.

PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90

PS Disclosure; Page 320-321; 389pp; English.

XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock
XX protein (HSP)-90, or selectively treating cells expressing (II)
XX involving administering HSP90-inhibitor. The method is useful for
XX treating genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL, and CMML,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This is the amino acid sequence of a human oncogenic protein.

XX Sequence 448 AA;

Query Match 96.6%; Score 2011; DB 23; Length 448;
Best Local Similarity 100.0%; Pred. No. 5,6e-176;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSTFDALSPSPALPSN 74
DB 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSTFDALSPSPALPSN 129
QY 75 TDYGPSPHSDVSPFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQGAIVRAM 134
DB 130 TDYGPSPHSDVSPFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQGAIVRAM 189
QY 135 PVYKKAHVTEVYKRCNHELSEFNEGQIAPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
DB 190 PVYKKAHVTEVYKRCNHELSEFNEGQIAPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGETFTTYLVYFMCNNSCVGGMNRRPILITVLETRDGOVLGRRCFEARICACP 254
DB 250 PYEPPOVGETFTTYLVYFMCNNSCVGGMNRRPILITVLETRDGOVLGRRCFEARICACP 309
QY 255 GRDKKADEDSIRKQOVSSTKNGDGTFRPRQNTHGIGOMTSIKRRSPDDELLYLPRGR 314
DB 310 GRDKKADEDSIRKQOVSSTKNGDGTFRPRQNTHGIGOMTSIKRRSPDDELLYLPRGR 369
QY 315 EYEMMLIKIKESLELMQYLPOHTIETRYRQOQOQHLLQKHLSACFRNELVEPRRETP 374
DB 370 EYEMMLIKIKESLELMQYLPOHTIETRYRQOQOQHLLQKHLSACFRNELVEPRRETP 429
QY 375 KQSDVFFRHSKPPNRSYYP 393
DB 430 KQSDVFFRHSKPPNRSYYP 448

RESULT 9

ABG95137 standard; Protein: 448 AA.

XX AC ABG95137;

XX 04-DEC-2002 (first entry)
DT Human oncogene p51 isoform TAp63gamma.
DE
XX
XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX Homo sapiens.
XX WO200269900-A2.
XX 12-SEP-2002.
XX 01-MAR-2002; 2002WO-US06518.
XX 01-MAR-2001; 2001US-272751P.
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX Filtz LC, Burrows FJ;
XX WPI: 2002-698710/75.
XX
XX Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90
PT
XX
XX Disclosure: Page 341-342; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock
CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
XX
XX Sequence 448 AA:
SQ

Query Match 96.6%; Score 2011; DB 23; Length 448;
Best Local Similarity 100.0%; Pred. No. 5.6e-176;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNNLGLNMDQIQNGSSSTSPYNDHANSTAPPAQSPSTDALSPSPAIRSN 74
DB 70 PQTNNLGLNMDQIQNGSSSTSPYNDHANSTAPPAQSPSTDALSPSPAIRSN 129
QY 75 TDYGPSPHSDVSPFOSSSTAKSATWTYSTELKKLYQAIKTPDIQIKWTPPGQAVITAM 134
DB 130 TDYGPSPHSDVSPFOSSSTAKSATWTYSTELKKLYQAIKTPDIQIKWTPPGQAVITAM 189
QY 135 PYVKAHEVTEVVKRCPNHELSPREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194

DB 190 PYVKAHEVTEVVKRCPNHELSPREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPQVGEFTTLYYNFMCNSSCYGANNRPILIIYVLETRDQVYLGRCFEARICACP 254
DB 250 PYEPQVGEFTTLYYNFMCNSSCYGANNRPILIIYVLETRDQVYLGRCFEARICACP 309
QY 255 GDRBRADSDIRKQOVSTKMGDCTKRPFRONTGICMTSTIKRRSPDDELLYIPVGR 314
DB 310 GDRBRADSDIRKQOVSTKMGDCTKRPFRONTGICMTSTIKRRSPDDELLYIPVGR 369
QY 315 EYEMLLIKESLEMOQLPQHTIETRYQQOQOQHLLQKHLISACFRNELVEPRRPTP 374
DB 370 EYEMLLIKESLEMOQLPQHTIETRYQQOQOQHLLQKHLISACFRNELVEPRRPTP 429
QY 375 KOSDVEFRHSKPPNRSYTP 393
DB 430 KOSDVEFRHSKPPNRSYTP 448

RESULT 10
ABG95143 standard; Protein: 448 AA.
XX
XX ABG95143;
XX
XX 04-DEC-2002 (first entry)
XX
XX Human oncogene p63 isoform.
XX
XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
XX Homo sapiens.
XX WO200269900-A2.
XX 12-SEP-2002.
XX 01-MAR-2002; 2002WO-US06518.
XX 01-MAR-2001; 2001US-272751P.
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX Filtz LC, Burrows FJ;
XX WPI: 2002-698710/75.
XX N-PSDB: ABS73335.
XX
XX Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90
PT
XX
XX Disclosure: Page 354-356; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock
CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease

(e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.

XX Sequence 448 AA:

SQ Query Match 96.6%; Score 2011; DB 23; Length 448;

Best Local Similarity 100.0%; Pred. No. 5,6e-176; Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSTFDALSPSPALPSN 74

Db 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSTFDALSPSPALPSN 129

QY 75 TDYGPSPFVDSFOQSSSTAKSATWTYSTELKLYCOJAKTCPIQIKWTPPPQGAIVRAM 134

Db 130 TDYGPSPFVDSFOQSSSTAKSATWTYSTELKLYCOJAKTCPIQIKWTPPPQGAIVRAM 189

QY 135 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPSPSHLIRVGNSHAQYVEDPITGRQSVLY 194

Db 190 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPSPSHLIRVGNSHAQYVEDPITGRQSVLY 249

QY 195 PYEPPQVGTETTYLYNPMCNSSCVGGMNRRPILITVLETRDQVLRGCFEARIACAP 254

Db 250 PYEPPQVGTETTYLYNPMCNSSCVGGMNRRPILITVLETRDQVLRGCFEARIACAP 309

QY 255 GRDKKADSDIRKQOVSDSTKNGDGTKRPFQNTNGIOMTSIKKRRSPDDELLYLPVGR 314

Db 310 GRDKKADSDIRKQOVSDSTKNGDGTKRPFQNTNGIOMTSIKKRRSPDDELLYLPVGR 369

QY 315 ETYEMLKIKESLEIMQYLPQHTIETYROOQOOQHLLQKHLISACFRNELVEPRRET 374

Db 370 ETYEMLKIKESLEIMQYLPQHTIETYROOQOOQHLLQKHLISACFRNELVEPRRET 429

QY 375 KQSDVFFRHSKPPNRSVYP 393

Db 430 KQSDVFFRHSKPPNRSVYP 448

RESULT 11

ABP61911 ID ABP61911 standard; Protein: 448 AA.

XX AC ABP61911;

D7 07-OCT-2002 (first entry)

XX Human lung cancer associated protein sequence SEQ ID NO:340.

XX Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO200247534-A2.

XX PD 20-JUN-2002.

XX PF 30-NOV-2001; 2001WO-US47576.

XX PR 12-DEC-2000; 2000US-0735705.

XX PR 07-MAY-2001; 2001US-0850716.

XX PR 28-JUN-2001; 2001US-0897778.

XX PA (CORI-) CORIXA CORP.

XX PI Wang T, Wang A, Skelky YAM, LI SX, Kalos MD, Henderson RA;

PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
XX WPI: 2002-583465/62.
DR N-PSDB: ABQ92434.

XX Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT by the polynucleotides, useful in pharmaceutical compositions such as
PT vaccines and as markers to indicate the presence of lung cancer
XX
PS Example 2; Page 329-330; 381pp; English.

XX The present invention describes isolated human lung carcinoma
CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC activity, and can be used in gene therapy and in vaccines. Compositions
CC comprising (I) or (II) can be used for stimulating an immune response in
CC a patient and for treating lung cancer in a patient. Oligonucleotides of
CC (I) can be used for detecting the presence of a cancer in a patient, by
CC obtaining a biological sample from the patient, contacting the
CC biological sample with the oligonucleotide, detecting in the sample, an
CC amount of polynucleotide that hybridises to the oligonucleotide and
CC comparing the amount of polynucleotide that hybridises to the
CC oligonucleotide to a predetermined cut-off value, and determining the
CC presence of a cancer in the patient. (I) and (II) are useful in
CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
CC indicate the presence or absence of a cancer such as lung cancer.
CC ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used
CC in the exemplification of the present invention.

SQ Sequence 448 AA:

Query Match 96.6%; Score 2011; DB 23; Length 448;

Best Local Similarity 100.0%; Pred. No. 5,6e-176; Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSTFDALSPSPALPSN 74

Db 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSTFDALSPSPALPSN 129

QY 75 TDYGPSPFVDSFOQSSSTAKSATWTYSTELKLYCOJAKTCPIQIKWTPPPQGAIVRAM 134

Db 130 TDYGPSPFVDSFOQSSSTAKSATWTYSTELKLYCOJAKTCPIQIKWTPPPQGAIVRAM 189

QY 135 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPSPSHLIRVGNSHAQYVEDPITGRQSVLY 194

Db 190 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPSPSHLIRVGNSHAQYVEDPITGRQSVLY 249

QY 195 PYEPPQVGTETTYLYNPMCNSSCVGGMNRRPILITVLETRDQVLRGCFEARIACAP 254

Db 250 PYEPPQVGTETTYLYNPMCNSSCVGGMNRRPILITVLETRDQVLRGCFEARIACAP 309

QY 255 GRDKKADSDIRKQOVSDSTKNGDGTKRPFQNTNGIOMTSIKKRRSPDDELLYLPVGR 314

Db 310 GRDKKADSDIRKQOVSDSTKNGDGTKRPFQNTNGIOMTSIKKRRSPDDELLYLPVGR 369

QY 315 ETYEMLKIKESLEIMQYLPQHTIETYROOQOOQHLLQKHLISACFRNELVEPRRET 374

Db 370 ETYEMLKIKESLEIMQYLPQHTIETYROOQOOQHLLQKHLISACFRNELVEPRRET 429

QY 375 KQSDVFFRHSKPPNRSVYP 393

Db 430 KQSDVFFRHSKPPNRSVYP 448

RESULT 12

ABB74991 ID ABB74991 standard; Protein: 448 AA.

XX AC ABB74991;

D7 01-MAY-2002 (first entry)

XX Human p53 homologue isoform, p53 (L5305) protein SEQ ID NO:340.

```

XX Human: lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KM immune response.
XX Homo sapiens.
XX WO200200174-A2.
XX 03-JAN-2002.
XX 28-JUN-2001; 2001WO-US21065.
XX 28-JUN-2000; 2000US-0606421.
XX 02-AUG-2000; 2000US-0630940.
XX 21-AUG-2000; 2000US-0643597.
XX 15-SEP-2000; 2000US-0662786.
XX 09-OCT-2000; 2000US-0685696.
XX 12-DEC-2000; 2000US-0735705.
XX 07-MAY-2001; 2001US-0850716.
XX (CORI-) CORIXA CORP.
XX Wang T, Wang A, Sheiky YAM, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Renter MW, Marnerakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX WPI: 2002-090513/12.
XX N-PSDB; ABL49248.
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
XX lung cancer or stimulating an immune response -
XX Example 2; Page 322-323; 374pp: English.
XX The present invention describes human lung tumor proteins. Human lung
XX tumor proteins and polynucleotides have cytostatic and immunostimulant
XX activities, and can be used in vaccine production. Compositions
XX comprising the lung tumor proteins, polynucleotides, antibodies,
XX fusion proteins, T cell populations, or antigen presenting cells that
XX express the lung tumor proteins are useful for treating lung cancer or
XX stimulating an immune response. ABL4895 to ABL49300 and ABL4946 to
XX ABL5070 represent sequences used in the exemplification of the present
XX invention.
XX Sequence 448 AA:
XX
XX Query Match 96.6%; Score 2011; DB 23; Length 448;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-176;
XX Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15 POYTMGLTNSMDQIQNGSSSTPYNTDHAQNSVTAPSPYAPSPSTPALSPPAIPSN 74
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 70 POYTMGLTNSMDQIQNGSSSTPYNTDHAQNSVTAPSPYAPSPSTPALSPPAIPSN 129
OY 75 TDYPPHSDVYFQOOSTAKSATMTWTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVIRAM 134
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 130 TDYPPHSDVYFQOOSTAKSATMTWTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVIRAM 189
OY 135 PYYKKAHEVTEYVKKCPNHELSEFNEGQIAPPSH.IRVEGNSHAQYEDPITGROSUVY 194
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 190 PYYKKAHEVTEYVKKCPNHELSEFNEGQIAPPSH.IRVEGNSHAQYEDPITGROSUVY 249
OY 195 PYPEPQVTEFTTYVYNFMCNCSGCGMMRRPILITVLETETDGOVLGRCEARICACP 254
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 250 PYPEPQVTEFTTYVYNFMCNCSGCGMMRRPILITVLETETDGOVLGRCEARICACP 309
OY 255 GDRRADESDIRKQOVSDSTKNGDGTKRPFQNTHGQIOWTSIKRRSPDELLYLPVGR 314
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 310 GDRRADESDIRKQOVSDSTKNGDGTKRPFQNTHGQIOWTSIKRRSPDELLYLPVGR 369
OY 315 EYEMLLIKESLEMOYLPOHTTETTYRQOQOQHLLQKLLSACFNNELVEFRRETP 374
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 370 EYEMLLIKESLEMOYLPOHTTETTYRQOQOQHLLQKLLSACFNNELVEFRRETP 429

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OY 375 KOSDVEFRSRKPPNRSVYP 393
DB ||||||||||||||||||
DB 430 KOSDVEFRSRKPPNRSVYP 448
RESULT 13
ABU56418
ID ABU56418 standard; Protein; 448 AA.
XX AC ABU56418;
XX 02-APR-2003 (first entry)
XX Lung cancer-associated polypeptide #11.
XX Lung cancer-associated polypeptide; cytostatic; emphysema;
XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX Unidentified.
XX WO200286443-A2.
XX 31-OCT-2002.
XX 18-APR-2002; 2002WO-US12476.
XX 18-APR-2001; 2001US-284770P.
XX 10-MAY-2001; 2001US-290492P.
XX 09-NOV-2001; 2001US-339245P.
XX 13-NOV-2001; 2001US-350666P.
XX 29-NOV-2001; 2001US-334370P.
XX 12-APR-2002; 2002US-372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Aziz N, Murray R;
XX WPI: 2003-093161/08.
XX N-PSDB; ABX76134.
XX Detecting a lung cancer-associated transcript in a cell from a patient
XX for treating lung cancer, by contacting a biological sample from the
XX patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer -
XX Claim 27; Page 196; 453pp: English.
XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridises
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung
XX cancer-associated polynucleotides and polypeptides are used for
XX identifying a compound that modulates a lung cancer-associated
XX polypeptide, for inhibiting proliferation of a lung cancer-associated
XX cell to treat lung cancer in a patient and for treating a mammal having
XX lung cancer by administering a modulatory compound identified. The
XX methods are useful for treating lung cancer, such as small cell lung
XX cancer, non-small cell lung cancer or other benign or precancerous
XX lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
XX pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
XX pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
XX and polypeptides are useful for diagnostic purposes and as targets for
XX screening for therapeutic compounds that modulate lung cancer, such as
XX antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated
XX polypeptides of the invention.
XX Sequence 448 AA:
XX

```

Query Match 96.6%; Score 2011; DB 24; Length 448;
 Best Local Similarity 100.0%; Pred. No. 5.6e-176;
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSSTFDALSPSPALPSN 74
 |||||||
 DB 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSSTFDALSPSPALPSN 129
 |||||||
 QY 75 TDYGPSPFVDSFOQSSSTAKSATWTYTELKLKCYQIAKTCPIQIKWTTPPGCAVIRAM 134
 |||||||
 DB 130 TDYGPSPFVDSFOQSSSTAKSATWTYTELKLKCYQIAKTCPIQIKWTTPPGCAVIRAM 189
 |||||||
 QY 135 PVYKKAHVTEVYKRCNHNELREFNEGQIAPPSHLIRVEGNSHAQYVEDPITRGQSVLV 194
 |||||||
 DB 190 PVYKKAHVTEVYKRCNHNELREFNEGQIAPPSHLIRVEGNSHAQYVEDPITRGQSVLV 249
 |||||||
 QY 195 PYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQVILGRCFEARIACAP 254
 |||||||
 DB 250 PYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQVILGRCFEARIACAP 309
 |||||||
 QY 255 GDRKKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIOMTSIRKRRSPDDELILYLRGR 314
 |||||||
 DB 310 GDRKKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIOMTSIRKRRSPDDELILYLRGR 369
 |||||||
 QY 315 ETYEMLIKESLELMQYLPOHTIETVYRQOQOQHLLQKHLISACFRNELVPRRETP 374
 |||||||
 DB 370 ETYEMLIKESLELMQYLPOHTIETVYRQOQOQHLLQKHLISACFRNELVPRRETP 429
 |||||||
 QY 375 KQSDVEFRHSKPPRSVYP 393
 |||||||
 DB 430 KQSDVEFRHSKPPRSVYP 448
 |||||||

RESULT 14
 ID AAY05964
 AAY05964 standard; Protein: 389 AA.

AC AAY05964;
 XX
 DT 16-AUG-1999 (first entry)
 DE
 XX
 DE Mouse cell regulatory protein p63, isoform deltaNp63 gamma, cDNA.
 XX
 KM Cell regulatory protein; p63; mu-deltaNp63 gamma; mouse;
 KM cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; therapy.
 XX
 OS Mus sp.
 XX
 PN W09919357-A2.
 XX
 PD 22-APR-1999.
 XX
 PE 02-OCT-1998; 98WO-US21992.
 XX
 PR 29-MAY-1998; 98US-0087216.
 XX
 PR 15-OCT-1997; 97US-0062076.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI McKeon F, Yang A;
 XX
 DR WPI: 1999-277595/23.
 DR N-PSDB: AAX58583.
 XX
 PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 XX
 PS Claim 23; Fig 20; 16pp; English.
 XX
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour

CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
 CC RACE. Sequencing of the amplification product indicated that the
 CC amplified cDNA possessed a truncated N-terminus, i.e. the
 CC transactivation domain was absent. Additional splice variants were
 CC identified by screening a cDNA library with a probe corresponding
 CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
 CC variants differing at the C-terminus are designated as alpha, beta
 CC and gamma forms, while p63 members differing in the N-terminus are
 CC designated as deltaN and TA forms, where the deltaN form lacks the
 CC transactivation domain. The present sequence represents mouse p63
 CC isoform mu-deltaNp63 gamma. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.

Sequence 389 AA;
 XX
 SQ

Query Match 96.5%; Score 2009; DB 20; Length 389;
 Best Local Similarity 97.2%; Pred. No. 7e-176;
 Matches 382; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

QY 1 MLYLENNAGQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 |||||||
 DB 1 MLYLENNAGQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 |||||||
 QY 61 TFDALSPSPALPSSTDPGPHSPVDSFOQSSSTAKSATWTYTELKLKCYQIAKTCPIQIK 120
 |||||||
 DB 61 TFDALSPSPALPSSTDPGPHSPVDSFOQSSSTAKSATWTYTELKLKCYQIAKTCPIQIK 120
 |||||||
 QY 121 VMTPPGCAVIRAMPYVYKKAHVTEVYKRCNHNELREFNEGQIAPPSHLIRVEGNSHAQ 180
 |||||||
 DB 121 VMTPPGCAVIRAMPYVYKKAHVTEVYKRCNHNELREFNEGQIAPPSHLIRVEGNSHAQ 180
 |||||||
 QY 121 VMTPPGCAVIRAMPYVYKKAHVTEVYKRCNHNELREFNEGQIAPPSHLIRVEGNSHAQ 180
 |||||||
 DB 121 VMTPPGCAVIRAMPYVYKKAHVTEVYKRCNHNELREFNEGQIAPPSHLIRVEGNSHAQ 180
 |||||||
 QY 181 VYEDPITRGQSVLYVYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQV 240
 |||||||
 DB 181 VYEDPITRGQSVLYVYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQV 240
 |||||||
 QY 181 VYEDPITRGQSVLYVYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQV 240
 |||||||
 DB 181 VYEDPITRGQSVLYVYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQV 240
 |||||||
 QY 241 LGRRCFEARICACGRRKKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIOMTSIRKRR 300
 |||||||
 DB 241 LGRRCFEARICACGRRKKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIOMTSIRKRR 300
 |||||||
 QY 301 SPDELILYLRVGRRETEMLKIKESLELMQYLPOHTIETVYRQOQOQHLLQKHLISA 360
 |||||||
 DB 297 SPDELILYLRVGRRETEMLKIKESLELMQYLPOHTIETVYRQOQOQHLLQKHLISA 356
 |||||||
 QY 361 CERNELVEPRRETPKQSDVEFRHSKPPRSVYP 393
 |||||||
 DB 357 CERNELVEPRRETPKQSDVEFRHSKPPRSVYP 389
 |||||||

RESULT 15
 ID AAY05961
 AAY05961 standard; Protein: 483 AA.

AC AAY05961;
 XX
 DT 16-AUG-1999 (first entry)
 DE
 XX
 DE Mouse cell regulatory protein p63, isoform muTAp63 gamma.
 XX
 KM Cell regulatory protein; p63; muTAp63 gamma; TAp63 gamma; mouse;
 KM cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; therapy.

```
XX OS Mus sp.
XX PN MO9919357-A2.
XX PD 22-APR-1999.
XX PF 02-OCT-1998; 98WO-US21992.
XX PR 29-MAY-1998; 98US-0087216.
XX PR 15-OCT-1997; 97US-0062076.
XX PA (HARD ) HARVARD COLLEGE.
XX PI MKeon F, Yang A;
XX DR WPI; 1999-277595/23.
XX DR N-PSDB; AAX58580.
XX PT New isolated p63 cell regulatory protein for. e.g. treatment of
XX PT tumours
XX PS Claim 23; Fig 17; 161pp; English.
XX CC The present invention concerns the discovery of a new family of
XX CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
XX CC which demonstrate certain sequence identity to known tumour
XX CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
XX CC RACE. Sequencing of the amplification product indicated that the
XX CC amplified cDNA possessed a truncated N-terminus, i.e. the
XX CC transactivation domain was absent. Additional splice variants were
XX CC identified by screening a cDNA library with a probe corresponding
XX CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
XX CC variants differing at the C-terminus are designated as alpha, beta
XX CC and gamma forms, while p63 members differing in the N-terminus are
XX CC designated as delta1 and TA forms, where the delta1 form lacks the
XX CC transactivation domain. The present sequence represents murine
XX CC p53 isotype mutant p63 gamma. p63 was detected in a variety of
XX CC human and mouse tissue. It demonstrates remarkably divergent
XX CC activities, such as the ability to transactivate p53 reporter genes
XX CC and induce apoptosis. Cessation or down-regulation of p63 expression
XX CC may play a critical role in the process of cervical squamous
XX CC differentiation, both benign and neoplastic. Delta1 isoforms of p63
XX CC act as dominant negatives towards transactivation by p53 and p63.
XX CC p63 may also be implicated in hematopoiesis, muscle wasting (e.g.
XX CC cachexia) and neuronal differentiation and related degenerative
XX CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
XX CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
XX CC identify compounds useful for treating disorders involving such
XX CC processes, in detection and diagnosis, and in the production of
XX CC transgenic animals.
SQ Sequence 483 AA;
Query Match 93.1%; Score 1938; DB 20; Length 483;
Best Local Similarity 97.1%; Pred. No. 3 2e-169;
Matches 368; Conservative 0; Mismatches 7; Indels 4; Gaps 1;
QY 15 PQTNLGLINSMDDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIIPSN 74
DB 109 PQTNLGLINSMDDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIIPSN 168
QY 75 TDYRPGHSDVAFQOOSTAKSATWTYSTRKLKLYCQIATCPQIKVMTPPPGAVIRAM 134
DB 169 TDYRPGHSDVAFQOOSTAKSATWTYSTRKLKLYCQIATCPQIKVMTPPPGAVIRAM 228
QY 135 PYYKKAENHTEVYKRCNPHELREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 194
DB 229 PYYKKAENHTEVYKRCNPHELREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 288
QY 195 PYEPPOVGTETFTVLYNFCNCSVCGMNRRLILVLTETRDGOVLGRRCFEARICACP 254
DB 289 PYEPPOVGTETFTVLYNFCNCSVCGMNRRLILVLTETRDGOVLGRRCFEARICACP 348
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```
QY 255 GRDRKADEDSIRKQVSDSTKNGDGTKRPPRONTGHIOMTSIKRRSPDDELILYLPVGR 314
DB 349 GRDRKADEDSIRKQVSDSAKNGDA---FRONTGHIOMTSIKRRSPDDELILYLPVGR 404
QY 315 ETEYMLKIKESLELMQYLPQHTIETYYRQOQOQHOLLOKHLISACFNELVEPRRETP 374
DB 405 ETEYMLKIKESLELMQYLPQHTIETYYRQOQOQHOLLOKHLISACFNELVEPRGEAP 464
QY 375 KQSDVFFRRSKPPNRSVYP 393
DB 465 TQSDVFFRRSNPNHSVYP 483
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Job time : 29.1034 secs

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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:54 ; Search time 10.8414 Seconds
(without alignments)
1533.769 Million cell updates/sec

Title: US-09-538-106-18

Perfect score: 2082

Sequence: 1 MLTYLNNAGQTFSEPOXTNL.....PKQSDVFRHSKPPNRSYYP 393

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA.*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCUTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2011	96.6	448	4	US-09-643-597-340
2	2011	96.6	448	4	US-09-542-615A-340
3	2011	96.6	448	4	US-09-606-421B-340
4	1884	90.5	461	4	US-09-643-597-343
5	1884	90.5	461	4	US-09-542-615A-343
6	1884	90.5	461	4	US-09-606-421B-343
7	1867	89.7	356	4	US-09-643-597-341
8	1867	89.7	356	4	US-09-277-196-2
9	1867	89.7	356	4	US-09-542-615A-341
10	1867	89.7	356	4	US-09-606-421B-341
11	1867	89.7	356	4	US-09-643-597-338
12	1867	89.7	356	4	US-09-542-615A-338
13	1867	89.7	356	4	US-09-606-421B-338
14	1860	89.3	586	4	US-09-643-597-152
15	1860	89.3	586	4	US-09-480-884A-152
16	1860	89.3	586	4	US-09-542-615A-152
17	1860	89.3	586	4	US-09-606-421B-152
18	1813	87.1	516	4	US-09-643-597-344
19	1813	87.1	516	4	US-09-542-615A-344
20	1813	87.1	516	4	US-09-606-421B-344
21	1813	87.1	641	4	US-09-643-597-339
22	1813	87.1	641	4	US-09-542-615A-339
23	1813	87.1	641	4	US-09-606-421B-339
24	1813	87.1	680	4	US-09-643-597-342
25	1813	87.1	680	4	US-09-542-615A-342
26	1813	87.1	680	4	US-09-606-421B-342
27	1807	86.8	426	4	US-09-277-196-19

28	1248.5	60.0	420	4	US-09-277-196-20	Sequence 20, Appl
29	1248.5	60.0	635	4	US-09-081-975-3	Sequence 3, Appl1
30	739	35.5	381	4	US-09-257-580-2	Sequence 27, Appl
31	711	34.1	393	1	US-08-047-041A-27	Sequence 8, Appl1
32	711	34.1	393	1	US-08-390-516C-8	Sequence 8, Appl1
33	711	34.1	393	2	US-08-390-515A-8	Sequence 8, Appl1
34	711	34.1	393	2	US-08-801-718-8	Sequence 2, Appl1
35	707	34.0	362	4	US-09-603-052-2	Sequence 17, Appl
36	707	34.0	363	2	US-08-697-221-17	Sequence 25, Appl
37	707	34.0	393	1	US-08-047-041A-25	Sequence 26, Appl
38	707	34.0	393	1	US-08-047-041A-26	Sequence 2, Appl1
39	707	34.0	393	1	US-08-347-792-2	Sequence 6, Appl1
40	707	34.0	393	1	US-08-390-516C-6	Sequence 2, Appl1
41	707	34.0	393	1	US-08-390-516C-7	Sequence 2, Appl1
42	707	34.0	393	1	US-08-431-357-2	Sequence 6, Appl1
43	707	34.0	393	1	US-08-390-515A-6	Sequence 7, Appl1
44	707	34.0	393	1	US-08-390-515A-7	Sequence 32, Appl
45	707	34.0	393	2	US-08-795-006A-32	

ALIGNMENTS

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RESULT 1
US-09-643-597-340
; Sequence 340, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-643-597-340

Query Match          96.6%; Score 2011; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.3e+14;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15  PQTMLGLNSDDOIONGSSSTSPYNTDHAONSTAPSPYQBPSTEDALSPSPATSN 74
    |||||||
70  PQTMLGLNSDDOIONGSSSTSPYNTDHAONSTAPSPYQBPSTEDALSPSPATSN 129
    |||||||
75  TDYPPHSDVSFOOSTRAKSTWYSTEKLKYQIAKTCPTQIKWMPPOGAVIRAM 134
    |||||||
130 TDYPPHSDVSFOOSTRAKSTWYSTEKLKYQIAKTCPTQIKWMPPOGAVIRAM 189
    |||||||
135 PYYKAEHVTEVVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQVEDPTGHSYLV 194
    |||||||
190 PYYKAEHVTEVVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQVEDPTGHSYLV 249
    |||||||
195 PYPPOVGTETFTVLYNFMCSNCCVGMNRRPILITVLETRDGOVLCRCEARICACP 254
    |||||||
250 PYPPOVGTETFTVLYNFMCSNCCVGMNRRPILITVLETRDGOVLCRCEARICACP 309
    |||||||
255 GDRRADEDSIRKQOVSDTKNGDCTKRPRONTNGIQMTSIRKRRSPDDELLYLPVGR 314
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Db 310 GRDRKADEDSIRKQVSDSTKNGDGTKRPRQNTHGIGMTSIRKRRSPDDELLYLPVGR 369
Qy 315 EYEMMLKIKESLELMQYLPOHTIETYROOQOOHOLHLOKHLISACFRNELVPRRETP 374
Db 370 EYEMMLKIKESLELMQYLPOHTIETYROOQOOHOLHLOKHLISACFRNELVPRRETP 429
Qy 375 KQSDVFFRHSKPPRRSYYP 393
Db 430 KQSDVFFRHSKPPRRSYYP 448
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RESULT 2

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US-09-542-615A-340
; Sequence 340, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-340
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Query Match 96.6%; Score 2011; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.3e-184;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 70 PÖTNGLILNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAPDSSFFDALSPSPALPSN 129
Qy 75 TDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPGAVIRAM 134
Db 130 TDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPGAVIRAM 189
Qy 135 PYKKAAHVTEYVKRCNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
Db 190 PYKKAAHVTEYVKRCNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
Qy 195 PYEPPOVGETTEFTYLYNFMCNNSCVGGMNRRPILIIYTLERDGOVGRRCFEARICACP 254
Db 250 PYEPPOVGETTEFTYLYNFMCNNSCVGGMNRRPILIIYTLERDGOVGRRCFEARICACP 309
Qy 255 GRDRKADEDSIRKQVSDSTKNGDGTKRPRQNTHGIGMTSIRKRRSPDDELLYLPVGR 314
Db 310 GRDRKADEDSIRKQVSDSTKNGDGTKRPRQNTHGIGMTSIRKRRSPDDELLYLPVGR 369
Qy 315 EYEMMLKIKESLELMQYLPOHTIETYROOQOOHOLHLOKHLISACFRNELVPRRETP 374
Db 370 EYEMMLKIKESLELMQYLPOHTIETYROOQOOHOLHLOKHLISACFRNELVPRRETP 429
Qy 375 KQSDVFFRHSKPPRRSYYP 393
Db 430 KQSDVFFRHSKPPRRSYYP 448
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RESULT 3
US-09-606-421B-340
; Sequence 340, Application US/09606421B
; Patent No. 6531315
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; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-340
```

```
Query Match 96.6%; Score 2011; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.3e-184;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 15 PÖYTNGLILNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAPDSSFFDALSPSPALPSN 74
Db 70 PÖTNGLILNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAPDSSFFDALSPSPALPSN 129
Qy 75 TDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPGAVIRAM 134
Db 130 TDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPGAVIRAM 189
Qy 135 PYKKAAHVTEYVKRCNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
Db 190 PYKKAAHVTEYVKRCNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
Qy 195 PYEPPOVGETTEFTYLYNFMCNNSCVGGMNRRPILIIYTLERDGOVGRRCFEARICACP 254
Db 250 PYEPPOVGETTEFTYLYNFMCNNSCVGGMNRRPILIIYTLERDGOVGRRCFEARICACP 309
Qy 255 GRDRKADEDSIRKQVSDSTKNGDGTKRPRQNTHGIGMTSIRKRRSPDDELLYLPVGR 314
Db 310 GRDRKADEDSIRKQVSDSTKNGDGTKRPRQNTHGIGMTSIRKRRSPDDELLYLPVGR 369
Qy 315 EYEMMLKIKESLELMQYLPOHTIETYROOQOOHOLHLOKHLISACFRNELVPRRETP 374
Db 370 EYEMMLKIKESLELMQYLPOHTIETYROOQOOHOLHLOKHLISACFRNELVPRRETP 429
Qy 375 KQSDVFFRHSKPPRRSYYP 393
Db 430 KQSDVFFRHSKPPRRSYYP 448
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RESULT 4
US-09-643-597-343
; Sequence 343, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
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;; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
;; FILE REFERENCE: 210121.455C11
;; CURRENT APPLICATION NUMBER: US/09/643,597
;; CURRENT FILING DATE: 2000-08-21
;; NUMBER OF SEQ ID NOS: 369
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 343
;; LENGTH: 461
;; TYPE: PR1
;; ORGANISM: Homo sapiens
US-09-643-597-343

Query Match
Best Local Similarity 93.3%; Pred. No. 2e-172;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MYLENNAOTOFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSS 60
DB 1 MYLENNAOTOFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPSNNDYPCGPHSFVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNNDYPCGPHSFVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEHTEVVKRCPNHLSRENEGQIAPPSHLIRVEGSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEHTEVVKRCPNHLSRENEGQIAPPSHLIRVEGSHAQ 180
QY 181 YVEDPITGQSVLYPVEPPQVGEFTTVLYNFMNCSSCVGMMRRPILIIIVLETRDGOV 240
DB 181 YVEDPITGQSVLYPVEPPQVGEFTTVLYNFMNCSSCVGMMRRPILIIIVLETRDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRFRONTGCIQMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRFRONTGCIQMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYROOQOQHLLQKHLISA 360
DB 301 SPDELLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYROOQOQHLLQKHLISA 360
QY 361 CERNELVEPRRETPKOSDVEFRHSKRP 387
DB 356 -----QTSIQSPSSYGNSSPP 371

RESULT 5
US-09-542-615A-343
; Sequence 343, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-542-615A-343

Query Match
Best Local Similarity 90.5%; Score 1884; DB 4; Length 461;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MYLENNAOTOFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSS 60
DB 1 MYLENNAOTOFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPSNNDYPCGPHSFVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNNDYPCGPHSFVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEHTEVVKRCPNHLSRENEGQIAPPSHLIRVEGSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEHTEVVKRCPNHLSRENEGQIAPPSHLIRVEGSHAQ 180
QY 181 YVEDPITGQSVLYPVEPPQVGEFTTVLYNFMNCSSCVGMMRRPILIIIVLETRDGOV 240
DB 181 YVEDPITGQSVLYPVEPPQVGEFTTVLYNFMNCSSCVGMMRRPILIIIVLETRDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRFRONTGCIQMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRFRONTGCIQMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYROOQOQHLLQKHLISA 360
DB 301 SPDELLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYROOQOQHLLQKHLISA 360
QY 361 CERNELVEPRRETPKOSDVEFRHSKRP 387
DB 356 -----QTSIQSPSSYGNSSPP 371

RESULT 6
US-09-606-421B-343
; Sequence 343, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-606-421B-343

Query Match
Best Local Similarity 90.5%; Score 1884; DB 4; Length 461;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MYLENNAOTOFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSS 60
DB 1 MYLENNAOTOFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPSNNDYPCGPHSFVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNNDYPCGPHSFVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEHTEVVKRCPNHLSRENEGQIAPPSHLIRVEGSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEHTEVVKRCPNHLSRENEGQIAPPSHLIRVEGSHAQ 180
QY 181 YVEDPITGQSVLYPVEPPQVGEFTTVLYNFMNCSSCVGMMRRPILIIIVLETRDGOV 240

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Db 181 YVEDPITGRQSVLPYPPQVGEFTTVLYNFMKNSSCVGGMNRPILIIYVLETRDGOV 240
QY 241 LGRRCFARICACGGRKKADEDSIRKQOYSDSTKNKGDTKRPROMTHGIOMTSIKRR 300
Db 241 LGRRCFARICACGGRKKADEDSIRKQOYSDSTKNKGDTKRPROMTHGIOMTSIKRR 300
QY 301 SPDELLYLVRGRETVEMLIKESLELMQYLPQHTIETTYRQOQOOHQHLLQKHLISA 360
Db 301 SPDELLYLVRGRETVEMLIKESLELMQYLPQHTIETTYRQOQOOHQHLLQK----- 355
QY 361 CFNRELVEPRRETPKQSDVFFRHSKRP 387
Db 356 -----QSTIOSSPSYGNSSPP 371
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RESULT 7
US-09-643-597-341
: Sequence 341, Application US/09643597
: Patent No. 6426072
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasar A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C11
: CURRENT APPLICATION NUMBER: US/09/643,597
: CURRENT FILING DATE: 2000-08-21
: NUMBER OF SEQ ID NOS: 369
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 341
: LENGTH: 356
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-643-597-341
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Query Match 89.7%; Score 1867; DB 4; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.9e-171;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNIGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
Db 1 MLYENNAQTOFSEPOYTNIGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY 61 TFDALSSPAIPSTVDYPGHSPFVSFOQSTAKSATWTSTELKIKLYCOIAKTCPIQIK 120
Db 61 TFDALSSPAIPSTVDYPGHSPFVSFOQSTAKSATWTSTELKIKLYCOIAKTCPIQIK 120
QY 121 VMTPPOGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
Db 121 VMTPPOGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLPYPPQVGEFTTVLYNFMKNSSCVGGMNRPILIIYVLETRDGOV 240
Db 181 YVEDPITGRQSVLPYPPQVGEFTTVLYNFMKNSSCVGGMNRPILIIYVLETRDGOV 240
QY 241 LGRRCFARICACGGRKKADEDSIRKQOYSDSTKNKGDTKRPROMTHGIOMTSIKRR 300
Db 241 LGRRCFARICACGGRKKADEDSIRKQOYSDSTKNKGDTKRPROMTHGIOMTSIKRR 300
QY 301 SPDELLYLVRGRETVEMLIKESLELMQYLPQHTIETTYRQOQOOHQHLLQK 355
Db 301 SPDELLYLVRGRETVEMLIKESLELMQYLPQHTIETTYRQOQOOHQHLLQK 355
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RESULT 8
US-09-277-196-2
: Sequence 2, Application US/09277196
: Patent No. 6476206
: GENERAL INFORMATION:
: APPLICANT: Trink, Barry
: APPLICANT: Jen, Jin
: APPLICANT: Ratovitski, Edward
: APPLICANT: Sidransky, David
: TITLE OF INVENTION: p40 Protein Acts as an Oncogene
: FILE REFERENCE: 01107.79765
: CURRENT APPLICATION NUMBER: US/09/277,196
: CURRENT FILING DATE: 1999-03-26
: EARLIER APPLICATION NUMBER: 60/079736
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 356
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-277-196-2
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Query Match 89.7%; Score 1867; DB 4; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.9e-171;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNIGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
Db 1 MLYENNAQTOFSEPOYTNIGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY 61 TFDALSSPAIPSTVDYPGHSPFVSFOQSTAKSATWTSTELKIKLYCOIAKTCPIQIK 120
Db 61 TFDALSSPAIPSTVDYPGHSPFVSFOQSTAKSATWTSTELKIKLYCOIAKTCPIQIK 120
QY 121 VMTPPOGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
Db 121 VMTPPOGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLPYPPQVGEFTTVLYNFMKNSSCVGGMNRPILIIYVLETRDGOV 240
Db 181 YVEDPITGRQSVLPYPPQVGEFTTVLYNFMKNSSCVGGMNRPILIIYVLETRDGOV 240
QY 241 LGRRCFARICACGGRKKADEDSIRKQOYSDSTKNKGDTKRPROMTHGIOMTSIKRR 300
Db 241 LGRRCFARICACGGRKKADEDSIRKQOYSDSTKNKGDTKRPROMTHGIOMTSIKRR 300
QY 301 SPDELLYLVRGRETVEMLIKESLELMQYLPQHTIETTYRQOQOOHQHLLQK 355
Db 301 SPDELLYLVRGRETVEMLIKESLELMQYLPQHTIETTYRQOQOOHQHLLQK 355
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```
RESULT 9
US-09-542-615A-341
: Sequence 341, Application US/09542615A
: Patent No. 6518256
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: FILE REFERENCE: 210121.455C8
: CURRENT APPLICATION NUMBER: US/09/542,615A
: CURRENT FILING DATE: 2000-04-14
: NUMBER OF SEQ ID NOS: 350
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 341
: LENGTH: 356
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-341

Query Match      89.7%; Score 1867; DB 4; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.9e-171;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLYENNAGTQFSEQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAGTQFSEQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOOSSTAKSATWTYSELKLLKLCQIAKTPIDIK 120
DB 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOOSSTAKSATWTYSELKLLKLCQIAKTPIDIK 120
QY 121 VMTPPGQAVIRAMPVYKKAHEVTEVVKRCPNHELSPREFNEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGQAVIRAMPVYKKAHEVTEVVKRCPNHELSPREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYVEPPQVGTETFTYLYNFMCMSSCVGNNRPILITVLETRDQV 240
DB 181 YVEDPITGRQSVLYVEPPQVGTETFTYLYNFMCMSSCVGNNRPILITVLETRDQV 240
QY 241 IGRRCFEARICACPGDRKKADEDSIRKQOVSSTNGDGTKRPFONTHGLOMTSIKRR 300
DB 241 IGRRCFEARICACPGDRKKADEDSIRKQOVSSTNGDGTKRPFONTHGLOMTSIKRR 300
QY 301 SPDELILYLVPGRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQK 355
DB 301 SPDELILYLVPGRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQK 355

RESULT 10
US-09-606-421B-341
; Sequence 341, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 341
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-341

Query Match      89.7%; Score 1867; DB 4; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.9e-171;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 121 VMTPPGQAVIRAMPVYKKAHEVTEVVKRCPNHELSPREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYVEPPQVGTETFTYLYNFMCMSSCVGNNRPILITVLETRDQV 240
DB 181 YVEDPITGRQSVLYVEPPQVGTETFTYLYNFMCMSSCVGNNRPILITVLETRDQV 240
QY 241 IGRRCFEARICACPGDRKKADEDSIRKQOVSSTNGDGTKRPFONTHGLOMTSIKRR 300
DB 241 IGRRCFEARICACPGDRKKADEDSIRKQOVSSTNGDGTKRPFONTHGLOMTSIKRR 300
QY 301 SPDELILYLVPGRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQK 355
DB 301 SPDELILYLVPGRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQK 355

RESULT 11
US-09-643-597-338
; Sequence 338, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-338

Query Match      89.7%; Score 1867; DB 4; Length 586;
Best Local Similarity 92.5%; Pred. No. 1.2e-170;
Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYENNAGTQFSEQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAGTQFSEQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOOSSTAKSATWTYSELKLLKLCQIAKTPIDIK 120
DB 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOOSSTAKSATWTYSELKLLKLCQIAKTPIDIK 120
QY 121 VMTPPGQAVIRAMPVYKKAHEVTEVVKRCPNHELSPREFNEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGQAVIRAMPVYKKAHEVTEVVKRCPNHELSPREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYVEPPQVGTETFTYLYNFMCMSSCVGNNRPILITVLETRDQV 240
DB 181 YVEDPITGRQSVLYVEPPQVGTETFTYLYNFMCMSSCVGNNRPILITVLETRDQV 240
QY 241 IGRRCFEARICACPGDRKKADEDSIRKQOVSSTNGDGTKRPFONTHGLOMTSIKRR 300
DB 241 IGRRCFEARICACPGDRKKADEDSIRKQOVSSTNGDGTKRPFONTHGLOMTSIKRR 300
QY 301 SPDELILYLVPGRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQK 356
DB 301 SPDELILYLVPGRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQOQHLLQK 355
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QY 361 CERNELVEPRRERPKQSDVEFFRHSKP 387
: : : : :
Db 356 -----QTSIQSPSSYGNSSPP 371

RESULT 12

US-09-542-615A-338
: Sequence 338, Application US/09542615A
: Patent No. 6518256
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: FILE REFERENCE: 210121.455C8
: CURRENT APPLICATION NUMBER: US/09/542.615A
: CURRENT FILING DATE: 2000-04-14
: NUMBER OF SEQ ID NOS: 350
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 338
: LENGTH: 386
: TYPE: PR
: ORGANISM: Homo sapiens
US-09-542-615A-338

Query Match 89.7%; Score 1867; DB 4; Length 586;
Best Local Similarity 92.5%; Pred. No. 1.2e-170;
Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYENNAQTOFSEPOYTNTGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
: : : : :
Db 1 MLYENNAQTOFSEPOYTNTGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSSP 60
: : : : :
QY 61 TFDALSSPAIPSTNDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIATCP1QIK 120
: : : : :
Db 61 TFDALSSPAIPSTNDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIATCP1QIK 120
: : : : :
QY 121 VMPRPBGAVIRAMPYVKKAEHTEYVKRCNHELSREFNEGOLAPSHLIRVGNSHAQ 180
: : : : :
Db 121 VMPRPBGAVIRAMPYVKKAEHTEYVKRCNHELSREFNEGOLAPSHLIRVGNSHAQ 180
: : : : :
QY 121 VMPRPBGAVIRAMPYVKKAEHTEYVKRCNHELSREFNEGOLAPSHLIRVGNSHAQ 180
: : : : :
Db 121 VMPRPBGAVIRAMPYVKKAEHTEYVKRCNHELSREFNEGOLAPSHLIRVGNSHAQ 180
: : : : :
QY 181 YVEDPITGRQSVLYVPEPQVGEFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETTRDGOV 240
: : : : :
Db 181 YVEDPITGRQSVLYVPEPQVGEFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETTRDGOV 240
: : : : :
QY 241 LGRRCFARICACGRRKADSDSIRKQOYSDSTKNDGTRKPRRONTHGIOMTSIKRR 300
: : : : :
Db 241 LGRRCFARICACGRRKADSDSIRKQOYSDSTKNDGTRKPRRONTHGIOMTSIKRR 300
: : : : :
QY 301 SPDELLYLVPVGRGETEMLKIKESLELMQYLPQHTIETRYRQOQOQOHHLLKLSA 360
: : : : :
Db 301 SPDELLYLVPVGRGETEMLKIKESLELMQYLPQHTIETRYRQOQOQOHHLLKLSA 360
: : : : :
QY 361 CERNELVEPRRERPKQSDVEFFRHSKP 387
: : : : :
Db 356 -----QTSIQSPSSYGNSSPP 371

RESULT 13
US-09-606-421B-338
: Sequence 338, Application US/09606421B
: Patent No. 6531315
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.

: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C9
: CURRENT APPLICATION NUMBER: US/09/606.421B
: CURRENT FILING DATE: 2000-06-28
: NUMBER OF SEQ ID NOS: 358
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 338
: LENGTH: 386
: TYPE: PR
: ORGANISM: Homo sapiens
US-09-606-421B-338

Query Match 89.7%; Score 1867; DB 4; Length 586;
Best Local Similarity 92.5%; Pred. No. 1.2e-170;
Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYENNAQTOFSEPOYTNTGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
: : : : :
Db 1 MLYENNAQTOFSEPOYTNTGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSSP 60
: : : : :
QY 61 TFDALSSPAIPSTNDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIATCP1QIK 120
: : : : :
Db 61 TFDALSSPAIPSTNDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIATCP1QIK 120
: : : : :
QY 121 VMPRPBGAVIRAMPYVKKAEHTEYVKRCNHELSREFNEGOLAPSHLIRVGNSHAQ 180
: : : : :
Db 121 VMPRPBGAVIRAMPYVKKAEHTEYVKRCNHELSREFNEGOLAPSHLIRVGNSHAQ 180
: : : : :
QY 181 YVEDPITGRQSVLYVPEPQVGEFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETTRDGOV 240
: : : : :
Db 181 YVEDPITGRQSVLYVPEPQVGEFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETTRDGOV 240
: : : : :
QY 241 LGRRCFARICACGRRKADSDSIRKQOYSDSTKNDGTRKPRRONTHGIOMTSIKRR 300
: : : : :
Db 241 LGRRCFARICACGRRKADSDSIRKQOYSDSTKNDGTRKPRRONTHGIOMTSIKRR 300
: : : : :
QY 301 SPDELLYLVPVGRGETEMLKIKESLELMQYLPQHTIETRYRQOQOQOHHLLKLSA 360
: : : : :
Db 301 SPDELLYLVPVGRGETEMLKIKESLELMQYLPQHTIETRYRQOQOQOHHLLKLSA 360
: : : : :
QY 361 CERNELVEPRRERPKQSDVEFFRHSKP 387
: : : : :
Db 356 -----QTSIQSPSSYGNSSPP 371

RESULT 14
US-09-643-597-152
: Sequence 152, Application US/09643597
: Patent No. 6426072
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C11
: CURRENT APPLICATION NUMBER: US/09/643.597
: CURRENT FILING DATE: 2000-08-21
: NUMBER OF SEQ ID NOS: 369
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 152

LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-643-597-152

Query Match 89.3%; Score 1860; DB 4; Length 586;
Best Local Similarity 92.2%; Pred. No. 5,9e-170;
Matches 357; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYENNAQTOFSEPOYTNLGLNSMDQOIQNGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
DB 1 MLYENNAQTOFSEPOYTNLGLNSMDQOIQNGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY 61 TFDALSPSPALPSNTDYGPHSFDVSVFOOSSSTAKSATWTYSELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYGPHSFDVSVFOOSSSTAKSATWTYSELKKLYCQIAKTCPIQIK 120
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DB 121 VMTPPGAVIRAMVYKKAHEVTEVVKRCPNHLSREFNEGOIAPSSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYPEPPQVGTETTYLYNFMCNSSCGGNRRPILITVLETRDQV 240
DB 181 YVEDPITGRQSVLYPEPPQVGTETTYLYNFMCNSSCGGNRRPILITVLETRDQV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHGHIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHGHIOMTSIKRR 300
QY 301 SPDELLVLPVGRRETYEMLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKHLISA 360
DB 301 SPDELLVLPVGRRETYEMLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKHLISA 360
QY 361 CERNLVEPRRETPKQSDVFFRHSKP 387
DB 361 CERNLVEPRRETPKQSDVFFRHSKP 387
QY 356 -----QTSIQSPSSYGNSSP 371
DB 356 -----QTSIQSPSSYGNSSP 371

RESULT 15
US-09-480-884A-152
Sequence 152, Application US/09480884A
Patent No. 6482397
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-480-884A-152

Query Match 89.3%; Score 1860; DB 4; Length 586;
Best Local Similarity 92.2%; Pred. No. 5,9e-170;
Matches 357; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYENNAQTOFSEPOYTNLGLNSMDQOIQNGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
DB 1 MLYENNAQTOFSEPOYTNLGLNSMDQOIQNGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY 61 TFDALSPSPALPSNTDYGPHSFDVSVFOOSSSTAKSATWTYSELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYGPHSFDVSVFOOSSSTAKSATWTYSELKKLYCQIAKTCPIQIK 120

QY 121 VMTPPGAVIRAMVYKKAHEVTEVVKRCPNHLSREFNEGOIAPSSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMVYKKAHEVTEVVKRCPNHLSREFNEGOIAPSSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYPEPPQVGTETTYLYNFMCNSSCGGNRRPILITVLETRDQV 240
DB 181 YVEDPITGRQSVLYPEPPQVGTETTYLYNFMCNSSCGGNRRPILITVLETRDQV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHGHIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHGHIOMTSIKRR 300
QY 301 SPDELLVLPVGRRETYEMLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKHLISA 360
DB 301 SPDELLVLPVGRRETYEMLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKHLISA 360
QY 361 CERNLVEPRRETPKQSDVFFRHSKP 387
DB 361 CERNLVEPRRETPKQSDVFFRHSKP 387
QY 356 -----QTSIQSPSSYGNSSP 371
DB 356 -----QTSIQSPSSYGNSSP 371

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 7, 2003, 09:46:34 ; Search time 16.7783 seconds
(without alignments)
2781.719 Million cell updates/sec

Title: US-09-538-106-18
Perfect score: 2082
Sequence: 1 MLTYLNNAGTQFSEPTNTL.....PKSDVFRHRSKPNRSVYP 393

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 segs, 118759770 residues
Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2011	96.6	448	9	US-09-735-705-340 Sequence 340, App
2	2011	96.6	448	10	US-09-850-716A-340 Sequence 340, App
3	2011	96.6	448	10	US-09-897-778-340 Sequence 340, App
4	1884	90.5	461	9	US-09-735-705-343 Sequence 343, App
5	1884	90.5	461	10	US-09-850-716A-343 Sequence 343, App
6	1884	90.5	461	10	US-09-897-778-343 Sequence 343, App
7	1867	89.7	356	9	US-09-735-705-341 Sequence 341, App
8	1867	89.7	356	10	US-09-850-716A-341 Sequence 341, App
9	1867	89.7	356	10	US-09-897-778-341 Sequence 341, App
10	1867	89.7	356	15	US-10-274-874-2 Sequence 2, Appl
11	1867	89.7	586	9	US-09-735-705-338 Sequence 338, App
12	1867	89.7	586	10	US-09-850-716A-338 Sequence 338, App
13	1867	89.7	586	10	US-09-897-778-338 Sequence 338, App
14	1860	89.3	586	9	US-09-735-705-152 Sequence 152, App
15	1860	89.3	586	10	US-09-850-716A-152 Sequence 152, App

16	1860	89.3	586	10	US-09-897-778-152	Sequence 152, App
17	1860	89.3	586	11	US-09-466-396A-152	Sequence 152, App
18	1813	87.1	516	9	US-09-735-705-344	Sequence 344, App
19	1813	87.1	516	10	US-09-850-716A-344	Sequence 344, App
20	1813	87.1	516	10	US-09-897-778-344	Sequence 344, App
21	1813	87.1	641	9	US-09-735-705-339	Sequence 339, App
22	1813	87.1	641	10	US-09-850-716A-339	Sequence 339, App
23	1813	87.1	641	10	US-09-897-778-339	Sequence 339, App
24	1813	87.1	680	9	US-09-735-705-342	Sequence 342, App
25	1813	87.1	680	10	US-09-850-716A-342	Sequence 342, App
26	1813	87.1	680	10	US-09-897-778-342	Sequence 342, App
27	1807	86.8	426	15	US-10-274-874-19	Sequence 19, Appl
28	1248.5	60.0	420	15	US-10-274-874-20	Sequence 20, Appl
29	1248.5	60.0	635	14	US-10-155-059-3	Sequence 3, Appl
30	1248.5	60.0	636	10	US-09-732-384-10	Sequence 10, Appl
31	707	34.0	393	9	US-09-776-695-32	Sequence 32, Appl
32	707	34.0	393	10	US-09-732-384-3	Sequence 3, Appl
33	707	34.0	393	10	US-09-860-211-9	Sequence 9, Appl
34	707	34.0	393	11	US-09-029-327-4	Sequence 4, Appl
35	707	34.0	393	11	US-09-860-286-9	Sequence 9, Appl
36	707	34.0	393	15	US-10-274-874-4	Sequence 4, Appl
37	707	34.0	393	15	US-10-160-290-2	Sequence 2, Appl
38	707	34.0	428	15	US-10-076-691-2	Sequence 2, Appl
39	703	33.8	401	10	US-09-968-851-34	Sequence 34, Appl
40	700.5	33.6	353	15	US-10-146-473-78	Sequence 78, Appl
41	699	33.6	390	15	US-10-038-010-6	Sequence 6, Appl
42	696	33.4	390	15	US-10-160-290-3	Sequence 3, Appl
43	694	33.3	394	14	US-10-155-059-4	Sequence 4, Appl
44	692	33.2	381	10	US-09-968-851-36	Sequence 36, Appl
45	679.5	32.6	374	10	US-09-968-851-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-735-705-340
Sequence 340, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 340
LENGTH: 448
TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-705-340

Query Match 96.6%; Score 2011; DB 9; Length 448;
Best local Similarity 100.0%; Pred. No. 3.4e-178;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 PQTNYGLNMSDQOIONGSSSTSPYNTDHAONSVTAPSPVQPSSTFDALSPSPAIRPN 74
DB 70 PQTNYGLNMSDQOIONGSSSTSPYNTDHAONSVTAPSPVQPSSTFDALSPSPAIRPN 129

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QY      75 TDYGPSPFVDSFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKWTPPGCAVIRAM 134
      |||
Db      130 TDYGPSPFVDSFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKWTPPGCAVIRAM 189
QY      135 PYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
      |||
Db      190 PYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY      195 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIYLETROGOVLGRRCFEARICACP 254
      |||
Db      250 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIYLETROGOVLGRRCFEARICACP 309
QY      255 GRDKKADEDSIRKQOVSSTKNGDGTKRPRFRONTNGIOMTSIKKRRSPDDELLYLPRGR 314
      |||
Db      310 GRDKKADEDSIRKQOVSSTKNGDGTKRPRFRONTNGIOMTSIKKRRSPDDELLYLPRGR 369
QY      315 EYEMMLKIKESLEIMQYLPQHTIETRYRQOQOOHQHLLQKHLKSACFRNELVEPRRET 374
      |||
Db      370 EYEMMLKIKESLEIMQYLPQHTIETRYRQOQOOHQHLLQKHLKSACFRNELVEPRRET 429
QY      375 KQSDVFFRHSKPPNRSYYP 393
      |||
Db      430 KQSDVFFRHSKPPNRSYYP 448

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RESULT 2

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US-09-850-716A-340
: Sequence 340, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kailos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Ketter, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716A
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 340
: LENGTH: 448
: TYPE: PR1
: ORGANISM: Homo sapiens
US-09-850-716A-340

```

```

Query Match      96.6%; Score 2011; DB 10; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.4e-178;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      15 PÖYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSPSTFDALSPSPALPSN 74
      |||
Db      70 PÖYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSPSTFDALSPSPALPSN 129
QY      75 TDYGPSPFVDSFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKWTPPGCAVIRAM 134
      |||
Db      130 TDYGPSPFVDSFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKWTPPGCAVIRAM 189
QY      135 PYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
      |||
Db      190 PYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY      195 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIYLETROGOVLGRRCFEARICACP 254
      |||
Db      250 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIYLETROGOVLGRRCFEARICACP 309
QY      255 GRDKKADEDSIRKQOVSSTKNGDGTKRPRFRONTNGIOMTSIKKRRSPDDELLYLPRGR 314
      |||
Db      310 GRDKKADEDSIRKQOVSSTKNGDGTKRPRFRONTNGIOMTSIKKRRSPDDELLYLPRGR 369
QY      315 EYEMMLKIKESLEIMQYLPQHTIETRYRQOQOOHQHLLQKHLKSACFRNELVEPRRET 374
      |||
Db      370 EYEMMLKIKESLEIMQYLPQHTIETRYRQOQOOHQHLLQKHLKSACFRNELVEPRRET 429

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```

QY      375 KQSDVFFRHSKPPNRSYYP 393
      |||
Db      430 KQSDVFFRHSKPPNRSYYP 448

```

RESULT 3

```

US-09-897-778-340
: Sequence 340, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Marnetakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Matanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 340
: LENGTH: 448
: TYPE: PR1
: ORGANISM: Homo sapiens
US-09-897-778-340

```

```

Query Match      96.6%; Score 2011; DB 10; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.4e-178;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      15 PÖYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSPSTFDALSPSPALPSN 74
      |||
Db      70 PÖYTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSPSTFDALSPSPALPSN 129
QY      75 TDYGPSPFVDSFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKWTPPGCAVIRAM 134
      |||
Db      130 TDYGPSPFVDSFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKWTPPGCAVIRAM 189
QY      135 PYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
      |||
Db      190 PYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY      195 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIYLETROGOVLGRRCFEARICACP 254
      |||
Db      250 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIYLETROGOVLGRRCFEARICACP 309
QY      255 GRDKKADEDSIRKQOVSSTKNGDGTKRPRFRONTNGIOMTSIKKRRSPDDELLYLPRGR 314
      |||
Db      310 GRDKKADEDSIRKQOVSSTKNGDGTKRPRFRONTNGIOMTSIKKRRSPDDELLYLPRGR 369
QY      315 EYEMMLKIKESLEIMQYLPQHTIETRYRQOQOOHQHLLQKHLKSACFRNELVEPRRET 374
      |||
Db      370 EYEMMLKIKESLEIMQYLPQHTIETRYRQOQOOHQHLLQKHLKSACFRNELVEPRRET 429
QY      375 KQSDVFFRHSKPPNRSYYP 393
      |||
Db      430 KQSDVFFRHSKPPNRSYYP 448

```

RESULT 4

```

US-09-735-705-343
: Sequence 343, Application US/09735705
: Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun

```



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Db 61 TFDLSPSPALPSTNDYDGPSPVDFVQSSTAKSATWTSTELKTKLYCOIAKCPIDQIK 120
Qy 121 VMPPPGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
Db 121 VMPPPGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
Qy 181 YVEDPITGRQSVLVYPPPOVGEFTTVLYNFMCNSSCVGGMNRPILLIIVTLETDRGOV 240
Db 181 YVEDPITGRQSVLVYPPPOVGEFTTVLYNFMCNSSCVGGMNRPILLIIVTLETDRGOV 240
Qy 241 LGRRCFARICACGRRKKADEDSIRKQOYSDSTKNGDGTKRPRONTGHIOMTSIKRR 300
Db 241 LGRRCFARICACGRRKKADEDSIRKQOYSDSTKNGDGTKRPRONTGHIOMTSIKRR 300
Qy 301 SPDELLYLPRVGRRETEYEMLIKESLELMQYLPQHTIETRYROOQOOHOLLQK 360
Db 301 SPDELLYLPRVGRRETEYEMLIKESLELMQYLPQHTIETRYROOQOOHOLLQK 360
Qy 361 CFRNELVPRRRETPKQSDVEFRHSKRP 387
Db 356 -----QTSTQSPSSYGNSSPP 371
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RESULT 7

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US-09-735-705-341
: Sequence 341, Application US/09735705
: Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangun, Chaltanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C14
: CURRENT FILING DATE: US/09/735,705
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 341
: LENGTH: 356
: TYPE: PR1
: ORGANISM: Homo sapiens
US-09-735-705-341
```

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Query Match 89.7%; Score 1867; DB 9; Length 356;
Best Local Similarity 99.7%; Pred. No. 5,7e-165;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
Db 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
Qy 61 TFDLSPSPALPSTNDYDGPSPVDFVQSSTAKSATWTSTELKTKLYCOIAKCPIDQIK 120
Db 61 TFDLSPSPALPSTNDYDGPSPVDFVQSSTAKSATWTSTELKTKLYCOIAKCPIDQIK 120
Qy 121 VMPPPGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
Db 121 VMPPPGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
Qy 181 YVEDPITGRQSVLVYPPPOVGEFTTVLYNFMCNSSCVGGMNRPILLIIVTLETDRGOV 240
Db 181 YVEDPITGRQSVLVYPPPOVGEFTTVLYNFMCNSSCVGGMNRPILLIIVTLETDRGOV 240
```

```
Qy 241 LGRRCFARICACGRRKKADEDSIRKQOYSDSTKNGDGTKRPRONTGHIOMTSIKRR 300
Db 241 LGRRCFARICACGRRKKADEDSIRKQOYSDSTKNGDGTKRPRONTGHIOMTSIKRR 300
Qy 301 SPDELLYLPRVGRRETEYEMLIKESLELMQYLPQHTIETRYROOQOOHOLLQK 355
Db 301 SPDELLYLPRVGRRETEYEMLIKESLELMQYLPQHTIETRYROOQOOHOLLQK 355
```

RESULT 8

```
US-09-850-716A-341
: Sequence 341, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT FILING DATE: US/09/850,716A
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 341
: LENGTH: 356
: TYPE: PR1
: ORGANISM: Homo sapiens
US-09-850-716A-341
```

```
Query Match 89.7%; Score 1867; DB 10; Length 356;
Best Local Similarity 99.7%; Pred. No. 5,7e-165;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
Db 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
Qy 61 TFDLSPSPALPSTNDYDGPSPVDFVQSSTAKSATWTSTELKTKLYCOIAKCPIDQIK 120
Db 61 TFDLSPSPALPSTNDYDGPSPVDFVQSSTAKSATWTSTELKTKLYCOIAKCPIDQIK 120
Qy 121 VMPPPGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
Db 121 VMPPPGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
Qy 181 YVEDPITGRQSVLVYPPPOVGEFTTVLYNFMCNSSCVGGMNRPILLIIVTLETDRGOV 240
Db 181 YVEDPITGRQSVLVYPPPOVGEFTTVLYNFMCNSSCVGGMNRPILLIIVTLETDRGOV 240
Qy 241 LGRRCFARICACGRRKKADEDSIRKQOYSDSTKNGDGTKRPRONTGHIOMTSIKRR 300
Db 241 LGRRCFARICACGRRKKADEDSIRKQOYSDSTKNGDGTKRPRONTGHIOMTSIKRR 300
Qy 301 SPDELLYLPRVGRRETEYEMLIKESLELMQYLPQHTIETRYROOQOOHOLLQK 355
Db 301 SPDELLYLPRVGRRETEYEMLIKESLELMQYLPQHTIETRYROOQOOHOLLQK 355
```

RESULT 9

```
US-09-897-778-341
: Sequence 341, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
```

```
: APPLICANT: Wang, Tongtong
: APPLICANT: Mainerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Matanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
```

```

: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 341
: LENGTH: 356
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-897-778-341

Query Match
Best Local Similarity 89.7%; Score 1867; DB 10; Length 356;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
DB 1 MYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPAIPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIK 120
QY 61 TFDALSPSPAIPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
QY 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
QY 181 YVEDPITGROSALVPEPPQVGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOV 240
DB 181 YVEDPITGROSALVPEPPQVGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPRONTHGIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPRONTHGIOMTSIKRR 300
QY 301 SPDDLLYLPVGRREYEMLKIKESLEMOYLPQHTIETRYQOQOQHHLQK 355
DB 301 SPDDLLYLPVGRREYEMLKIKESLEMOYLPQHTIETRYQOQOQHHLQK 355

RESULT 10
US-10-274-874-2
: Sequence 2, Application US/10274874
: Publication No. US20030113774A1
: GENERAL INFORMATION:
: APPLICANT: Trlink, Barry
: APPLICANT: Jen, Jim
: APPLICANT: Ratovitski, Edward
: APPLICANT: Sidoransky, David
: TITLE OF INVENTION: p40 Protein Acts as an Oncogene
: FILE REFERENCE: 01107.79765
: CURRENT APPLICATION NUMBER: US/10/274,874
: CURRENT FILING DATE: 2002-10-22
: PRIOR APPLICATION NUMBER: US/09/277,196
: PRIOR FILING DATE: 1999-03-26
: PRIOR APPLICATION NUMBER: 60/079736
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 356
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-274-874-2

Query Match
Best Local Similarity 89.7%; Score 1867; DB 15; Length 356;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
```

```

DB 1 MYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPAIPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIK 120
QY 61 TFDALSPSPAIPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
QY 181 YVEDPITGROSALVPEPPQVGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOV 240
DB 181 YVEDPITGROSALVPEPPQVGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPRONTHGIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPRONTHGIOMTSIKRR 300
QY 301 SPDDLLYLPVGRREYEMLKIKESLEMOYLPQHTIETRYQOQOQHHLQK 355
DB 301 SPDDLLYLPVGRREYEMLKIKESLEMOYLPQHTIETRYQOQOQHHLQK 355

RESULT 11
US-09-735-705-338
: Sequence 338, Application US/09735705
: Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skelvy, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C14
: CURRENT APPLICATION NUMBER: US/09/735,705
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 338
: LENGTH: 586
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-735-705-338

Query Match
Best Local Similarity 89.7%; Score 1867; DB 9; Length 586;
Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;

QY 1 MYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
DB 1 MYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPAIPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIK 120
QY 61 TFDALSPSPAIPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNDYDPGPHSFVDSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
QY 181 YVEDPITGROSALVPEPPQVGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOV 240
DB 181 YVEDPITGROSALVPEPPQVGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOV 240
```

```

QY      241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTGTRPRRONTGHIOMTSIKRR 300
        |||||||
Db      241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTGTRPRRONTGHIOMTSIKRR 300
QY      301 SPDELLYLPRGRETETMLKIKESLELMQYLPQHTIETTRQOQOQHLLQKHLISA 360
        |||||||
Db      301 SPDELLYLPRGRETETMLKIKESLELMQYLPQHTIETTRQOQOQHLLQKHLISA 360
QY      361 CFRNELVEPRRETPKQSDVEFFRHSKPP 387
        :| | | :| | |
Db      356 -----QTISIQSPSSSYGNSSPP 371

```

```

RESULT 12
US-09-850-716A-338
: Sequence 338, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Reltter, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 338
: LENGTH: 586
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-850-716A-338

```

```

Query Match      89.7%: Score 1867; DB 10; Length 586;
Best Local Similarity 92.5%: Pred. No. 1.2e-164;
Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;

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QY      1  MLYENNAGTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
        |||||||
Db      1  MLYENNAGTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY      61 TFDALSSPAIPSTNDYPGPHSDVSPFOQSSSTAKSATWTYSTELKLYCOIANTCPIQIK 120
        |||||||
Db      61 TFDALSSPAIPSTNDYPGPHSDVSPFOQSSSTAKSATWTYSTELKLYCOIANTCPIQIK 120
QY      121 VMTPPGAVIRAMPYVKKAEHTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
        |||||||
Db      121 VMTPPGAVIRAMPYVKKAEHTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY      181 YVEDPITGRQSVLVPYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIYVLTETRDGOV 240
        |||||||
Db      181 YVEDPITGRQSVLVPYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIYVLTETRDGOV 240
QY      241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTGTRPRRONTGHIOMTSIKRR 300
        |||||||
Db      241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTGTRPRRONTGHIOMTSIKRR 300
QY      301 SPDELLYLPRGRETETMLKIKESLELMQYLPQHTIETTRQOQOQHLLQKHLISA 360
        |||||||
Db      301 SPDELLYLPRGRETETMLKIKESLELMQYLPQHTIETTRQOQOQHLLQKHLISA 360
QY      361 CFRNELVEPRRETPKQSDVEFFRHSKPP 387
        :| | | :| | |
Db      356 -----QTISIQSPSSSYGNSSPP 371

```

```

RESULT 13
US-09-897-778-338
: Sequence 338, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:

```

```

: APPLICANT: Wang, Tongtong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 338
: LENGTH: 586
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-897-778-338

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```

Query Match      89.7%: Score 1867; DB 10; Length 586;
Best Local Similarity 92.5%: Pred. No. 1.2e-164;
Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;

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QY      1  MLYENNAGTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
        |||||||
Db      1  MLYENNAGTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY      61 TFDALSSPAIPSTNDYPGPHSDVSPFOQSSSTAKSATWTYSTELKLYCOIANTCPIQIK 120
        |||||||
Db      61 TFDALSSPAIPSTNDYPGPHSDVSPFOQSSSTAKSATWTYSTELKLYCOIANTCPIQIK 120
QY      121 VMTPPGAVIRAMPYVKKAEHTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
        |||||||
Db      121 VMTPPGAVIRAMPYVKKAEHTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY      181 YVEDPITGRQSVLVPYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIYVLTETRDGOV 240
        |||||||
Db      181 YVEDPITGRQSVLVPYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIYVLTETRDGOV 240
QY      241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTGTRPRRONTGHIOMTSIKRR 300
        |||||||
Db      241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTGTRPRRONTGHIOMTSIKRR 300
QY      301 SPDELLYLPRGRETETMLKIKESLELMQYLPQHTIETTRQOQOQHLLQKHLISA 360
        |||||||
Db      301 SPDELLYLPRGRETETMLKIKESLELMQYLPQHTIETTRQOQOQHLLQKHLISA 360
QY      361 CFRNELVEPRRETPKQSDVEFFRHSKPP 387
        :| | | :| | |
Db      356 -----QTISIQSPSSSYGNSSPP 371

```

```

RESULT 14
US-09-735-705-152
: Sequence 152, Application US/09735705
: Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

```

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRN
ORGANISM: Homo sapien
US-09-735-705-152

Query Match 89.3%; Score 1860; DB 9; Length 586;
Best Local Similarity 92.2%; Pred. No. 5,3e-164;
Matches 357; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYLNNMQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
DB 1 MLYLNNMQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDFVSFOOSTAKSATWTSTELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSFDFVSFOOSTAKSATWTSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPVYKKAHVTEVYKRCPNHELRENEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPVYKKAHVTEVYKRCPNHELRENEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVYEPPOVGTETTYLYNFMCNSSCYGNNRRPILITVLTETRDGV 240
DB 181 YVEDPITGRQSVLVYEPPOVGTETTYLYNFMCNSSCYGNNRRPILITVLTETRDGV 240
QY 241 LGRCFEARIACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRONTHGIDMTSIKRR 300
DB 241 LGRCFEARIACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRONTHGIDMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLTKIKESLELMQYLPQHTIETRYQOOOQOHHLQKHLISA 360
DB 301 SPDELLYLPVGRRETYEMLTKIKESLELMQYLPQHTIETRYQOOOQOHHLQKHLISA 360
QY 361 CFRNELVEPRRETPKQSDVFFRHSKRP 387
DB 361 CFRNELVEPRRETPKQSDVFFRHSKRP 387
QY 356 -----QTSIQSPSSSYGNSSP 371
DB 356 -----QTSIQSPSSSYGNSSP 371

RESULT 15
US-09-850-716A-152
Sequence 152, Application US/09850716A
Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRN
ORGANISM: Homo sapien
US-09-850-716A-152

Query Match 89.3%; Score 1860; DB 10; Length 586;
Best Local Similarity 92.2%; Pred. No. 5,3e-164;
Matches 357; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYLNNMQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
DB 1 MLYLNNMQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSS 60

QY 61 TFDALSPSPALPSNTDYPGPHSFDFVSFOOSTAKSATWTSTELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSFDFVSFOOSTAKSATWTSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPVYKKAHVTEVYKRCPNHELRENEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPVYKKAHVTEVYKRCPNHELRENEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVYEPPOVGTETTYLYNFMCNSSCYGNNRRPILITVLTETRDGV 240
DB 181 YVEDPITGRQSVLVYEPPOVGTETTYLYNFMCNSSCYGNNRRPILITVLTETRDGV 240
QY 241 LGRCFEARIACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRONTHGIDMTSIKRR 300
DB 241 LGRCFEARIACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRONTHGIDMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLTKIKESLELMQYLPQHTIETRYQOOOQOHHLQKHLISA 360
DB 301 SPDELLYLPVGRRETYEMLTKIKESLELMQYLPQHTIETRYQOOOQOHHLQKHLISA 360
QY 361 CFRNELVEPRRETPKQSDVFFRHSKRP 387
DB 361 CFRNELVEPRRETPKQSDVFFRHSKRP 387
QY 356 -----QTSIQSPSSSYGNSSP 371
DB 356 -----QTSIQSPSSSYGNSSP 371

Search completed: August 7, 2003, 09:57:12
Job time : 17.7783 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:03; Search time 12.3901 Seconds

(without alignments)
3050.350 Million cell updates/sec

Title: US-09-538-106-18

Perfect score: 2082

Sequence: 1 MLYLENNAGTQFSEPDITNL.....PKQSDVFRHRSKPPNRSYTP 393

Scoring table: BIOSDM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	839.5	40.3	396	1 JH0631	cellular tumor ant
2	762	36.6	363	1 A29376	cellular tumor ant
3	758.5	36.4	367	1 S02193	cellular tumor ant
4	745.5	35.8	386	1 S51648	cellular tumor ant
5	720	34.6	391	1 S02192	cellular tumor ant
6	712.5	34.2	396	1 JH0633	cellular tumor ant
7	707	34.0	393	1 DNR053	cellular tumor ant
8	703	33.8	393	1 S06594	cellular tumor ant
9	700	33.6	390	1 DNMS53	cellular tumor ant
10	698	33.5	391	2 J06193	tumor suppressor p
11	698	33.5	393	2 J06176	tumor suppressor p
12	687	33.0	381	2 S38824	cellular tumor ant
13	259.5	12.5	77	2 146226	cellular tumor ant
14	111.5	5.4	1819	2 T32008	hypothetical prote
15	109	5.2	3942	2 T42730	Bassoon protein -
16	109	5.2	4273	2 C69679	transcription fact
17	108	5.2	2529	2 A56923	transcription fact
18	104.5	5.0	1691	1 D54689	protein-tyrosine-p
19	104.5	5.0	1703	2 S15047	SNF protein - yea
20	104.5	5.0	1894	2 C54689	protein-tyrosine-p
21	104.5	5.0	1912	2 A56178	transcription fact
22	104	5.0	2578	2 A56922	transcription fact
23	102	4.9	947	2 T23107	hypothetical prote
24	100	4.8	628	2 S19150	hypothetical prote
25	99.5	4.8	1203	2 T17415	mycelial surface a
26	99	4.8	1456	2 T01397	LTR gag/pol polyp
27	98	4.7	751	2 AC2098	hypothetical prote
28	98	4.7	1144	2 T20218	hypothetical prote
29	98	4.7	1487	2 S62048	probable membrane

30	97	4.7	710	2 T41586	hypothetical serin
31	96.5	4.6	797	1 VGBEX1	glycoprotein X pre
32	96.5	4.6	866	2 T45462	membrane glycoprot
33	96.5	4.6	1445	2 A59437	KIAA1204 protein l
34	96	4.6	427	2 F85436	hypothetical prote
35	96	4.6	628	2 J00110	hypothetical 69K p
36	96	4.6	890	2 E86530	initiation factor-
37	96	4.6	890	2 E81576	translational initia
38	96	4.6	890	2 F72093	translational initia
39	96	4.6	1106	2 T31742	hypothetical prote
40	96	4.6	1203	2 B55094	chromosomal protei
41	95.5	4.6	1505	2 JC4851	hypoxia-inducible
42	95.5	4.6	2409	1 A60979	versican precursor
43	95	4.6	466	2 A88868	protein T23B5.3 [l
44	95	4.6	490	2 T23147	hypothetical prote
45	95	4.6	628	2 S01955	hypothetical prote

ALIGNMENTS

RESULT 1
JH0631
cellular tumor antigen p53 - rainbow trout.
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0631
R:de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A:Reference number: JH0631; MUID:92210006; PMID:1339362
A:Accession: JH0631
A:Molecule type: mRNA
A:Residues: 1-396 <DEF>
A:Cross-References: GB:M75145; NID:9213828; PIDN:AAA49605.1; PID:9213829
A:Experimental source: Liver
A:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match	40.3%	Score	839.5	DB 1	Length	396
Best Local Similarity	55.2%	Pred. No.	2.6e-58			
Matches	169	Conservative	47	Mismatches	79	Indels 11; Gaps 6;
QY	49	VTPSPYAPPS-STPDALS-PSPAIPSNWDYPGPHSPFVSFOQSSTANSATWTSTELKK	106			
DB	61	VSATPEPAPQPSISTIDTGSPTSTVPTSDYDGAIGFQRLRFLQSSSTAKSVCTYSPDLNK	120			
QY	107	LYCQIAKTCPIQIKVMTPEPPGAVIRAMPYKKAHEVTEVYKRCFNHLSREFNEGQIAP	166			
DB	121	LEFQIAKTCPIQIVVDHPDPGAVVRAIAIYKKSIDVADVYVRCCHOSTSNNNGP-AP	179			
QY	167	PSHLIRVGNSSHAQVVEPIRGROSVLVYEPPOVGTETTLVLFNFMNSSCGVMNRP	226			
DB	180	RGHILRVBGNORSEYMEGNTLRHSVLVYEPPOVGSSECTVTLVLFNFMNSSCGVMNRP	239			
QY	227	ILIIYTLFEDGQVGRRCFEARICACPGPRKADKEDSIRKQ---VSDSTKNGDGTARP	283			
DB	240	ILIIYTLFEDGQVGRRCFEARICACPGPRKADKEDSIRKQ---VSDSTKNGDGTARP	299			
QY	284	FRO-NFHGIQMTSIRKRS---PDDELIYLPVGRRETYEMILTKRESLELMQYIPQHTI	338			
DB	300	MEASLIPAPQPGASKRTSSPAVSDDEIYTLQIRKREYEMILTKRESLELMQYIPQHTI	359			
QY	339	ETTYROO 344				
DB	360	DKYRQK 365				
RESULT 2	A29376					


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Db      239 MNRRLPILITITLEDSCGNLGRNSFEVACGRCRDRRTREENLRKKGSCEPPEPRSTRK 298
      282 RPRRQTHGIOMTSIKKRSP--DDELLYLVRGRREYEMILKIKESLELMQYLPQITIEF 340
      299 RALPMT-----SSPPKKRPDLGGEFTTQIRSEFKYEMFRELNDALDEL----KDALQ 349
QY      341 YRQOQOQH-OHLQKHLIS-ACFRNELVEPRRET 374
      350 RERGSRASHSHLKKRRSPSCHKPKML--KREGP 383

RESULT 5
S02192
cellular tumor antigen p53 - rat
N:Alternate names: gene p53 protein; nuclear oncoprotein p53
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02192; S41149
R:Sousai, T.; de Fromental, C.C.; Breugnot, C.; May, E.
Nucleic Acids Res. 16, 11384, 1988
A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A:Reference number: S02192; M01D:89083585; PMID:3060862
A:Accession: S02192
A:Molecule type: mRNA
A:Residues: 1-391 <SOU>
A:Cross-references: EMBL:X13058; NID:g56828; PIDN:CAA31457.1; PID:g56829
R:Nulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A:Title: Structure of the rat p53 tumor suppressor gene.
A:Reference number: S41149; M01D:93181268; PMID:8441680
A:Accession: S41149
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173, 'W', 175-391 <HDL>
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:
A:introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F:174,177,230,240/Binding site: zinc (Cys, His, Cys) #status predicted
F:190/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match      34.6%; Score 720; DB 1; Length 391;
Best local Similarity 46.1%; Pred. No. 6.4e-49;
Matches 149; Conservative 56; Mismatches 98; Indels 20; Gaps 7;

QY      18 TNLGLNSMDQ-----QIQNGSSSTSPYNTDHAQNSVT--APSPYAQPSSTFDALSPS 68
      35 TANGSPNSMEDLFLLPDVAELLEGPPEALQVSAIPAQDEPGETAPAVAVASATPWLSSS 94
      69 PALPSTIDVPGFHSFVDSQOSTAKSATWYSTEKLKYLCOIAKTCPIQIKWTPPPQG 128
      95 --VPSSQKTYQNGVFLGSLQSTAKSVACVYSISLNKLFQCLAKCPVQLWVTSTPPG 152
QY      129 AVIRAPVYKKAHVTEVVKRCPNHLSREFNEGQ--IAPPSHILIRVGNASHQYVEDPIT 187
      153 TRVRAMAIITKKSOMHEVVRCPHNE--RCSGDGLAPQHLIRVGNASHQYVEDPIT 209
      188 GRQSVLYPEPPOVGTFTTVLVNFMKNSSCVGMNRRPILITVLETRDGOVLGRCFE 247
      210 FRHSVVPYEPPEVGSDDYTTIHKKYKNSCGMGNRRPILITITLEDSSGNLGDSE 269
      248 ARICACPGDRKADDESIRKQVSDSTKKGDTKRRPFRONTGHIOMTSIKKRSP--DDEL 306
      270 VRCACAPGDRKRENEFRKKEHCPELPPGSAKRALPTST-----SSSPQKKKPLDGEY 325
QY      307 LYLPRVGRREYEMILKIKESLEL 329
      326 FTLIKIRGRERFRELNELEL 348
Db
```

```
RESULT 6
JH0633
cellular tumor antigen p53 - golden hamster
N:Alternate names: tumor-suppressor protein p53
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0633
R:Legros, Y.; McIntyre, P.; Sousai, T.
Gene 112, 247-250, 1992
A:Title: The cDNA cloning and immunological characterization of hamster p53.
A:Reference number: JH0633; M01D:92210007; PMID:1355773
A:Accession: JH0633
A:Molecule type: mRNA
A:Residues: 1-396 <LEG>
A:Cross-references: GB:M75144; NID:9191414; PIDN:AAA37085.1; PID:g191415
A:Experimental source: kidney, strain M21
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F:179,182,241,245/Binding site: zinc (Cys, His, Cys) #status predicted
F:195/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match      34.2%; Score 712.5; DB 1; Length 396;
Best local Similarity 40.9%; Pred. No. 2.5e-48;
Matches 155; Conservative 61; Mismatches 128; Indels 35; Gaps 7;

QY      2 LYENNAQTOFSPQOTNIGLNSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAQPSST 61
      44 LFLSENV-----AGWLEDDPEALQGSAAAAAPAAEDPAETPAVAVASAPAT 92
      62 FDALSPPAIPSTNDVPGFHSFVDSQOSTAKSATWYSTEKLKYLCOIAKTCPIQIKY 121
      93 PRLSSS--VPSTKTYQGDYGRFLGHSHTAKSVTCYSISLNKLFQCLAKTCPIQLWY 150
      122 MPRPQGAIVIRAMPYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHILIRVGNASHQY 181
      151 SSPPPGTRVRAVAITKQIKYMTVEVVRCPHHERSSE--GDG--LAPQHLIRVGNNAHEY 208
      182 VEDPITGRQSVLYPEPPOVGTFTTVLVNFMKNSSCVGMNRRPILITVLETRDGOVL 241
      209 LDDKQFRHSVVPYEPPEVGSDDYTTIHKKYKNSCGMGNRRPILITITLEDPSGNLL 268
      242 GRGCFARICACPGDRKADDESIRKQVSDSTKKGDTKRRPFRONTGHIOMTSIKKR 301
      269 GRHSFEVRLICACGRRRRRFEKRFKKGECPELPKSAKRALPTMT-----SSSPQKKRT 325
      302 PDELLYLVRGRREYEMILKIKESLELMQYLPQITIE-----TYRQOQOQHLLQ 355
      326 LDGEYFTLIKIRGGERFKMFQELNEALELKDQAQLKASEDSGAHSYLSKKGSAKRLK 385
QY      356 HLISACFRNELVEPRRET 374
      386 LMT-----KREGP 393
Db

RESULT 7
DNH053
cellular tumor antigen p53 [validated] - human
N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppr
C:Species: Homo sapiens (man)
C>Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C:Accession: A25224; A43073; J04036; S40773; S42669; A25397; B25397;
4905; I58354; I78850; I52861; S60153
R:Lamb, P.; Crawford, E.
Mol. Cell. Biol. 6, 1379-1385, 1986
A:Title: Characterization of the human p53 gene.
A:Reference number: A25224; M01D:87064416; PMID:2946935
A:Accession: A25224
A:Molecule type: DNA
A:Residues: 1-393 <LAM>
A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1;
R:Buchanan, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
```

Gene 70, 245-252, 1988
A:Title: A variation in the structure of the protein-coding region of the human p53 gene
A:Reference number: J70436; MUID:89108008; PMID:2905688
A:Accession: A43073
A:Molecule type: DNA
A:Residues: 1-393 <BUC1>
A:Cross-references: EMBL:M22898; NID:q189474
A:Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro all
A:Accession: J70436
A:Molecule type: DNA
A:Residues: 1-71, 'P', '73-393 <BUC2>
A:Cross-references: EMBL:M23898; NID:q189474; PIDN:AAA5998.1; PID:q189476
A:Note: this 72-Pro allele was found in both normal and malignant cell lines
R:Chumakov, P.M.; Almazov, V.P.; Jenklns, J.R.
submitted to the EMBL Data library, August 1990
A:Reference number: S40773
A:Accession: S40773
A:Molecule type: DNA
A:Residues: 1-393 <CHD>
A:Cross-references: EMBL:X54156; NID:q35213; PIDN:CAA38095.1; PID:q35214
R:Malashewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, S.
EMBO J. 3, 3257-3262, 1984
A:Title: Isolation and characterization of a human p53 cDNA clone: expression of the hu
A:Reference number: S42669; MUID:85126934; PMID:6396087
A:Accession: S42669
A:Molecule type: mRNA
A:Residues: 101-393 <MKI1>
A:Cross-references: EMBL:X01405; NID:q35215; PIDN:CAA2652.1; PID:g642241
R:Zakut-Houri, R.; Blenz-Tadmor, B.; Givol, D.; Oren, M.
EMBO J. 4, 1251-1255, 1985
A:Title: Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.
A:Reference number: A22837; MUID:85230577; PMID:4006916
A:Accession: A22837
A:Molecule type: mRNA
A:Residues: 1-71, 'P', '73-393 <ZAK>
A:Cross-references: EMBL:X02469; EMBL:M60950; NID:q35209; PIDN:CAA26306.1; PID:q35210
R:Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Biol. 5, 1601-1610, 1985
A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tu
A:Reference number: A55060; MUID:85267676; PMID:3894933
A:Accession: A55060
A:Molecule type: mRNA
A:Residues: 1-71, 'P', '73-272, 'H', '274-393 <HAR>
A:Cross-references: GB:K03199; NID:q189478; PIDN:AAA59989.1; PID:q189479
R:Harlow, E.; Brill, E.; Shokat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Rotter, V.
Mol. Cell. Biol. 6, 4650-4656, 1986
A:Title: Molecular basis for heterogeneity of the human p53 protein.
A:Reference number: A93086; MUID:87089826; PMID:3025664
A:Accession: A25397
A:Molecule type: mRNA
A:Residues: 1-78, 'T', '80-393 <HAR1>
A:Cross-references: EMBL:M4694; NID:q339813; PIDN:AAA61211.1; PID:q339814
A:Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
A:Accession: B25397
A:Molecule type: mRNA
A:Residues: 1-71, 'P', '73-78, 'T', '80-393 <HAR2>
A:Cross-references: EMBL:M4695; NID:q339813; PIDN:AAA61212.1; PID:q339816
A:Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
R:Malashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
Mol. Cell. Biol. 7, 961-963, 1987
A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.
A:Reference number: S42452; MUID:87144273; PMID:3547088
A:Accession: S42452
A:Molecule type: mRNA; DNA
A:Residues: 66-71, 'P', '73-79 <MKI2>
A:Experimental source: clone lambda C113
A:Note: 72-Cys was also found, and appears to represent a polymorphism
A:Accession: S42453
A:Molecule type: mRNA; DNA
A:Residues: 66-79 <MKI3>
A:Experimental source: clone J6K
R:Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.; Crook, T.

EMBO J. 10, 2879-2887, 1991
A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
A:Reference number: I38082; MUID:92007731; PMID:1915267
A:Accession: I38082
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189, 'LSTLSEWKEICVSIWMTETLFDIYWCMSRLRLALT', 'VPSTTTCTVTPMAA' <F01>
A:Cross-references: EMBL:X60010; NID:q506432; PIDN:CAA42625.1; PID:q506433
A:Note: deletion of a C nucleotide causes a frameshift at position 566
A:Accession: I38083
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-192, 'R', '194-393 <F02>
A:Cross-references: EMBL:X60011; NID:q506434; PIDN:CAA42626.1; PID:q506435
A:Accession: I38084
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-393 <F03>
A:Cross-references: EMBL:X60012; NID:q506436; PIDN:CAA42627.1; PID:q506437
A:Accession: I38085
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-245, 'T', '247-393 <F04>
A:Cross-references: EMBL:X60013; NID:q506438; PIDN:CAA42628.1; PID:q506439
A:Accession: I38086
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-236, 'T', '238-393 <F05>
A:Cross-references: EMBL:X60014; NID:q506440; PIDN:CAA42629.1; PID:q506441
A:Accession: I38087
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247, 'Q', '249-393 <F06>
A:Cross-references: EMBL:X60015; NID:q506442; PIDN:CAA42630.1; PID:q506443
A:Accession: I38088
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71, 'P', '73-237, 'Y', '239-393 <F07>
A:Cross-references: EMBL:X60016; NID:q506444; PIDN:CAA42631.1; PID:q506445
A:Accession: I38089
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247, 'Q', '249-393 <F08>
A:Cross-references: EMBL:X60017; NID:q506446; PIDN:CAA42632.1; PID:q506447
A:Accession: I38090
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71, 'P', '73-162, 'H', '164-393 <F09>
A:Cross-references: EMBL:X60018; NID:q506448; PIDN:CAA42633.1; PID:q506449
A:Accession: I38091
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212, 'Q', '214-393 <F10>
A:Cross-references: EMBL:X60019; NID:q506450; PIDN:CAA42634.1; PID:q506451
A:Accession: I38092
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-253, 'D', '255-393 <F11>
A:Cross-references: EMBL:X60020; NID:q506452; PIDN:CAA42635.1; PID:q506453
A:Note: all sequences submitted to the EMBL/GenBank/DBJ databases June 1991
R:Farrell, P.A.; Barrett, J.C.; Wiseman, R.W.
Nucleic Acids Res. 19, 6977, 1991
A:Title: An Ala polymorphism intragenic to the TP53 gene.
A:Reference number: I38093; MUID:92107726; PMID:11762941
A:Accession: I38093
A:Molecule type: DNA
A:Residues: 1-393 <FUT>
A:Cross-references: EMBL:X54156; NID:q35213; PIDN:CAA38095.1; PID:q35214
R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakata
Cancer Res. 51, 5800-5805, 1991
A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell l
A:Reference number: A44905; MUID:92034678; PMID:1933850

A:Accession: AA4905
A:Molecule type: DNA
A:Residues: 246-247, 'W', 249-250 <YAM>
A:Cross-references: GB:563157; NID:g4237829; PIDN:AA20140.1; PID:g237830
A:Note: sequence extracted from NCBI backbone (NCBIN:63157, NCBIPI:63158)
R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
Oncogene 6, 1067-1071, 1991
A:Title: Use of the single strand conformation polymorphism technique and PCR to detect
A:Reference number: 158354; MUID:91296386; PMID:1648702
A:Accession: 158354
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 244-247, 'W', 249-252 <HEN1>
A:Cross-references: GB:541969; NID:g1679931; PIDN:AA19324.1; PID:g232814
A:Accession: 178850
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 274-277, 'S', 279-282 <HEN2>
A:Cross-references: GB:541977; NID:g1679932; PIDN:AA19325.1; PID:g232816
R:Chow, V.T.; Quek, H.H.; Toock, E.P.C.
Cancer Lett. 73, 141-148, 1993
A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphoblastoid cell line
A:Reference number: 152681; MUID:94036762; PMID:8221626
A:Accession: 152681
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 327-331, 'DQTSFQKENC' <CHO>
A:Cross-references: GB:566666; NID:g436292; PIDN:AA28601.1; PID:g436293
R:Peterson, G.; Song, D.; Huegler-Boert, B.; Oldenburg, I.; Baur, E.K.F.
Mol. Gen. Genet. 249, 425-431, 1995
A:Title: Mapping of 11ner epitopes recognized by monoclonal antibodies with gene-fragments
A:Reference number: 560151; MUID:96133682; PMID:8552047
A:Accession: 560153
A:Molecule type: DNA
A:Residues: 3-44 <PET>
R:Dang, C.V.; Lee, W.M.F.
J. Biol. Chem. 264, 18019-18023, 1989
A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, N-myc, p53, HSP70, and p135

[illegible]

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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:32:13 ; Search time 6.96946 Seconds

(without alignments)
2651.784 Million cell updates/sec

Title: US-09-538-106-18

Sequence: 1 MYLENNAGTQSEPDYTNL.....PKSDVFRHRSKPNRSVYP 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1248.5	60.0	636	P73_HUMAN	O15330 homo sapien
2	1247.5	59.9	637	P73_CERAE	O9XSK8 cercopithec
3	839.5	40.3	369	P53_ONCMY	P25035 oncorhynchu
4	819.5	39.4	369	P53_BARBU	O9W678 barbuis barb
5	806.5	38.7	373	P53_BRARE	P79734 brachydania
6	800	38.4	376	P53_ICTPU	O93379 ictalurus p
7	762	36.6	363	P53_XENLA	P07193 xenopus lae
8	758.5	36.4	367	P53_CHICK	P10360 gallus gall
9	757.5	36.2	386	P53_PIG	O9TUB2 sus scrofa
10	753.5	35.8	386	P53_FELCA	P41685 felis silve
11	745.5	35.8	386	P53_BOVIN	O29668 bos taurus
12	745	35.8	367	P53_TETMU	O9W679 tetraodon m
13	739	35.5	381	P53_CANFA	O29537 canis famli
14	737.5	35.4	352	P53_ORYLA	P79820 oryza lat
15	736.5	35.4	391	P53_MARMO	O36006 marmota mon
16	725.5	34.8	382	P53_SHEEP	P51664 ovis aries
17	720	34.6	391	P53_RAT	P10361 rattus norv
18	719	34.5	391	P53_CAVPO	O9WUR6 cavia porce
19	719	34.5	393	P53_TUPGB	O9TET1 tupia glis
20	717.5	34.5	366	P53_PLAHE	O12946 platichthys
21	712.5	34.2	396	P53_MESAU	O00366 mesocricetu
22	707	34.0	393	P53_HUMAN	P04637 homo sapien
23	703	33.8	314	P53_SPEBE	O64662 speimophilu
24	703	33.8	393	P53_CERAE	P13481 cercopithec
25	703	33.8	393	P53_MACFA	P56423 macaca fasc
26	703	33.8	393	P53_MACFA	P56423 macaca fasc
27	702.5	33.7	342	P53_XIPHE	O57338 xiphophorus
28	702.5	33.7	342	P53_XIPHE	O92143 xiphophorus
29	702	33.7	393	P53_CRIGR	O02185 cricetus
30	700	33.6	390	P53_MOUSE	P02340 mus musculu
31	700	33.6	391	P53_RABIT	O95330 oryctolagus
32	689.5	33.1	280	P53_HORSE	P79892 equus cabal
33	591.5	28.4	207	P53_EQUAS	O29480 equus asinu

ALIGNMENTS

RESULT 1	ID	P73_HUMAN	STANDARD	PRT	636 AA.
AC	O15350	O15351	O9WTR8		
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Tumor protein p73 (p53-like transcription factor) (p53-related protein)				
GN	TP73 OR P73.				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).				
RC	TISSUE=Colon;				
RX	MEDLINE=97433090; PubMed=9288759;				
RA	Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A., Minty A., Chalton P., Lelias J.-M., Dumont X., Ferrara P., McKeon F., Caput D.;				
RT	"Monoclonally deleted expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers.";				
RL	Cell 90:809-819(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).				
RX	MEDLINE=98389621; PubMed=9721206;				
RA	Jenkin M., Huang H., Reed C., Qian C., Smith J.S., Alderete B., Yoshikawa H., Nagashima M., Khan M.A., McEnamin M.G., Hagihara K., Harris C.C.;				
RT	"Mutational analysis of p73 and p53 in human cancer cell lines.";				
RL	Oncogene 18:3415-3421(1999).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).				
RX	MEDLINE=98389621; PubMed=9721206;				
RA	Jenkin M., Huang H., Reed C., Qian C., Smith J.S., Alderete B., Yoshikawa H., Nagashima M., Khan M.A., McEnamin M.G., Hagihara K., Harris C.C.;				
RT	"Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions.";				
RL	Genomics 51:359-363(1998).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).				
RX	TISSUE=Neuroblastoma;				
RA	MEDLINE=99021697; PubMed=9802988;				
RT	De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M., Annichiarico-Petruzzelli M., Levrero M., Melino G.;				
RL	"Two new p73 splice variants, gamma and delta, with different transcriptional activity.";				
RN	J. Exp. Med. 188:1763-1768(1998).				
RP	[5]				
RX	SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).				
RA	TISSUE=Breast cancer, Hepatoma, Lymphocytes, and Skin;				
RT	MEDLINE=99310938; PubMed=10381648;				
RL	De Laurenzi V., Catali M.V., Terrinoni A., Corazzari M., Melino G., Costanzo A., Levrero M., Knight R.A.;				
RT	"Additional complexity in p73: induction by mitogens in lymphoid cells and identification of two new splicing variants epsilon and zeta.";				

RL Cell Death Differ. 6:389-390(1999).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM KAPPA).
 RA Thomas D.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
 RA MEDLINE-99318135; PubMed-10391251;
 RX MEDLINE-99318135; PubMed-10391251;
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Khairbanda S., Weichselbaum R., Kute D.;
 RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
 RT to DNA damage.";
 RL Nature 399:814-817(1999).
 RN [8]
 RP ERRATUM.
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Khairbanda S., Weichselbaum R., Kute D.;
 RL Nature 400:792-792(1999).
 RN [9]
 RP FUNCTION.
 RX MEDLINE-99217940; PubMed-10203277;
 RA Kaelin M.G. Jr.;
 RT "The emerging p53 gene family.";
 RL J. Natl. Cancer Inst. 91:594-598(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 439-506.
 RX MEDLINE-99380160; PubMed-10449409;
 RA Chi S.W., Ayed A., Arrowsmith C.H.;
 RT "Solution structure of a conserved C-terminal domain of p73 with
 RT structural homology to the SAM domain.";
 RL EMBO J. 18:4438-4445(1999).
 CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
 CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
 CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
 CC PROTEIN.
 CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
 CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
 CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
 CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
 CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-7;
 CC Name-Alpha;
 CC IsoId=O15350-1; Sequence=Displayed;
 CC Name-Beta;
 CC IsoId=O15350-2; Sequence=VSP_006539;
 CC Name-Gamma;
 CC IsoId=O15350-3; Sequence=VSP_006540, VSP_006541;
 CC Note-The splicing of exon 11 results in a frameshift from the
 CC original reading frame;
 CC Name-Delta;
 CC IsoId=O15350-4; Sequence=VSP_006542, VSP_006543;
 CC Name-Epsilon;
 CC IsoId=O15350-5; Sequence=VSP_006544, VSP_006545;
 CC Note-The splicing of exon 11 results in a frameshift from the
 CC original reading frame. The splicing of exon 13 reverts the
 CC reading frame to the sequence of isoform Alpha;
 CC Name-Zeta;
 CC IsoId=O15350-6; Sequence=VSP_006546;
 CC Name-Kappa;
 CC IsoId=O15350-7; Sequence=VSP_006538;
 CC -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
 CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
 CC -1- INDUCTION: NOT INDUCED BY DNA DAMAGE.
 CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
 CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
 CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
 CC -1- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERS
 CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
 CC IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
 CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC				-----
DR	EMBL	Y11416; CAA72220.1;	-	
DR	EMBL	Y11416; CAA72221.1;	-	
DR	EMBL	Y11416; CAA72219.1;	-	
DR	EMBL	AF077628; AAC61887.1;	-	
DR	EMBL	AF077616; AAC61887.1;	JOINED.	
DR	EMBL	AF077617; AAC61887.1;	JOINED.	
DR	EMBL	AF077619; AAC61887.1;	JOINED.	
DR	EMBL	AF077620; AAC61887.1;	JOINED.	
DR	EMBL	AF077621; AAC61887.1;	JOINED.	
DR	EMBL	AF077624; AAC61887.1;	JOINED.	
DR	EMBL	AF077625; AAC61887.1;	JOINED.	
DR	EMBL	AF077626; AAC61887.1;	JOINED.	
DR	EMBL	AF077627; AAC61887.1;	JOINED.	
DR	EMBL	AF079094; AAD39696.1;	-	
DR	EMBL	AF079082; AAD39696.1;	JOINED.	
DR	EMBL	AF079083; AAD39696.1;	JOINED.	
DR	EMBL	AF079084; AAD39696.1;	JOINED.	
DR	EMBL	AF079085; AAD39696.1;	JOINED.	
DR	EMBL	AF079086; AAD39696.1;	JOINED.	
DR	EMBL	AF079087; AAD39696.1;	JOINED.	
DR	EMBL	AF079088; AAD39696.1;	JOINED.	
DR	EMBL	AF079089; AAD39696.1;	JOINED.	
DR	EMBL	AF079091; AAD39696.1;	JOINED.	
DR	EMBL	AF079092; AAD39696.1;	JOINED.	
DR	EMBL	AF079093; AAD39696.1;	JOINED.	
DR	EMBL	AL136528; CAB82742.1;	-	
DR	PDB	1COK; 17-AUG-99.		
DR	PDB	IDXS; 08-AUG-01.		
DR	TRANSFAC	T04931;	-	
DR	GeneW	HGNC:12003; TP73.		
DR	MIM	601990;	-	
DR	GO	GO:0003700; F:transcription factor activity; TAS.		
DR	GO	GO:0008630; P:Induction of apoptosis by DNA damage; TAS.		
DR	GO	GO:0006298; P:mismatch repair; TAS.		
DR	InterPro	IPIR002117; P53.		
DR	InterPro	IPIR001660; SAM.		
DR	Pfam	PF00870; P53; 1.		
DR	Pfam	PF00536; SAM; 1.		
DR	PRINTS	PR00386; P53SUPPRESSOR.		
DR	ProDom	PD002681; P53; 1.		
DR	SMART	SM00454; SAM; 1.		
DR	PROSITE	PS00348; P53; 1.		
KM	Transcription regulation; Activator; DNA-binding; Anti-oncogene; Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing; 3d-structure.			
FT	DOMAIN	1	46	TRANSACTIVATION (BY SIMILARITY).
FT	DOMAIN	1	55	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	287	304	NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT	DOMAIN	346	435	MEDIATES OLIGOMERIZATION (POTENTIAL).
FT	DOMAIN	168	171	POLY-PRO.
FT	DOMAIN	391	394	POLY-GUN.
FT	DOMAIN	483	486	POLY-PRO.
FT	DOMAIN	131	310	DNA-BINDING (POTENTIAL).
FT	MOD_RES	99	99	PHOSPHORYLATION (BY ABL) (IN ISOFORM BETA).
FT	VARSPLIC	282	282	G->GNTCRHWVLCGRGLSRPYLGSPSG (In isoform kappa).
FT	VARSPLIC	495	636	SFLNGSLGPCNTEIEFTSSQGLSTIYHLONTIEDGALKIPE QYRTITWGGLDDVGHDYSTAQOQLRSNNATISGSGE LQRORVMEAVHFRVRHTITIPNRGGPGGGPMADFDPD DCKARKODIKKEEFTAEIETH -> RTWGP (In isoform beta)

	Query Match	60.0%	Score 1248.5;	DB 1;	Length 636;	
	Best Local Similarity	70.6%;	Pred. No. 1.2e-87;			
	Matches 238;	Conservative 37;	Mismatches 55;	Indels 7;	Gaps 4;	
QY	22 LLSNMDPOINGSSSTSPYTMDAONSVTAPSPAPCSPTEDALSPSPAIPSNIDYPGP	81				
Db	11::: ::: ::: ::: ::: ::: ::: ::: :::					
Db	67 LLSSTMQMSSRRASASPRTPEHNA-SVPHSPPAQPSSTFDMSPAVIPSNDYDGPB	125				
QY	82 SFDVSFOQSSTANSATWTTSTELKKLYCQIAKTCPIQIKWTPPPQGAVIRAMFYKAE	141				
Db	126 HFEFTFOQSSTAKSATWTWSPLLKLKCQIAKTCPIDQIKVSTPPPQGAIRAMPYYKAE	185				
QY	142 HVEYVVRKCNHHELSREFNEGQIALPBPRLIRVENENSAQVEDBITGNOSVLVEYPEPV	201				
Db	186 HYDVYVRCPPHELGRPFNEQSPASHLLRVESNNLSAQYDDVTGGQSVVVEYPEPV	245				
QY	202 GTETTYLVNPMNCSCVGCGNNRPRIILIVLETRDCOVLGRCFEARIACAPGRDRKAD	261				
Db	246 GTEETTYLVNPMNCSCVGCGNNRPRIIITLEMRDQVGLGRSFGERTICACPGRDRAD	305				
QY	262 EDSIRKOQV--SDSTKNQDGTKRFPRONTNGION--TSIKRSRSPDEDLIPLYRGRETY	317				
Db	306 EDHRREQQALESNAKNGASKRAFKOSPAPVAPLIGAGVKRKRRHGDEDTYLQVKGREN	365				
QY	318 EMALKIKESLEIMOYLPOHTTETYROOOQ--QQHQHL 352					
Db	366 EIMLKKESEFLMELVPQLVDSTRQOOQLLRSHL 402					
RESULT 2						
p73_CERAE	STANDARD;	PRT:	637 AA.			
ID	p73_CERAE					
AC	O9XSK8: O9TSO9;					
DT	16-OCT-2001 (Rel. 40, Created)					
DT	16-OCT-2001 (Rel. 40, Last sequence update)					
DT	28-FEB-2003 (Rel. 41, Last annotation update)					
DE	Tumor protein p73 (p53-like transcription factor) (p53-related					
DE	protein).					
GN	TP73 OR P73.					
OS	Cercopithecus aethiops (Green monkey) (Grivet).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;					
OC	Cercopitheciinae; Cercopithecus.					
OX	NCBI_Taxid=9534;					
RN	[1]					
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).					
RC	TISSUE=Kidney;					
RA	Caput D.;					
CC	submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.					
CC	-1 FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.					
CC	WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE					
CC	PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN					
CC	(BY SIMILARITY).					
CC	-1 SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL					
CC	TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY					
CC	AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.					
CC	-1 SUBCELLULAR LOCATION: Nuclear.					
CC	-1 ALTERNATIVE PRODUCTS:					
CC	Event=Alternative splicing; Named isoforms=2;					
CC	Name=Alpha;					
CC	isoId=O9XSK8-1; Sequence=Displayed;					
CC	Name=Beta;					
CC	isoId=O9XSK8-2; Sequence=VSP_006537;					
CC	-1 DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA					
CC	BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS					
CC	TO THE ABL TYROSINE KINASE SH3 DOMAIN.					
CC	-1 SIMILARITY: BELONGS TO THE P53 FAMILY.					
CC	-----					
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DR EMBL; Y11419; CAAT2224.1; -;
DR EMBL; Y11419; CAAT72225.1; -;
DR HSSP; O15350; ILOK.
DR InterPro; IPRO02117; P53.
DR InterPro; IPRO01660; SAM.
DR Pfam; PF00870; P53; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PRO0386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SMO0454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Transcription regulation; Activator; DNA-binding; Anti-oncogene;
KW Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing.
FT FT
FT VARSPLIC 495 637
FT
FT
FT
SQ SEQUENCE 637 AA; 69630 MM; 7GBD200B919C9C70A CRC64;
/FtId=VSP_006537.
Query Match 59.9%; Score 1247.5; DB 1; Length 637;
Best Local Similarity 70.3%; Pred. No. 1.4e-87;
Matches 237; Conservative % 38; Mismatches 55; Indels 7; Gaps 4;

QY 22 LLSNMDIOIQNGSSSTSPYNDAHONSVTAPSPAOSPTFDALSPSPAIPSNIDYPGH 81
Db LLSSTDMOIMSRRASASAPIPEEHA-SVPHSPYAOPSSTFDISPAPVYSNTDYPCGP 125
11:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 82 SFDSFOOSSPAKSATWTYTEELKKLYCOLAKTPIDQIKVTIPPPOGAVIRAMPYYKKA 141
Db LFEVTFPOOSSPAKSATWTYTEELKKLYCOLAKTKPIDQIKVSAPPFGAIRAMPYYKKA 185
11:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 142 HVEIVVKRCENHELREPNESQIAPPSHLRVESNSHAQVYEDPIITGQSVLVPEPPQY 201
Db HTVDIVKRCPEHLEGRFNEGOSAPASHLIVEGNMNLISQYDDVDTGROSVVVPEPPQY 245
11:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 202 GTETTYLVNPMNCSSCGVGNNRPDLITVLTFRDOGVLRGRCFEARICACPGDRKAD 261
Db GTETTYLVNPMNCSSCGVGNNRPDLITVLTFRDOGVLRGRSFEGRICACPGDRKAD 305
11:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 246 GTEFTTLTNFMCMSSCVGGNNRPDLITVLTFRDOGVLRGRSFEGRICACPGDRKAD 305
Db EDSTRKOQV--SDSTKNKGDFKRFPFONTHIGM--TSIKRSRSPDELLTLPVPRGRETY 317
262 262
QY 306 EDHRREGDALNESSAKKGAASKRAFKOSPAPVPALGCEVKKRRRGDEDITYLYQVRGNF 365
Db 306 306
11:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 318 EMILKIKESLELMQLPDQHTLETYRQQQ--QQHQHL 352
Db 366 ELMLKIKESLELMELVQPPLDVSRQQQQLQLRSHL 402
11:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 3
P53_ONCMY STANDARD; PRT; 396 AA.
ID ID P53_ONCMY STANDARD; PRT; 396 AA.
AC AC P25035;
DT DT 01-MAY-1992 (Rel. 22, Created)
DT DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN GN TP53.
OS OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX OX NCBI_TaxID=8022;
RN RN [1]
RP SEQUENCE FROM N.A.
RX RX MEDLINE=92210006; PubMed=1339362;
RA RA de Fromentel C.C., Padet F., Chapus A., Baney C., May P., Soussi T.;
"Rainbow trout p53: cDNA cloning and biochemical characterization.";

RL Gene 112:241-245(1992).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC -----
 CC EMBL: M75145; AAA49605.1; -
 CC PIR: JH0631; JH0631.
 CC HSP: P04637; ITUP.
 CC InterPro: IPR002117; P53.
 CC Pfam: PF00870; P53; 1.
 CC PRINTS: PR00386; P53SUPPRESSR.
 CC ProDom: PD002681; P53; 1.
 CC PROSITE: PS00348; P53; 1.
 CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 CC Nuclear protein; Phosphorylation; Apoptosis.
 CC KM Nuclear protein; Phosphorylation; Transcription regulation; Activator;
 CC FT DNA BIND 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
 CC FT DOMAIN 90 281 BY SIMILARITY.
 CC FT DOMAIN 325 356 OLIGOMERIZATION.
 CC FT DOMAIN 325 356 BASIC (REPRESSION OF DNA-BINDING).
 CC FT DOMAIN 303 318 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC FT MOD.RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
 CC FT MOD.RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
 CC SQ SEQUENCE 396 AA; 43966 MW; 8422250765545A1C CRC64;
 CC -----
 CC Query Match 40.3%; Score 839.5; DB 1; Length 396;
 CC Best Local Similarity 55.2%; Pred. No. 9.4e-57;
 CC Matches 169; Conservative 47; Mismatches 79; Indels 11; Gaps 6;
 CC
 CC QY 49 VTAPSPYAPS-STFDALS-PSPALPSNTDYPGPHSFVDSFQSSSTAKSATWTSTELKK 106
 CC DB 61 VSATPPAPQPSISTIDTGSPTSTVPTSDYDGAIGFOLRFQSSSTAKSVCTSPDLNK 120
 CC QY 107 LYCOLAKTCPIQIKMTPPGAVIRAMPVYKKAHEVTEVYKRCNHNELREFNGQIAP 166
 CC DB 121 LFCQLAKTCPIQIVVDHPPPGAVVRAIAIKKISDVADVARCPHSTSENNEGP-AP 179
 CC QY 167 PSHLRVGENSHAOYVEDPITGRQSVLVPEPPQVTEFTYLVYFMCSSCVGGMNRRP 226
 CC DB 180 RGLVLRVGENSHAOYVEDPITGRQSVLVPEPPQVTEFTYLVYFMCSSCVGGMNRRP 239
 CC QY 227 ILIYVLTGQVIGRCFEGARICACPGDRKKADEDSIRKQ---VSDSTKNGDGTARP 283
 CC DB 240 ILIYVLTGQVIGRCFEGARICACPGDRKKADEDSIRKQ---VSDSTKNGDGTARP 299
 CC QY 284 FRO-NTHGIGMTSIRKRS---PDDELLYLIPVGRREYEMLKIKESLELMQYIPORTI 338
 CC DB 300 MEKALPAPDQASAKTKSSPAVSDELYTLQIRKERYEMLKIKESLELMQYIPORTI 359
 CC QY 339 ETRYROO 344
 CC DB 360 DKYRQK 365
 CC
 CC RESULT 4
 CC P53_BARBU
 CC ID P53_BARBU STANDARD; PRT; 369 AA.
 CC AC Q9W678;

DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Barbus barbus (Barbel).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Barbus.
 OC NCBI_TaxId:40830;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
 RT "Evolutionary conservancy of p53 gene sequences in fish."
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF071570; AAD34212.1; -
 CC HSP: P04637; ITUP.
 CC InterPro: IPR002117; P53.
 CC Pfam: PF00870; P53; 1.
 CC PRINTS: PR00386; P53SUPPRESSR.
 CC ProDom: PD002681; P53; 1.
 CC PROSITE: PS00348; P53; 1.
 CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 CC Nuclear protein; Phosphorylation; Apoptosis.
 CC KM Nuclear protein; Phosphorylation; Transcription regulation; Activator;
 CC FT DNA BIND 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).
 CC FT DOMAIN 66 256 BY SIMILARITY.
 CC FT DOMAIN 298 329 OLIGOMERIZATION.
 CC FT DOMAIN 342 365 BASIC (REPRESSION OF DNA-BINDING).
 CC FT DOMAIN 276 292 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC FT MOD.RES 368 368 PHOSPHORYLATION (BY SIMILARITY).
 CC SQ SEQUENCE 369 AA; 41233 MW; 0BE2CF2CEA74C304 CRC64;
 CC -----
 CC Query Match 39.4%; Score 819.5; DB 1; Length 369;
 CC Best Local Similarity 51.2%; Pred. No. 2.8e-55;
 CC Matches 167; Conservative 49; Mismatches 87; Indels 23; Gaps 8;
 CC
 CC QY 29 QIONGSSSTPYNTDHAQNSVT-APSPYAPSSTFDALSPSPALPSNTDYPGPHSFVDSF 87
 CC DB 26 ELINDEYLPSSDPDPIFNVLQEQPQSTP-----PLASVVAVDYGEHGFKGF 77
 CC QY 88 QOSSTAKSATWTSTELKKLYCQIAKTCPIQIKMTPPGAVIRAMPVYKKAHEVTEV 147
 CC DB 78 PQSGTAKSVTCYSSDLKLFQCLAKTCPIQIVVDHPPPGAVVRAIAIKKISDVADVARCPHSTSENNEGP-AP 137
 CC QY 148 KCRPHHELSREFNEQIAPPSHLIRVGENSHAOYVEDPITGRQSVLVPEPPQVTEFTY 207
 CC DB 138 RCRPHHEKTPD-GDG-LAPAAHLIRVGENSHAOYVEDPITGRQSVLVPEPPQVTEFTY 195
 CC QY 208 VLYNFMCSSCVGGMNRRPILITVLTFRDQVIGRCFEGARICACPGDRKKADEDSIRK 267
 CC DB 196 VLYNFMCSSCVGGMNRRPILITVLTFRDQVIGRCFEGARICACPGDRKKADEDSIRK 255

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OY 268 QOVSDSTKNGD----GTRPF-RONTGIGIOMTSIKRR----SPDELLYLVRGREYE 318
DB 256 DQ---ETKLDKIPANKRSILKSTSSVPRREGSKAKLSSSDEIITLYOVRKERE 312
OY 319 MLKIKESLEIMQYLPQHTIETYYROO 344
DB 313 MLKINDSLEISDVVPSEMDRYROK 338

RESULT 5
P53_BRARE
ID P53_BRARE STANDARD: PRT: 373 AA.
AC P53734; Q90440;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR DRP53.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE-97344388; PubMed-9200835;
RA Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
RA Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;
RA "zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
RT expression during embryogenesis.";
RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
RN [2]
RP SEQUENCE OF 140-212 FROM N.A.
RA Winge P.;
RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL: U60804; AAB0617.1; -
DR EMBL: U66693; AAB57408.1; -
DR HSSP: P04637; ITDP.
DR ZFIN: ZDB-GENE-990415-270; tp53.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 70 260
FT DOMAIN 301 332 OLIGOMERIZATION.
FT DOMAIN 345 366 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 280 296 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 372 372 PHOSPHORYLATION (BY SIMILARITY).

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SQ SEQUENCE 373 AA; 41899 MW; AC7AB724FA6B61FE CRC64;
Query Match 38.7%; Score 806.5; DB 1; Length 373;
Best Local Similarity 48.0%; Pred. No. 2,8e-54;
Matches 171; Conservative 55; Mismatches 97; Indels 33; Gaps 10;

OY 5 ENNAOTGSEPOYTNL-----GLNMDQOIQNGSSSTSPYNTDHQNSVTAPS 53
DB 3 QNDQO-EFAELWEKNIITPPGGGSCWDITN--DESYLPDS-----FDNFEN-VLEEQ 53
OY 54 PYAOPSSTFDALSPSPALPSNTDYPGPHSFDVSPQSSSTAKSATWTYSTELKLYCOIAK 113
DB 54 P--QPST-----LPPISTVETSDYDPGDHGFRLRPPQSGTAKSVTCTYPSDLKLLKCOIAK 107
OY 114 TCEPIQIKVTPPPGCVIRAMPVYKKAHYEVYKRCRPNHELSREPNESQILAPPSHLIRV 173
DB 108 TCEPVQVVDVAPPGGVAVRATAYKSEHVAVVRCPHNE--RPDGNMLAPAGHLIRV 165
OY 174 EGNSHAQVYEDDITGOSLVLPYEPPOVGTFTYVLYNPMCNSSCGVGNRRPILITVTL 233
DB 166 EGNQRANRYEDNITLHSHVFPYEPQDLAEWTVLNTMCSNCGMKNRRPILITVTL 225
OY 234 ETRDQVIGRCFPEARICACPGDRKADSDIRK-QOVSDSTKNGDGTAKRPFRONTGIGIO 292
DB 226 ETQEGQLLRSEFEVAVCACPGDRKTEESNFKKQDETMTAKTTTGTRSLVKESSSAT 285
OY 293 M----TSIKRSPDELLYLVRGREYEMLKIKESLEIMQYLPQHTIETYYROO 344
DB 286 LRPEGSKAKKSSSDEIITLYOVRGERERYEILKINDSLEISDVVPASDAERYROK 341

RESULT 6
P53_ICTPU
ID P53_ICTPU STANDARD: PRT: 376 AA.
AC 093379;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxId=7996;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE-99071979; PubMed-9854815;
RA Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
RA "Identification and characterization of the tumor suppressor p53 in
RT channel catfish (Ictalurus punctatus).";
RL Comp. Biochem. Physiol. 120B:675-682(1998).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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DR EMBL: AF074967; AAC26824.1; -.
DR HSSP: P04637; 1TUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 36 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 77 268 BY SIMILARITY.
FT DOMAIN 303 334 OLIGOMERIZATION.
FT DOMAIN 347 372 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 286 298 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 375 375 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 376 AA; 41989 MM; 1B89CD98DB3289F2 CRC64;

Query Match 38.4%; Score 800; DB 1; Length 376;
Best Local Similarity 50.8%; Pred. No. 8.9e-54;
Matches 164; Conservative 45; Mismatches 94; Indels 20; Gaps 5;

OY 53 SPYAPSTTFALSPSPAINPTDYPGPHSFDVSPFOSSSTAKSATWTSTELKLYCOIA 112
DB 56 SDMLQPGSS--SSPTSTVPTSDYPLNLTILHQSSEGTKSVTCTTSPDLNKLFCOLA 113
OY 113 KTCPLQIKVMPPPGAVIRAMPYKKAHYTEVVKRPNHLSREFNEGOTAPPSHLIR 172
DB 114 KTCPLVLMVSSPPGSLATATAYKRESEHVAEYVRCRPHHERSNDSDGP-APPGHLIR 172
OY 173 VEGNSHAYVEDPITGRQSVLYVPEPPVGTETFTVLYNFCNCSGCVGGMNRPILLIYT 232
DB 173 VEGNSRAYIQEDGNTQAHSVVPEPPVGSOSTVLVNYMNCSSCMGMNRPILLITIT 232
OY 233 LETFDGQVLYGRCEFEARICACPRGRKADSDSIRKQVSDSTKNDGTRKPPRQNTGICQ 292
DB 233 LETDGHILGRTEFEVRKACPRGRKTESNFKKQ-EPRTSGTLTKRMSKADPPSHE 291
OY 293 MTSIKRRSPDELLYLPVGRRETYEMLIKESLELMQVLPQHTIETFRQOQOQHOL 352
DB 292 ASKRSKSSSDDELYTLQVRKEREFLKINDGLESDVPADQEKYRQK----- 343
OY 353 LQKHLISACFRNE---LVEPRR 371
DB 344 ----LLSKTCRKRERDGAAGEPKR 362

RESULT 7
P53_XENLA
ID P53_XENLA STANDARD: PRT: 363 AA.
AC P07193;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=88143684; PubMed=2830576;
RX Soussi T., de Fromental C.C., Mechali M., May P., Kress M.;
RX "Cloning and characterization of a cDNA from Xenopus laevis coding
RX for a protein homologous to human and murine p53."
RX Oncogene 1:71-78(1987).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=94114403; PubMed=8302570;
RX Hoever M., Clement J.H., Medlich D., Montenarh M., Knoechel W.;
RX "Overexpression of wild-type p53 interferes with normal development
RX in Xenopus laevis embryos."

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RL Oncogene 9:109-120(1994).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC Bax and Fas antigen expression, or by repression of Bcl-2
CC expression (by similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (by similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M36962; AAA49923.1; -.
DR EMBL: X05191; CA28821.1; -.
DR EMBL: X77546; CA54672.1; -.
DR PIR: A29376; A29376.
DR HSSP: P04637; 1TUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 29 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 76 267 BY SIMILARITY.
FT DOMAIN 300 331 OLIGOMERIZATION.
FT DOMAIN 344 356 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 281 293 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 362 362 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 52 52 T->S (IN REF. 2).
FT CONFLICT 71 71 MISSING (IN REF. 2).
FT CONFLICT 296 296 MISSING (IN REF. 2).
SQ SEQUENCE 363 AA; 40692 MM; CE1F3E58F020D74D CRC64;

Query Match 36.6%; Score 762; DB 1; Length 363;
Best Local Similarity 54.5%; Pred. No. 6.7e-51;
Matches 151; Conservative 42; Mismatches 68; Indels 16; Gaps 5;

OY 68 SPAIPSTNDYGPSPHSFDVSPFOSSSTAKSATWTSTELKLYCOIAKTCPIQIKWTPPQ 127
DB 68 SCAVPSYDIDYAGKGLQDLPQNGTAKSVTCTYSELNKLKFCQIAKTCPLLYRVESPPR 127
OY 128 GAVIRAMPYKKAHYTEVVKRPNHLSREFNEGQIAPPSHLIRVEGNSHAYVEDPIT 187
DB 128 GSILRATVAYKRSHEVAEVVRCRPHHERSVRPG-DAAPPSHLIRVEGNSHAYVEDPIT 186
OY 188 GRSVLYVPEPPVGTETFTVLYNFCNCSGCVGGMNRPILLIYTLEFRQSVLYGRCFE 247
DB 187 GRHSVCVPEEGPOVTECTVLYNFCNCSGCMGMNRPILLITTELEPODILGRCFE 246
OY 248 ARICACPRGRKADSDSIRKQVSDSTKNDGTRKPPRQNTG-GLIOMTSIKRR--S 301
DB 247 VRVCACPRGRKADSDSIRKQVSDSTKNDGTRKPPRQNTG-GLIOMTSIKRR--S 301
OY 302 PDELLYLPVGRRETYEMLIKESLELMQVLPQHTI 338
DB 298 DDEIFTLIRKGRSREYEMIKKINDALEIQLDQOKV 334

RESULT 8

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P53_CHICK STANDARD; PRT; 367 AA.

AC P10360;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor p53).

GN TP53.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RP SEQUENCE FROM N.A.

RC STRAIN=SPAFAS;

RX MEDLINE=89083584; PubMed=3060861;

RA Soussi T.;

RT "Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein."

RL Nucleic Acids Res. 16:11383-11383(1988).

CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of Bax and Fas antigen expression, or by repression of Bcl-2 expression (By similarity).

CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC EMBL: X13057; CAJ31456.1; -

DR PIR: S02193; S02193.

DR HSSP: P04637; ITPP.

DR InterPro: IPR002117; P53.

DR Pfam: PF00870; P53; 1.

DR PRINTS: PR00386; P53SUPPRESSR.

DR PRODOM: PD002681; P53; 1.

DR PROSITE: PS00348; P53; 1.

KW Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.

FT DOMAIN 1 30 TRANSCRIPTION ACTIVATION (ACIDIC).

FT DNA_BIND 87 278 BY SIMILARITY.

FT DOMAIN 308 339 OLIGOMERIZATION.

FT DOMAIN 347 364 BASIC (REPRESSION OF DNA-BINDING).

FT DOMAIN 292 306 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).

SO SEQUENCE 367 AA; 40169 MW; FC37D0CFD919586 CRC64;

Query Match 36.4%; Score 758.5; DB 1; Length 367;

Best Local Similarity 52.8%; Pred. No. 1.3e-50;

Matches 151; Conservative 42; Mismatches 80; Indels 13; Gaps 5;

QY 48 SVTAPSYAOPSSFDALSPSPALPSNTDYGPHSPVFSQGSSTAKSATWTYTELKL 107

DB 61 AAAPPLPBP--TPPRAASPVVSTEDYGDGDFRGEAEAGTAKSVCTYSPVLNKV 118

QY 108 YCOIAKCPQIKYMPPPGAVIRAMPYKKAHVEYVKKRCNHELRFENSGOAPP 167

DB 119 YCRLAKCPQVQVRGAVAPRSSSLRAVAAYKKSHSEVAEVRCHHRCGGGTDG-LAPA 177

QY 168 SHLIRVEGNSHAQVEDPITGRQSVLVPYPPQVGTFTVLVNFMCNSSCVGGMNRRPI 227

DB 178 OHLIRVEGNPOARHDEDETKRHSVVPYEPPEVSGDCTVLVNFMCNSSCMGMMNRRPI 237

QY 228 LIIVTLETROGVIGRCRCFARICACGRRKRADEDSIRKQVSDSTKNDG--TKPRFR 265

DB 238 LTITLTGPGQLGRRCFCFVRVACGRRKTEENFR-----RGAGGVAKRAMS 290

QY 286 ONFHGIQMTSIRKRPDDELTPVRGREYEMLRKESLEIMQ 331

DB 291 PPTAPPEPK-KRYLNPNDNEIFLYQVGRKRYEMLRKESLEIMQ 335

RESULT 9

P53_PIG STANDARD; PRT; 386 AA.

AC O9TUB2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor p53).

GN TP53 OR P53.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

OX NCBI_TaxID=9823;

RP SEQUENCE FROM N.A.

RX MEDLINE=99422034; PubMed=10490836;

RA Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;

RT "Nucleotide sequence of the porcine p53 cDNA, and the detection of recombinant porcine p53 expressed in vitro with a variety of anti-p53 antibodies."

RL Oncogene 18:5005-5009(1999).

CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of Bax and Fas antigen expression, or by repression of Bcl-2 expression.

CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC EMBL: AF098067; AAF04620.1; -

DR HSSP: P04637; IC26.

DR InterPro: IPR002117; P53.

DR Pfam: PF00870; P53; 1.

DR PRINTS: PR00386; P53SUPPRESSR.

DR PRODOM: PD002681; P53; 2.

DR PROSITE: PS00348; P53; 1.

KW Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.

FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).

FT DNA_BIND 94 285 BY SIMILARITY.

FT DOMAIN 318 349 OLIGOMERIZATION.

FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).

FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY SIMILARITY).

FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 386 AA: 42862 MM; AAC3D88EDDF55162 CRC64;
 Query Match 36.4%; Score 753.5; DB 1; Length 386;
 Best Local Similarity 43.0%; Pred. No. 1.6e-50;
 Matches 157; Conservative 63; Mismatches 104; Indels 41; Gaps 8;

QY 24 NSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSPFDALSPSPALPSNTDYPGPRSF 83
 DB 51 NWLDENPDADSRVAP-----PAAAPAPAPAPAPATSMPL--SSFPQSKTYGSDVF 101
 QY 84 DVSQGSSTAKSATMTYSTELKLLKLCQIAKTCPIQIKWTTPPGCAVIRAMPYKAEHV 143
 DB 102 RLGFHSHSTAKSVYCTYSPALNKLFCQIAKTCVPQVLWSSPPPGTRVRAAIVYKSSYM 161
 QY 144 TEVVKRCPSHLSREFNGQIAPSHLIRVEGNSHAQYVEDPITGRQSLVPEPPQVGT 203
 DB 162 TEVVRRCCHHRRSSSDSG-LAPQHLIRVEGNLAELDLDRNTRHSHVYVEPEPEGS 220
 QY 204 EFTVLVYFMCNSSCVGGMNRPILITVLETRDGOVIGRCFEARICACPRGRKADED 263
 DB 221 DCTIHYFMCNSSCMGMNRRPILITITLEDASGNLGRNSFEVRVACACPRDRTEEE 280
 QY 264 SIRKQVSDSRKNGDTRKPRFRONTHGQMTSIRKRSRDPDELLAPYRGRETYMLKI 323
 DB 281 NFKLKGQSCPEPPPGSTKRALPTST--SSSPVQKKKPLDGEYFTLQIRGRERFEMREL 337
 QY 324 KESLELMQYLPQHTIEYRQ--QQQOQHQLKHLKLSACFENLVEERRETPOKQDVEF 381
 DB 338 NDALFKD-----AQTRAREGENNAHSHLSK-----KGQSPS----- 371
 QY 382 RHSKP 386
 DB 372 RHKKP 376

RESULT 10
 P53_FELCA STANDARD; PRT: 386 AA.
 ID P53_FELCA AC P41685;
 AC P41685;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR TRP53.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph node;
 RX MEDLINE=9433960; PubMed=8056458;
 RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y.,
 RA Watari T., Goitsuka R., Tsujimoto H., Hasegawa A.;
 RT "Cloning of feline p53 tumor suppressor gene and its aberration in
 RT hematopoietic tumors";
 RL Int. J. Cancer 58:602-607(1994).
 RM [2]
 RN SEQUENCE OF 34-354 FROM N.A.
 RX MEDLINE=94114699; PubMed=8286534;
 RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T., Goitsuka R.,
 RA O'Brien S.J., Tsujimoto H., Hasegawa A.;
 RT "Molecular cloning and chromosomal mapping of feline p53 tumor
 RT suppressor gene";
 RL J. Vet. Med. Sci. 55:801-805(1993).
 CC -i- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of

CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression.
 CC -i- SUBUNIT: Binds DNA as a homotetramer (by similarity).
 CC -i- SUBCELLULAR LOCATION: Nuclear.
 CC -i- DISEASE: p53 is found in increased amounts in a wide variety
 CC of transformed cells. p53 is frequently mutated or inactivated
 CC in many types of cancer.
 CC -i- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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DR EMBL: D26608; BAA05653.1; -;
 DR EMBL: D16460; BAA03927.1; -;
 DR HSSP: P04637; 10LG.
 DR pfam: PF00870; P53.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PROSITE: PS00348; P53; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Anticarcinogenic; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 94 285 BY SIMILARITY.
 FT DOMAIN 318 349 OLIGOMERIZATION.
 FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 15 PHOSPHORYLATION (BY PRPK) (BY
 FT SIMILARITY).
 FT MOD_RES 15 PHOSPHORYLATION (BY PRPK) (BY
 FT SIMILARITY).
 FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 285 K -> R (IN REF. 2).
 FT SEQUENCE 386 AA: 42692 MM; D08B43BA1BC8B78 CRC64;
 SQ SEQUENCE 386 AA: 42692 MM; D08B43BA1BC8B78 CRC64;

Query Match 36.2%; Score 753.5; DB 1; Length 386;
 Best Local Similarity 49.8%; Pred. No. 3.2e-50;
 Matches 147; Conservative 49; Mismatches 82; Indels 17; Gaps 4;

QY 43 DHAQNSVTAPSPYAPSPFDALSPSPALPSNTDYPGPRSF 94
 DB 58 DDASGMSAVPAPAPAPAT-----PAPAIWPLSPFVSQATYGVAGYFHLGFLQSGTAK 112
 QY 95 SATMTYSELKLLKLCQIAKTCPIQIKWTTPPGCAVIRAMPYKAEHVYKRCPNHE 154
 DB 113 SVTCTYSPPLKLLKLCQIAKTCPIQIKWTTPPGCAVIRAMPYKAEHVYKRCPNHE 172
 QY 155 LSREFNGQIAPSHLIRVEGNSHAQYVEDPITGRQSLVPEPPQVGTFTVLYNEMC 214
 DB 173 RCPDSDG-LAPQHLIRVEGNLAELDLDRNTRHSHVYVEPEPEVSDCTTHYNMC 231
 QY 215 NSSCVGGMNRRPILITVLETRDGOVIGRCFEARICACPRGRKADEDSTRKQVNST 274
 DB 232 NSSCVGGMNRRPILITVLETRDGOVIGRCFEARICACPRGRKADEDSTRKQVNST 291
 QY 275 KNGDTRKPRFRONTHGQMTSIRKRSRDPDELLAPYRGRETYMLKI 329
 DB 292 PPQSTKRALPTST--SSFPQKKKPLDGEYFTLQIRGRERFEMRELNALEL 343

RESULT 11
 P53_BOVIN STANDARD; PRT: 386 AA.
 ID P53_BOVIN AC O29628;
 AC O29628;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53.
 OS Bos taurus (Bovine), and

OS Bos indicus (zebu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 NC NCBITaxID=9913, 9915;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Bovine; TISSUE-Liver;
 RX MEDLINE=95352829; PubMed=7626789;
 RA Dequiedt F., Kettmann R., Burny A., Willems L.;
 RT "Nucleotide sequence of the bovine p53 tumor-suppressor cDNA.";
 RL DNA Seq. 5:261-264(1995).
 RN [2]
 RP SEQUENCE OF 13-386 FROM N.A.
 RC SPECIES-Bovine; STRAIN-Holstein; TISSUE-thymus;
 RX MEDLINE=96401400; PubMed=8807776;
 RA Komori H., Ishiguro N., Horieuchi M., Shitagawa M., Alda Y.;
 RT "Prominant p53 mutations in enzootic bovine leukemic cell lines.";
 RL Vet. Immunol. Immunopathol. 52:53-63(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-B. indicus; STRAIN-Boran; TISSUE-Blood;
 RA Bishop R.P., Godright E.E.I.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression.
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC -----
 DR EMBL: X81704; CA57348.1; -
 DR EMBL: D49825; BAA08629.1; -
 DR EMBL: U74486; AAB51214.1; -
 DR PIR: S51648; S51648.
 DR HSSP: P04637; 1TUP.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PRO0386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR PROSITE: PS00348; P53; 1.
 KM Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 44
 FT DNAS_BIND 94 285
 FT DOMAIN 318 349
 FT DOMAIN 361 380
 FT DOMAIN 304 316
 FT MOD_RES 15 15
 FT MOD_RES 385 385
 FT CONFLICT 380 380
 FT SEQUENCE 386 AA; 43255 MW; 222473F28C548F31 CRC4;
 SO
 Query Match 35.8%; Score 745.5; DB 1; Length 386;
 Best local similarity 41.7%; Pred. No. 1.3e-49;

Matches 165; Conservative 67; Mismatches 119; Indels 45; Gaps 13;
 QY 5 ENNAQRFSEPPQYTNIGL-----NSMDQIQNSSSTSYN-----TDHAQNSVTPAP--- 52
 DB 7 ELNVEPPLSOEFPSDLMNLLPENNLISSELSAPVDLLPTDYATVLDLDECPNE--APQNP 64
 QY 53 ---SPYAPSPSPFEDALSPSPA-----IPSNWDYCPHSPFVSPFQOSTAKSATWTS 101
 DB 65 EPAPAPAPPPAT-----PAPATSWPLSFFPSQKTPGNGVFLGLQSGTAKSVTCYS 119
 QY 102 TELKRLCYIAKTQPIQIKVMPPPGAVIRAMPVYKKAHVTEVVKCPNHELSEENE 161
 DB 120 PSLNKLFCOLAKTCPOVLWVDSPPPGTRVAMAIYKLEHMEVVRCPHHERSDYSD 179
 QY 162 GQIAPSHLIRVGNHQAQYVEPITGRSVLYVPEPPQVGFTEFTVLVNFKNSSCVG 221
 DB 180 G-LAPPQHILIRVGNLRAEVLDRNFRSHVVPYSPESLDSCTTIIHNFKNSSCKMG 238
 QY 222 MNRPLITLITVETFRGOVLYGRRCFARICACGPRDKADEDSIRKQOVSSTKNGDGTR 281
 DB 239 MNRPLITLITLEDSCGNLIGRNSFEVRCACGGRDRTEENLRKKGSCPEPPRSTR 298
 QY 282 RPERQNTHTGIQMTSIRKRSP--DDELLYLPVREGTEYEMLLKIKESLELMQYLPQHTIET 340
 DB 299 RALPTNV-----SSSPQPKKKPLDGEYFTLIRGFKRYEMREIDALDEL-----KDALDG 349
 QY 341 YRQOQOQOH-QHLOKHLS-ACFRNEIVEPRETP 374
 DB 350 REPESRAHSHLSKRKSPSCHKRPML--KREGP 383
 RESULT 12
 ID P53_TETMU STANDARD: PRT; 367 AA.
 AC Q9W679;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Tetradodon maurus (Congo puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 NC NCBITaxID=94908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
 RT "Evolutionary conservancy of p53 gene sequences in fish.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC -----

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DR EMBL: AF071571; AAD34213.1; -.
DR HSSP: P04637; ITUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR Prodom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 86 273 BY SIMILARITY.
FT DOMAIN 308 337 OLIGOMERIZATION.
FT DOMAIN 342 363 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 288 301 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 367 AA; 41266 MW; ACC10BEE2P5FCDF CRC64;

Query Match 35.8%; Score 745; DB 1; Length 367;
Best Local Similarity 51.9%; Pred. No. 1.3e-49;
Matches 148; Conservative 43; Mismatches 76; Indels 18; Gaps 3;

OY 57 QPSSFDALSPSPATPSNTDYGPHSPFVSSFOSSSTAKSATWTSTELKLYCOIAKCP 116
DB 67 EPPSMDGANSSPVYPTDIPGEYFKLRFOKSTAKSVSTSEILNKLFCQIAKTSL 126
OY 117 IQIKVTPPPGAVIRAMPVYKKAHVTEVYKRCNHELSTREFNGQIAPSHLIRVGN 176
DB 127 VEVLGKDPMGAVLRATAIKTEHVAVRCPHHQ-----NDLSAHSRLIRMGSS 181
OY 177 SHAQVEDPITGROSVLYPEPPQVGTETTYLVNFMKNSSCVCGMNRPIIIVTLETR 236
DB 182 ERAQYFEPHPTKRKOSVTPVPEPQSGSEPTILLSPKNSSCGMNRPPIITITILETQ 241
OY 237 DGQVGRRCFEARICACPGDRKADEDSIRKQOVSSTKNGDGTGRPPFRONTHTGIQMTSI 296
DB 242 EGIYVGRRCFEVYACGDRKRTKETSTKQ-----NDAKAKRKSVPPTDSTTI 294
OY 297 KKRNS-----PDDELIVPVKRGRETYEMLLKIKESLEIMOYLPQ 335
DB 295 KKSSTASSAEDNNEVYTLQIRGRKRYEMLLKINDGLLEKPK 339

RESULT 13
P53_CANFA STANDARD; PRT; 381 AA.
AC Q29537; Q9TV78;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Leukocyte;
RX MEDLINE=98178696; PubMed=9519881;
RA Veldhoen N., Milner J.;
RT "Isolation of canine p53 cDNA and detailed characterization of the
RT full length canine p53 protein.";
RL Oncogene 16:1077-1084(1998).
RN [2]
RC SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RA Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
RA Watarai T., Hasegawa A., Tsujimoto H.;
RT "Alterations of p53 tumor suppressor gene in various spontaneous
RT tumors in the dog.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 25-300 FROM N.A.

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RC STRAIN=Beagle;
RX MEDLINE=95323915; PubMed=7600529;
RA Kraelig S.A., Pazzi K.A., Madewell B.R.;
RT "Sequence analysis of canine p53 in the region of exons 3-8.";
RL Cancer Lett. 92:181-186(1995).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC Bax and Fas antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotetramer (by similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL: AF060514; AAC16909.1; -.
DR EMBL: AB020761; BAA78379.1; -.
DR EMBL: S77819; AAB42022.1; -.
DR HSSP: P04637; IOLG.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR Prodom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 89 280 BY SIMILARITY.
FT DOMAIN 313 344 OLIGOMERIZATION.
FT DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 299 311 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
FT SIMILARITY).
FT MOD_RES 380 380 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 1 4 MEES -> MDRP (IN REF. 2).
FT CONFLICT 378 378 L -> P (IN REF. 2).
SQ SEQUENCE 381 AA; 42486 MW; 761A718FDC93DA59 CRC64;

Query Match 35.5%; Score 739; DB 1; Length 381;
Best Local Similarity 46.5%; Pred. No. 4e-49;
Matches 153; Conservative 52; Mismatches 102; Indels 22; Gaps 7;

OY 5 ENNAQTQSPFQYNTL-----GLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYQPS 60
DB 28 ENNVSSSLCRAVADDELLPESVWNKLD-----DSDDAPRNP--ATSAFTAPGP--APSW 78
OY 61 TFDALSPSPATPSNTDYGPHSPFVSSFOSSSTAKSATWTSTELKLYCOIAKCPQIQ 120
DB 79 PL-----SSVSPSPPTYPGTGFRGLGFLHSGTAKSVTWTYPLNKLFCQIAKCPQV 133
OY 121 VMTPPGAVIRAMPVYKKAHVTEVYKRCNHELSTREFNGQIAPSHLIRVGNSHAO 180
DB 134 VSSPPPTCVRAVAIVKKSSEFVEVARCPHHHECCSSDQ-LAPQHLIRVGNLRAK 192
OY 181 YVEDPITGROSVLYPEPPQVGTETTYLVNFMKNSSCVCGMNRPIIIVTLETRDGOV 240
DB 193 YLDRNPTFRHSVYVPEPEVGSDDTYTHHYKNCNSCGMGNRPPIITITLDDSSGNV 252
OY 241 LGRRCFEARICACPGDRKADEDSIRKQOVSSTKNGDGTGRPPFRONTHTGIQMTSIKKR 300

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Db 253 LGRNSEVAVACACPGDRRTTEENFKKCEPCEPPGSTKRALPST---SSPPQKKK 309
OY 301 SPDELLYLPVNGRETYEMLKIKESLEL 329
Db 310 PLDGEYFTLQINGRERYEMFRNLNEALEL 338

RESULT 14
P53_ORYLA
ID P53_ORYLA STANDARD: PRT: 352 AA.
AC P79820; Q9PSU7; Q9PSU8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97305153; PubMed=9161419;
RA Krause M.K., Rhodes L.D., van Beneden R.J.;
RT "Cloning of the p53 tumor suppressor gene from the Japanese medaka (Oryzias latipes) and evaluation of mutational hotspots in MNNG-exposed fish."
RL Gene 189:101-106(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT THR-91.
RC STRAIN=Himedaka;
RA Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;
RT "Isolation of cDNAs encoding the p53 tumor suppressor gene in the Japanese Medaka (Oryzias latipes).";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
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CC -----
CC EMBL: U57306; AAC60146.1; -
CC EMBL: AF003949; AAD01195.1; -
CC EMBL: AF003950; AAD01196.1; -
CC HSSP: P04637; IYCS.
CC InterPro: IPR002117; P53.
CC Pfam: PF00870; P53; 1.
CC PRINTS: PR00386; P53SUPPRESSR.
CC ProDom: PD002681; P53; 1.
CC PROSITE: PS00348; P53; 1.
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
CC Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.
CC FT DOMAIN 1 48 TRANSCRIPTION ACTIVATION (ACIDIC).
CC FT DNA_BIND 87 273 BY SIMILARITY.

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FT DOMAIN 302 331 OLIGOMERIZATION.
FT DOMAIN 334 350 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 283 295 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 351 351 PHOSPHORYLATION (BY SIMILARITY).
FT VARIANT 91 91 S -> T.
FT CONFLICT 22 22 MISSING (IN REF. 1).
SQ SEQUENCE 352 AA; 39753 MW; 196868A6531BF5 CRC64;

Query Match 35.4%; Score 737.5; DB 1; Length 352;
Best Local Similarity 52.5%; Pred. No. 4,7e-49;
Matches 148; Conservative 40; Mismatches 67; Indels 27; Gaps 5;

OY 57 QPSTFDALSPSPAINSDYDPGPHSFDSFOOSSTAKSATMTYSELKLVQIAKCP 116
Db 68 EPVPTNEVNPPTVTVDYDPSYLELRFQSGTAKSYSTYSTELKLVQIAKTP 127
OY 117 IQIKVTPPGGAVIRAMPYKKAHVTEVYKRCNPHLSREFNEQIAPSHLRVEGN 176
Db 128 IEVRSKEPKKALILATAVYKTEHVADVVRRCPHHQ-----NEDSVHRSHLRVEGS 182
OY 177 SHAQYVEDPTTGQSVLYVEPQVETFTTYLYNMCSSCYGKNNRRPILITVLETR 236
Db 183 QLAQYFEDPYTKQSVTVPEEPQPSGEMTTLLSYMCNCSGCGNNRRPILITVLETR 241
OY 237 DGOVLGRCPPEARICACPGDRKADSDSIRKQOVSDSTFKNGDTRKPPNTHGIQMTSI 296
Db 242 EGVLRGRCPPEARICACPGDRKTEESRKQTPK-----KKKVPNT-----SSS 287
OY 297 KKRRS-----PDDELLYLPVNGRETYEMLKIKESLEIMQ 331
Db 288 KRKSHSGGEEDNRVFPVEVYGRERYEFLKINDGLELLE 329

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RESULT 15
P53_MARMO
ID P53_MARMO STANDARD: PRT: 391 AA.
AC Q36006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97376996; PubMed=9233767;
RA Feltelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
RT "Partial characterization of the woodchuck tumor suppressor, p53, and its interaction with woodchuck hepatitis virus X antigen in hepatocarcinogenesis.";
RL Oncogene 15:327-336(1997).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression.
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
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CC -----
 DR EMBL; AJ001022; CAA04478.1; -.
 DR HSSP; P04637; 1TUP.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR002681; P53; 1.
 DR PRODOM; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 100 290 BY SIMILARITY.
 FT DOMAIN 323 354 OLIGOMERIZATION.
 FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 15 15 PHOSPHORYLATION (BY PRK) (BY
 FT SIMILARITY).
 FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 391 AA; 43468 MW; EID5DB84BA40182 CRC64;

Query Match 35.4%; Score 736.5; DB 1; Length 391;
 Best Local Similarity 41.5%; Pred. No. 6.5e-49;
 Matches 159; Conservative 63; Mismatches 126; Indels 35; Gaps 8;

OY 5 ENNAOTOFSEPOYTNGLINSNDQOIQNGSSSTSPYNTDHAQNSVYAPAPYAQPSSTFDA 64
 DB 28 ENNVLSPLSPMDL-LIASED--VENWFDK---GPDEALQMSAAPAKAPPAASTL 80
 OY 65 LSPSPA-----IPSNIDYGPSPSEFVSQOOSTAKATWYSTELKLYCOIAKTCP 116
 DB 81 AAPSPATSWPLSSSVSONTYPGVYGFRLGLHSGTAKSVCTYSPSLNKLFCQLAKTCP 140
 OY 117 IQIKVMPPPPOGAVIRAMPVYKKAHVYEVVKRCPNHELSEFNEGQIAPSHLIRVEGN 176
 DB 141 VQLWWDSPPPGTRAVAMAIIKKSQHMTEVVRCPNHE--KCSDSGLAPQHLIRVEGN 198
 OY 177 SHAOYVEDPITGROSVLYPEPPPOVGTFTVLYNEMCNSSCGVMNRPIITVLETR 236
 DB 199 LRAETLDIDRNTFRHSVYVPEPEVSECTIHYNYMCNSSCMGMNRRPIITVILEGS 258
 OY 237 DGOVIGRCFCFARICACPGDRKADSDSIRKOQVSDSTKNGDGTKRPPRONT-----HGI 291
 DB 259 SGNLIGRNSFEYKVCACGRDRKTEENFRKR-----GECPEPPPRSTKRALPMGT 310
 OY 292 QMTSIKRRSPDDELLYLPVGRRETYEMLKIKESLELMOYLPOHTIETVYRQOOQOQH 351
 DB 311 SSSPOPKKPLDGEFTLKIRGARAFEMFOELNEALELKDAQAEK-----EPGESRPHPS 365
 OY 352 LLOKHLISACFRNELVEPRRET 374
 DB 366 YLKSRRKGGSTSRHKKIIFKREGP 388

Search completed: August 7, 2003, 09:47:30
 Job time : 7.96946 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: August 7, 2003, 09:41:09 ; Search time 31.6207 Seconds
(without alignments)
3207.225 Million cell updates/sec

Title: US-09-538-106-18
Perfect score: 2082
Sequence: 1 MYLENNAGTQFSEPGYTNL.....PKQSDVFFRRSKRPNSRVP 393

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhcc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rviro:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2082	100.0	393	4	075922 homo sapien
2	2039	97.9	393	11	099309 ratu
3	2011	96.6	487	4	09H3D2
4	2009	96.5	389	11	088899 mus musculu
5	1973	94.8	470	11	099309 ratu
6	1973	94.8	487	11	099309 ratu
7	1938	93.1	483	11	088897 mus musculu
8	1884	90.5	416	4	09P1B6
9	1884	90.5	461	4	09P1B5
10	1884	90.5	461	4	09P266
11	1884	90.5	586	4	09UBV9
12	1884	90.5	586	4	09P1B4
13	1882	90.4	461	11	09QWY9
14	1882	90.4	586	11	089097
15	1873	90.0	461	11	099306
16	1873	90.0	586	11	099302

17	1867	89.7	356	4	09UP74	09UP74 homo sapien
18	1867	89.7	586	4	075080	075080 homo sapien
19	1813	87.1	471	4	09NP87	09NP87 homo sapien
20	1813	87.1	516	4	09P1B7	09P1B7 homo sapien
21	1813	87.1	555	4	09H3D3	09H3D3 homo sapien
22	1813	87.1	641	4	075195	075195 homo sapien
23	1813	87.1	680	4	09H3D4	09H3D4 homo sapien
24	1813	87.1	680	4	09UE10	09UE10 homo sapien
25	1811	87.0	555	11	09QWZ0	09QWZ0 mus musculu
26	1811	87.0	680	11	088898	088898 mus musculu
27	1808	86.8	582	13	09DEC7	09DEC7 gallus gall
28	1807	86.8	538	11	0993D7	0993D7 ratu
29	1807	86.8	555	11	0993D8	0993D8 ratu
30	1807	86.8	663	11	0993J3	0993J3 ratu
31	1807	86.8	680	11	0937P6	0937P6 ratu
32	1722	82.7	355	13	098SW0	098SW0 xenopus lae
33	1591.5	76.4	457	13	08UH25	08UH25 brachydanto
34	1551.5	74.5	576	13	08JFE3	08JFE3 brachydanto
35	1551.5	74.5	588	13	08JH26	08JH26 brachydanto
36	1489	71.5	284	11	08C826	08C826 mus musculu
37	1381.5	66.4	501	4	09H3P8	09H3P8 homo sapien
38	1272	61.1	580	11	0937P1	0937P1 mus musculu
39	1268	60.9	631	11	0937P2	0937P2 mus musculu
40	1268	60.9	641	13	09W664	09W664 barbus barb
41	1256.5	60.4	426	4	08NHM9	08NHM9 homo sapien
42	1253.5	60.2	450	4	08TDY5	08TDY5 homo sapien
43	1253.5	60.2	587	4	08TDY6	08TDY6 homo sapien
44	1217	58.5	232	4	096KR0	096KR0 homo sapien
45	1085.5	52.1	514	11	09C077	09C077 mus musculu

ALIGNMENTS

RESULT 1
ID 075922 PRELIMINARY; PRT; 393 AA.
AC 075922;
DT 01-NOV-1998 (TREMUREL.08, Created)
DT 01-NOV-1998 (TREMUREL.08, Last sequence update)
DT 01-OCT-2002 (TREMUREL.22, Last annotation update)
DE P51 isoform DELGAMMA (DN P53 gamma) (Cellular tumor antigen p53).
DE P53.
GN P53.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE-20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S., Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
RN 12;
RP SEQUENCE FROM N.A.
RX MEDLINE-98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKeon F.;
RT "p53, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN 13;
RP SEQUENCE FROM N.A.
RA Higawara K., McManamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.

CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION (BY SIMILARITY).
 CC -1- SUBUNIT: BINDS DNA AS A HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
 CC MANY TYPES OF CANCER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC EMBL; AF075429; AAC62634.1; -.
 CC EMBL; AF116770; AAF43490.1; -.
 CC EMBL; AF116758; AAF43490.1; JOINED.
 CC EMBL; AF116759; AAF43490.1; JOINED.
 CC EMBL; AF116760; AAF43490.1; JOINED.
 CC EMBL; AF116761; AAF43490.1; JOINED.
 CC EMBL; AF116762; AAF43490.1; JOINED.
 CC EMBL; AF116763; AAF43490.1; JOINED.
 CC EMBL; AF116764; AAF43490.1; JOINED.
 CC EMBL; AF116765; AAF43490.1; JOINED.
 CC EMBL; AF124540; AAG45612.1; -.
 CC EMBL; AF124530; AAG45612.1; JOINED.
 CC EMBL; AF124531; AAG45612.1; JOINED.
 CC EMBL; AF124532; AAG45612.1; JOINED.
 CC EMBL; AF124533; AAG45612.1; JOINED.
 CC EMBL; AF124534; AAG45612.1; JOINED.
 CC EMBL; AF124535; AAG45612.1; JOINED.
 CC HSSP; P04637; IYCS.
 CC InterPro: IPR002117; P53.
 CC Pfam: PF00870; P53; 1.
 CC PRINTS: PR00386; P53SUPPRESSR.
 CC ProDom: PD002681; P53; 1.
 CC PROSITE: PS00348; P53; 1.
 CC Activator: Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
 CC Phosphorylation; Transcription; Transcription regulation.
 CC SEQUENCE 393 AA; 44658 MW; C6689B83FD701610 CRC64;
 SQ
 Query Match 100.0%; Score 2082; DB 4; Length 393;
 Best Local Similarity 100.0%; Pred. No. 3.7e-178;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLYENNAQOFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 DB 1 MLYENNAQOFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 QY 61 TFDALSPSPALPSNTDYPGPHSPDVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 DB 61 TFDALSPSPALPSNTDYPGPHSPDVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 QY 121 VMTPPQGAIVRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVSGNSHAQ 180
 DB 121 VMTPPQGAIVRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVSGNSHAQ 180
 QY 181 YVEDPITGRQSVLVYEPPEVPGVTEFTTVLYNFMKNSSCVCGMNRPLIITYTLETROGOV 240
 DB 181 YVEDPITGRQSVLVYEPPEVPGVTEFTTVLYNFMKNSSCVCGMNRPLIITYTLETROGOV 240
 QY 241 LGRRCFEARICACGRRKADSDSIKQOVSSTKNGDGTTRPRRONTGHIOMTSIKRR 300
 DB 241 LGRRCFEARICACGRRKADSDSIKQOVSSTKNGDGTTRPRRONTGHIOMTSIKRR 300
 QY 301 SPDELLLYLPVGRGETEYMLKIKESLELMQYLPQHTIETRYRQOQOOQHLLKHLISA 360
 DB 301 SPDELLLYLPVGRGETEYMLKIKESLELMQYLPQHTIETRYRQOQOOQHLLKHLISA 360
 QY 361 CERNELVEPRRETQKQSDVFFRRHSKPPNRSYYP 393
 DB 361 CERNELVEPRRETQKQSDVFFRRHSKPPNRSYYP 393
 RESULT 2
 ID 099JUD9 PRELIMINARY; PRT: 393 AA.
 AC 099JUD9;

DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE DN KET gamma protein (cellular tumor antigen p53).
 GN P53.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=wislat; TISSUE=Tongue;
 RX MEDLINE=21363378; PubMed=11470269;
 RA Bamberger C., Schmale H.;
 RT "Identification and tissue distribution of novel KET/p53 splice
 RT variants";
 RL FEBS Lett. 501:121-126(2001).
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS
 CC A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION
 CC BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF
 CC THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION (BY SIMILARITY).
 CC -1- SUBUNIT: BINDS DNA AS A HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
 CC MANY TYPES OF CANCER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC EMBL; AJ277450; CAC37102.1; -.
 CC HSSP; P04637; IYCS.
 CC InterPro: IPR002117; P53.
 CC Pfam: PF00870; P53; 1.
 CC PRINTS: PR00386; P53SUPPRESSR.
 CC ProDom: PD002681; P53; 1.
 CC PROSITE: PS00348; P53; 1.
 CC Activator: Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
 CC Phosphorylation; Transcription; Transcription regulation.
 CC SEQUENCE 393 AA; 44471 MW; 1A310CA6CB276DB CRC64;
 SQ
 Query Match 97.9%; Score 2039; DB 11; Length 393;
 Best Local Similarity 98.0%; Pred. No. 2.7e-174;
 Matches 385; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MLYENNAQOFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 DB 1 MLYENNAQOFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 QY 61 TFDALSPSPALPSNTDYPGPHSPDVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 DB 61 TFDALSPSPALPSNTDYPGPHSPDVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 QY 121 VMTPPQGAIVRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVSGNSHAQ 180
 DB 121 VMTPPQGAIVRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVSGNSHAQ 180
 QY 181 YVEDPITGRQSVLVYEPPEVPGVTEFTTVLYNFMKNSSCVCGMNRPLIITYTLETROGOV 240
 DB 181 YVEDPITGRQSVLVYEPPEVPGVTEFTTVLYNFMKNSSCVCGMNRPLIITYTLETROGOV 240
 QY 241 LGRRCFEARICACGRRKADSDSIKQOVSSTKNGDGTTRPRRONTGHIOMTSIKRR 300
 DB 241 LGRRCFEARICACGRRKADSDSIKQOVSSTKNGDGTTRPRRONTGHIOMTSIKRR 300
 QY 301 SPDELLLYLPVGRGETEYMLKIKESLELMQYLPQHTIETRYRQOQOOQHLLKHLISA 360
 DB 301 SPDELLLYLPVGRGETEYMLKIKESLELMQYLPQHTIETRYRQOQOOQHLLKHLISA 360
 QY 361 CERNELVEPRRETQKQSDVFFRRHSKPPNRSYYP 393
 DB 361 CERNELVEPRRETQKQSDVFFRRHSKPPNRSYYP 393

DB 361 CERNELVESRRAPTOGDVFFRHSNPNHNSVYP 393

RESULT 3

Q9H3D2 PRELIMINARY: PRT: 487 AA.

AC Q9H3D2; 076078: 16, Created)

DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)

DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)

DE TA p53 gamma (P51 isoform TAP63GAMMA).

GN p53.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-98448095; PubMed-9774969;

RA Yang A., Kaghad M., Wang Y., Gilliet E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., Mckeon F.;

RT "p53, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities.";

RL Mol. Cell 2:305-316(1998).

RN [2]

RP SEQUENCE FROM N.A.

RA Hagihara K., McMenamin M.G., Harris C.C.;

RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.

RN [3]

RP SEQUENCE OF 40-487 FROM N.A.

RC TISSUE=Skeletal muscle;

RX MEDLINE-98324755; PubMed-9662378;

RA Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I., Ikawa Y., Nimura Y., Nakagawara A., Odinata M., Ikawa S.;

RT Cloning and functional analysis of human p51, which structurally and functionally resembles p53.";

RL Nat. Med. 4:839-843(1998).

RN [4]

RP SEQUENCE OF 40-487 FROM N.A.

RX MEDLINE-20388515; PubMed-10935472;

RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S., Yokota J.;

RT "Mutation and expression of the p51 gene in human lung cancer.";

RL Neoplasia 1:71-79(1999).

CC -1- SUPRACELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL: AF124540; AAG45609.1; -.

DR EMBL: AF124528; AAG45609.1; JOINED.

DR EMBL: AF124529; AAG45609.1; JOINED.

DR EMBL: AF124531; AAG45609.1; JOINED.

DR EMBL: AF124532; AAG45609.1; JOINED.

DR EMBL: AF124533; AAG45609.1; JOINED.

DR EMBL: AF124534; AAG45609.1; JOINED.

DR EMBL: AF075428; AAC62633.1; -.

DR EMBL: AB016072; BAA32592.1; -.

DR EMBL: AF116770; AAF43486.1; -.

DR EMBL: AF116756; AAF43486.1; JOINED.

DR EMBL: AF116757; AAF43486.1; JOINED.

DR EMBL: AF116759; AAF43486.1; JOINED.

DR EMBL: AF116760; AAF43486.1; JOINED.

DR EMBL: AF116761; AAF43486.1; JOINED.

DR EMBL: AF116762; AAF43486.1; JOINED.

DR EMBL: AF116763; AAF43486.1; JOINED.

DR EMBL: AF116764; AAF43486.1; JOINED.

DR EMBL: AF116765; AAF43486.1; JOINED.

DR HSSP: P04637; 1YCS.

DR InterPro: IPR002117; P53.

DR Pfam: PF00870; P53; 1.

DR PRINTS: PR00386; P53SUPPRESSOR.

DR PRODOM: PD002681; P53; 1.

DR PROSITE: PS00348; P53; 1.

KW Nuclear protein.

SQ SEQUENCE 487 AA; 55687 MW; 86CC865BDF2643DD CRC64;

Query Match 96.6%; Score 2011; DB 4; Length 487;

Best Local Similarity 100.0%; Pred. No. 1,1e-171;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLINSMDOOLONGSSSTSPYNTDHAONSTAPSPYAOPOSTPDALSPSPAIPSN 74

DB 109 PQTNLGLINSMDOOLONGSSSTSPYNTDHAONSTAPSPYAOPOSTPDALSPSPAIPSN 168

QY 75 TDYPSHSPDVSFOOSTSKASATWTYSTELKLYCOIAKTCPIQIKVMPPOGAVIRAM 134

DB 169 TDYPSHSPDVSFOOSTSKASATWTYSTELKLYCOIAKTCPIQIKVMPPOGAVIRAM 228

QY 135 PYKKAHEVTEYVKRCPNHLSRENEGCIAPPSHLIRREGSHAQYVDPTTGROSVLY 194

DB 229 PYKKAHEVTEYVKRCPNHLSRENEGCIAPPSHLIRREGSHAQYVDPTTGROSVLY 288

QY 195 PYEPPOVGTETTYLYNFMCNSSCVGMMRRPILITVLETDGQVIGRCEARICACP 254

DB 289 PYEPPOVGTETTYLYNFMCNSSCVGMMRRPILITVLETDGQVIGRCEARICACP 348

QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGIGQWTSIKRRSPDDELLYLPVGR 314

DB 349 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGIGQWTSIKRRSPDDELLYLPVGR 408

QY 315 EYEMILTKESLELMQYLPQTTIETTYROOOOHOHLQKLLSACRFNELYERRRET 374

DB 409 EYEMILTKESLELMQYLPQTTIETTYROOOOHOHLQKLLSACRFNELYERRRET 468

QY 375 KOSDVFRRSKPPNSVYP 393

DB 469 KOSDVFRRSKPPNSVYP 487

RESULT 4

088899 PRELIMINARY: PRT: 389 AA.

AC 088899;

DT 01-NOV-1998 (TREMblrel. 08, Created)

DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)

DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)

DE DN p53 gamma (Cellular tumor antigen p53).

GN TRP63.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-98448095; PubMed-9774969;

RA Yang A., Kaghad M., Gilliet E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., Mckeon F.;

RT "p53, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities.";

RL Mol. Cell 2:305-316(1998).

CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION (BY SIMILARITY).

CC -1- SUBUNIT: BINDS DNA AS A HOMOTETRAMER (BY SIMILARITY).

CC -1- SUPRACELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL: AF075437; AAC62642.1; -.

DR HSSP: P04637; 1YCS.

DR MGD; MGI:1330810; Ttp63.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
 KW Phosphorylation; Transcription; Transcription regulation.
 SQ SEQUENCE 389 AA; 43970 MW; FEBB4A859C5F00B CRC64;

Query Match 96.5%; Score 2009; DB 11; Length 389;
 Best Local Similarity 97.2%; Pred. No. 1.3e-171;
 Matches 382; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

OY 1 MLYLENNATQTFSEPOYNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 DB 1 MLYLENNATQTFSEPOYNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 OY 61 TFDALSPSPALPSNTDYGPHSFVDSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 DB 61 TFDALSPSPALPSNTDYGPHSFVDSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 OY 121 VMTPEPGAVIRAMVYKKAHEVYKRCRNHELSREFNEQIAPPSHLIVEGNSHAQ 180
 DB 121 VMTPEPGAVIRAMVYKKAHEVYKRCRNHELSREFNEQIAPPSHLIVEGNSHAQ 180
 OY 181 YVEDPITRGOSVLYEPEPOVGTETTYLYNFMCSGCGMNRRLILYVLETRDQGV 240
 DB 181 YVEDPITRGOSVLYEPEPOVGTETTYLYNFMCSGCGMNRRLILYVLETRDQGV 240
 OY 241 LGRRCFEARICACPRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGIIOMTSIKRR 300
 DB 241 LGRRCFEARICACPRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGIIOMTSIKRR 300
 OY 301 SPDELLLYPYKGRREYEMLLIKESLELMQYLPQHTIETRYQOQOQHLLQKHLISA 360
 DB 297 SPDELLLYPYKGRREYEMLLIKESLELMQYLPQHTIETRYQOQOQHLLQKHLISA 356
 OY 361 CFRNELVEPRRETQKQSVFFRHSKPPNRSYVP 393
 DB 357 CFRNELVEPRGEAPQSDVFFRHSNPNNHSYVP 389

RESULT 5

O99JEU1 PRELIMINARY: PRT; 470 AA.
 AC O99JEU1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE TAI1 KET gamma protein.
 GN P63.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Tongue;
 RX MEDLINE=21363378; PubMed=11470269;
 RA Bamberger C., Schmale H.;
 RT "Identification and tissue distribution of novel KET/p63 splice variants."
 RL FEBS Lett. 501:121-126(2001).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AJ277448; CAC37100.1; -.
 DR HSSP; P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.

KW Nuclear protein.
 SQ SEQUENCE 470 AA; 53399 MW; 96B7ED2FB30DD394 CRC64;

Query Match 94.8%; Score 1973; DB 11; Length 470;
 Best Local Similarity 98.2%; Pred. No. 2.8e-168;
 Matches 372; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 15 PQTMLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSTFDALSPSPALPSN 74
 DB 92 PQTMLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSTFDALSPSPALPSN 151
 OY 75 TDYEPGPHSFVDSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPEPGAVIRAM 134
 DB 152 TDYEPGPHSFVDSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPEPGAVIRAM 211
 OY 135 PYKKAHEVTEYKRCRNHELSREFNEQIAPPSHLIVEGNSHAQYVEDPITRGOSVLY 194
 DB 212 PYKKAHEVTEYKRCRNHELSREFNEQIAPPSHLIVEGNSHAQYVEDPITRGOSVLY 271
 OY 195 PYEPPOVGTETTYLYNFMCSGCGMNRRLILYVLETRDQGVLRGRFEARICACP 254
 DB 272 PYEPPOVGTETTYLYNFMCSGCGMNRRLILYVLETRDQGVLRGRFEARICACP 331
 OY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHGIIOMTSIKRRSPDELLLYPYRGR 314
 DB 332 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHGIIOMTSIKRRSPDELLLYPYRGR 391
 OY 315 ETYEMLLIKESLELMQYLPQHTIETRYQOQOQHLLQKHLISACFRNELVESRREAP 374
 DB 392 ETYEMLLIKESLELMQYLPQHTIETRYQOQOQHLLQKHLISACFRNELVESRREAP 451
 OY 375 KQSDVFFRHSKPPNRSYVP 393
 DB 452 KQSDVFFRHSNPNNHSYVP 470

RESULT 6

O99JEU0 PRELIMINARY: PRT; 487 AA.
 AC O99JEU0;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE TAI2 KET gamma protein.
 GN P63.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Tongue;
 RX MEDLINE=21363378; PubMed=11470269;
 RA Bamberger C., Schmale H.;
 RT "Identification and tissue distribution of novel KET/p63 splice variants."
 RL FEBS Lett. 501:121-126(2001).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AJ277449; CAC37101.1; -.
 DR HSSP; P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 487 AA; 55499 MW; A688F392F32B3039 CRC64;

Query Match 94.8%; Score 1973; DB 11; Length 487;
 Best Local Similarity 98.2%; Pred. No. 2.9e-168;
 Matches 372; Conservative 0; Mismatches 7; Indels 0; Gaps 0;


```

QY 15 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 74
Db 109 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 168
QY 75 TDYPGPHFDVFSFOSSSTAKSATWTYITELKKLYCOIAKTCTPIQIKVMTPPPGAVIRAM 134
Db 169 TDYPGPHFDVFSFOSSSTAKSATWTYITELKKLYCOIAKTCTPIQIKVMTPPPGAVIRAM 228
QY 135 PVYKAEHVTEVVKPCPNHLSRENEGIIAPPSSHLIRVEGNSHAQYVEDPTTGRQSVLV 194
Db 229 PVYKAEHVTEVVKPCPNHLSRENEGIIAPPSSHLIRVEGNSHAQYVEDPTTGRQSVLV 288
QY 195 PYEPQVQTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGGVLRRCFEARICACP 254
Db 289 PYEPQVQTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGGVLRRCFEARICACP 348
QY 255 GDRKADSDSRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDELLYLPVGR 314
Db 349 GDRKADSDSRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDELLYLPVGR 408
QY 315 EYEMLLKIKESLELMQVLPQHTIETIRQOQOQOHHLLQKHLKSACFNLVEPRRTP 374
Db 409 EYEMLLKIKESLELMQVLPQHTIETIRQOQOQOHHLLQKHLKSACFNLVEPRRTP 468
QY 375 KQSDVFFRHSKPPNRSVYP 393
Db 469 TQSDVFFRHSNPNHSVYP 487

RESULT 7
O88897 ID O88897 PRELIMINARY; PRT; 483 AA.
AC O88897;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE TA-p63 gamma.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKoon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC EMBL; AF075434; AAC62639.1; -.
CC HSP; P04637; IYCS.
CC MGD; MGI:1330810; Trp63.
CC InterPro; IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PR00386; P53SUPPRESSR.
CC ProDom; PD002881; P53; 1.
CC PROSITE; PS00348; P53; 1.
CC Nuclear protein.
SQ SEQUENCE 483 AA; 54969 MW; A90ED0C110C50EAD CRC64;

Query Match 93.1%; Score 1938; DB 11; Length 483;
Best Local Similarity 97.1%; Pred. No. 3.9e-165;
Matches 368; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

QY 15 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 74
Db 109 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 168
QY 75 TDYPGPHFDVFSFOSSSTAKSATWTYITELKKLYCOIAKTCTPIQIKVMTPPPGAVIRAM 134

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Db 169 TDYPGPHFDVFSFOSSSTAKSATWTYITELKKLYCOIAKTCTPIQIKVMTPPPGAVIRAM 228
QY 135 PVYKAEHVTEVVKPCPNHLSRENEGIIAPPSSHLIRVEGNSHAQYVEDPTTGRQSVLV 194
Db 229 PVYKAEHVTEVVKPCPNHLSRENEGIIAPPSSHLIRVEGNSHAQYVEDPTTGRQSVLV 288
QY 195 PYEPQVQTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGGVLRRCFEARICACP 254
Db 289 PYEPQVQTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGGVLRRCFEARICACP 348
QY 255 GDRKADSDSRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDELLYLPVGR 314
Db 349 GDRKADSDSRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDELLYLPVGR 404
QY 315 EYEMLLKIKESLELMQVLPQHTIETIRQOQOQOHHLLQKHLKSACFNLVEPRRTP 374
Db 409 EYEMLLKIKESLELMQVLPQHTIETIRQOQOQOHHLLQKHLKSACFNLVEPRRTP 464
QY 375 KQSDVFFRHSKPPNRSVYP 393
Db 469 TQSDVFFRHSNPNHSVYP 483

RESULT 8
O9P1B6 ID O9P1B6 PRELIMINARY; PRT; 416 AA.
AC O9P1B6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 22, Last annotation update)
DE P51 isoform delNGelta (Cellular tumor antigen p53).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS
CC A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION
CC BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF
CC THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: BINDS DNA AS A HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
CC MANY TYPES OF CANCER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC EMBL; AF116769; AAF43493.1; -.
CC EMBL; AF116758; AAF43493.1; JOINED.
CC EMBL; AF116759; AAF43493.1; JOINED.
CC EMBL; AF116760; AAF43493.1; JOINED.
CC EMBL; AF116761; AAF43493.1; JOINED.
CC EMBL; AF116762; AAF43493.1; JOINED.
CC EMBL; AF116763; AAF43493.1; JOINED.
CC EMBL; AF116764; AAF43493.1; JOINED.
CC EMBL; AF116765; AAF43493.1; JOINED.
CC EMBL; AF116766; AAF43493.1; JOINED.
CC HSP; P04637; IYCS.
CC InterPro; IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PR00386; P53SUPPRESSR.
CC ProDom; PD002681; P53; 1.
CC PROSITE; PS00348; P53; 1.

```

KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
 KW Phosphorylation; Transcription; Transcription regulation.
 SQ SEQUENCE 416 AA; 46589 MW; A5974A14B25E3118 CRC64;

Query Match 90.5%; Score 1884; DB 4; Length 416;
 Best Local Similarity 93.3%; Pred. No. 2.2e-160;
 Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MLYLENNAOQTFSEPOYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
 DB 1 MLYLENNAOQTFSEPOYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
 QY 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 DB 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 QY 121 VMTPPQGVIRAMPYVYKKAHVTEVVKRCPNHELREFNEGQIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPPQGVIRAMPYVYKKAHVTEVVKRCPNHELREFNEGQIAPPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMMNRRLIIVTLETDRGOV 240
 DB 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMMNRRLIIVTLETDRGOV 240
 QY 241 LGRRCFEARICACGDRKDAEDSIRKQVSDSTKNGDGTKRFRQNTGHGQIOMTSIKKRR 300
 DB 241 LGRRCFEARICACGDRKDAEDSIRKQVSDSTKNGDGTKRFRQNTGHGQIOMTSIKKRR 300
 QY 301 SPDELLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOQOOHOLLOKLLSA 360
 DB 301 SPDELLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOQOOHOLLOKLLSA 360
 QY 361 CFNRELVEPRRETPKQSDVFFRHSKPP 387
 DB 356 -----QTSIQSPSSYGNSSPP 371

RESULT 9
 Q9P1B5 PRELIMINARY; PRT; 461 AA.
 AC Q9P1B5
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE P51 Isoform delNbeta.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20388515; PubMed=10935472;
 RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
 RA Yokota J.;
 RT "Mutation and expression of the p51 gene in human lung cancer."
 RL Neoplasia 1:71-79(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AF116769; AAF43492.1; JOINED.
 DR EMBL; AF116758; AAF43492.1; JOINED.
 DR EMBL; AF116759; AAF43492.1; JOINED.
 DR EMBL; AF116760; AAF43492.1; JOINED.
 DR EMBL; AF116761; AAF43492.1; JOINED.
 DR EMBL; AF116762; AAF43492.1; JOINED.
 DR EMBL; AF116763; AAF43492.1; JOINED.
 DR EMBL; AF116764; AAF43492.1; JOINED.
 DR EMBL; AF116765; AAF43492.1; JOINED.
 DR EMBL; AF116766; AAF43492.1; JOINED.
 DR EMBL; AF116767; AAF43492.1; JOINED.
 DR HSSP; P04637; LYCS.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSOR.

DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 461 AA; 51305 MW; 58B63547B81C1B05 CRC64;

Query Match 90.5%; Score 1884; DB 4; Length 461;
 Best Local Similarity 93.3%; Pred. No. 2.6e-160;
 Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MLYLENNAOQTFSEPOYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
 DB 1 MLYLENNAOQTFSEPOYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
 QY 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 DB 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 QY 121 VMTPPQGVIRAMPYVYKKAHVTEVVKRCPNHELREFNEGQIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPPQGVIRAMPYVYKKAHVTEVVKRCPNHELREFNEGQIAPPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMMNRRLIIVTLETDRGOV 240
 DB 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMMNRRLIIVTLETDRGOV 240
 QY 241 LGRRCFEARICACGDRKDAEDSIRKQVSDSTKNGDGTKRFRQNTGHGQIOMTSIKKRR 300
 DB 241 LGRRCFEARICACGDRKDAEDSIRKQVSDSTKNGDGTKRFRQNTGHGQIOMTSIKKRR 300
 QY 301 SPDELLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOQOOHOLLOKLLSA 360
 DB 301 SPDELLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOQOOHOLLOKLLSA 360
 QY 361 CFNRELVEPRRETPKQSDVFFRHSKPP 387
 DB 356 -----QTSIQSPSSYGNSSPP 371

RESULT 10
 Q9UP26 PRELIMINARY; PRT; 461 AA.
 AC Q9UP26
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE DN P63 beta.
 GN P63.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kagnad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKeon F.;
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities."
 RL Mol. Cell 2:305-316(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hagiwara K., McMenamin M.G., Harris C.C.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AF075433; AAC62638.1; JOINED.
 DR EMBL; AF124539; AAG45611.1; JOINED.
 DR EMBL; AF124530; AAG45611.1; JOINED.
 DR EMBL; AF124531; AAG45611.1; JOINED.
 DR EMBL; AF124532; AAG45611.1; JOINED.
 DR EMBL; AF124533; AAG45611.1; JOINED.
 DR EMBL; AF124534; AAG45611.1; JOINED.
 DR EMBL; AF124535; AAG45611.1; JOINED.

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EMBL; AF124536; AAG45611.1; JOINED.
EMBL; AF124537; AAG45611.1; JOINED.
HSP; P04637; 1YCS.
InterPro: IPR002117; P53.
Pfam: PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSOR.
PRODOM; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 461 AA; 51404 MW; 68B63547A46C1B05 CRC64;

Query Match          90.5%; Score 1884; DB 4; Length 461;
Best Local Similarity 93.3%; Pred. No. 2.6e-160;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MLYLNNNAOTQFSEPOYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
DB 1 MLYLNNNAOTQFSEPOYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60

QY 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120

QY 121 VMTPPQGVIRAMPYVYKKAHVTEVVKRCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGVIRAMPYVYKKAHVTEVVKRCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQ 180

QY 181 YVEDPITGRQSVLPVPEPQVGTFTVLYNFCNSCVGGMNRRPILIIIVTLETRDQGV 240
DB 181 YVEDPITGRQSVLPVPEPQVGTFTVLYNFCNSCVGGMNRRPILIIIVTLETRDQGV 240

QY 241 LGRRCFEARICACGPRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRR 300
DB 241 LGRRCFEARICACGPRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRR 300

QY 301 SPDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETYRQOQQOQHLLQKHLLSA 360
DB 301 SPDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETYRQOQQOQHLLQKHLLSA 360

QY 361 CFNRELVEPRRTPKQSDVFFRHSKPP 387
DB 356 -----QTSIQSPSSYGNSSPP 371

RESULT 11
Q9UBV9
ID Q9UBV9 PRELIMINARY; PRT; 586 AA.
AC Q9UBV9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DN P63 alpha.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKenon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lee L.A., Walsh P., Prater C.A., Su L., Marchbank A., Egbert T.B.,
RA DeLavallée R.P., Targoff I.N., Kaufman K.M., Chorzelski T.P.,
RA Jablonska S.;
RT "Characterization of an autoantigen associated with chronic ulcerative
RT stomatitis: The CUSP autoantigen is a member of the p53 family.";
RL J. Invest. Dermatol. 0:0-0(1999).
```

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[3]
RN SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF091627; AAC62636.1; -.
DR EMBL; AF091627; AAC43038.1; -.
DR EMBL; AF124539; AAG45610.1; -.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR HSP; P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSOR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 586 AA; 65756 MW; 2E2F92ABF1AF8629 CRC64;

Query Match          90.5%; Score 1884; DB 4; Length 586;
Best Local Similarity 93.3%; Pred. No. 3.5e-160;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MLYLNNNAOTQFSEPOYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
DB 1 MLYLNNNAOTQFSEPOYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60

QY 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120

QY 121 VMTPPQGVIRAMPYVYKKAHVTEVVKRCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGVIRAMPYVYKKAHVTEVVKRCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQ 180

QY 181 YVEDPITGRQSVLPVPEPQVGTFTVLYNFCNSCVGGMNRRPILIIIVTLETRDQGV 240
DB 181 YVEDPITGRQSVLPVPEPQVGTFTVLYNFCNSCVGGMNRRPILIIIVTLETRDQGV 240

QY 241 LGRRCFEARICACGPRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRR 300
DB 241 LGRRCFEARICACGPRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRR 300

QY 301 SPDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETYRQOQQOQHLLQKHLLSA 360
DB 301 SPDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETYRQOQQOQHLLQKHLLSA 360

QY 361 CFNRELVEPRRTPKQSDVFFRHSKPP 387
DB 356 -----QTSIQSPSSYGNSSPP 371

RESULT 12
Q9P1B4
ID Q9P1B4 PRELIMINARY; PRT; 586 AA.
AC Q9P1B4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 isoform del.Nalpa.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF116769; AAF43491.1; JOINED.
DR EMBL; AF116758; AAF43491.1; JOINED.
DR EMBL; AF116759; AAF43491.1; JOINED.
DR EMBL; AF116760; AAF43491.1; JOINED.
DR EMBL; AF116761; AAF43491.1; JOINED.
DR EMBL; AF116762; AAF43491.1; JOINED.
DR EMBL; AF116763; AAF43491.1; JOINED.
DR EMBL; AF116764; AAF43491.1; JOINED.
DR EMBL; AF116765; AAF43491.1; JOINED.
DR EMBL; AF116766; AAF43491.1; JOINED.
DR EMBL; AF116767; AAF43491.1; JOINED.
DR EMBL; AF116768; AAF43491.1; JOINED.
DR HSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 586 AA; 65726 MW; 9A2316B631AF8634 CRC64;

Query Match 90.5%; Score 1884; DB 4; Length 586;
Best Local Similarity 93.3%; Pred. No. 3.5e-160;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MLYENNAQTFSEPOYTNGLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAQTFSEPOYTNGLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPNTDYPGPHSFDVSPQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPNTDYPGPHSFDVSPQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGROSVLVPYEPPOVGTEFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDQV 240
DB 181 YVEDPITGROSVLVPYEPPOVGTEFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDQV 240
QY 241 LGRRCFARICACPGDRKKADEDSIRKQVSDSTKNGDGTGKPRFRONTGHIQMTSIKRR 300
DB 241 LGRRCFARICACPGDRKKADEDSIRKQVSDSTKNGDGTGKPRFRONTGHIQMTSIKRR 300
QY 301 SPDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIRQQQQQHOHLQKLLSA 360
DB 301 SPDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIRQQQQQHOHLQKLLSA 360
QY 361 CFRNELVEPRETPKQSDVFRHSKPP 387
DB 356 -----QTSIQSSPSYGNSSPP 371

RESULT 13
Q9QWY9 ID Q9QWY9 PRELIMINARY; PRT; 461 AA.
AC Q9QWY9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kachad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF075438; AAC62643.1; JOINED.
DR HSP; P04637; IYCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51455 MW; 7613296F2F85DBC8 CRC64;

Query Match 90.4%; Score 1882; DB 11; Length 461;
Best Local Similarity 93.0%; Pred. No. 3.9e-160;
Matches 360; Conservative 3; Mismatches 8; Indels 16; Gaps 1;

QY 1 MLYENNAQTFSEPOYTNGLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAQTFSEPOYTNGLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
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DB 61 TFDALSPSPALPNTDYPGPHSFDVSPQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGROSVLVPYEPPOVGTEFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDQV 240
DB 181 YVEDPITGROSVLVPYEPPOVGTEFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDQV 240
QY 241 LGRRCFARICACPGDRKKADEDSIRKQVSDSTKNGDGTGKPRFRONTGHIQMTSIKRR 300
DB 241 LGRRCFARICACPGDRKKADEDSIRKQVSDSTKNGDGTGKPRFRONTGHIQMTSIKRR 300
QY 301 SPDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIRQQQQQHOHLQKLLSA 360
DB 301 SPDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIRQQQQQHOHLQKLLSA 360
QY 361 CFRNELVEPRETPKQSDVFRHSKPP 387
DB 356 -----QTSIQSSPSYGNSSPP 371

RESULT 14
O89097 ID O89097 PRELIMINARY; PRT; 586 AA.
AC O89097;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DN P63 alpha.
GN Trp63 OR P73H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kachad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RT Caput D., McKean F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RT Mol. Cell 2:305-316(1998).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Thymus;
RC MEDLINE=98369596; PubMed=9703973;
RA Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,
RA Tanaka T., Shinkai Y., Kato H.;
RT "A second p53-related protein, p73l, with high homology to p73.";
RT Biochem. Biophys. Res. Commun. 248:603-607(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF075439; AAC62644.1; -;
DR EMBL: AB010152; BAA32432.1; -;
DR HSSP: P04637; 1YCS.
DR MGD: MG1:1330810; Trp63.
DR Interpro: IPR002117; P53.
DR Interpro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 586 AA; 65789 MW; 622E24085B8BDCE7 CRC64;

Query Match 90.4%; Score 1882; DB 11; Length 586;
Best Local Similarity 93.0%; Pred. No. 5.3e-160;
Matches 360; Conservative 3; Mismatches 8; Indels 16; Gaps 1;
QY 1 MYLENNAGTQFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
DB 1 MYLENNAGTQFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPAIIPSNNTDYPGPHSFDVSFOQSTAKSATWTSTELKLYCOIACTCPQIK 120
DB 61 TFDALSPSPAIIPSNNTDYPGPHSFDVSFOQSTAKSATWTSTELKLYCOIACTCPQIK 120
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DB 121 VMTPPPGAVIRAMPYKKAHEVTEYVKRCPNHELSEFNEGQIAPSHLIRVGNHQAQ 180
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DB 181 YVEDPITGRQSVLVPEPPQVGTETTVLYNFMCNSSCVGGMNRRPILITVLETRDGY 240
QY 241 LGRRCFEARICACPGDRKADSDSIRKQVSDSKNGDGTKRPFROTHGIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKADSDSIRKQVSDSKNGDGTKRPFROTHGIOMTSIKRR 300
QY 301 SPDELLIYLPVRGRETYEMLIKESLELMQYLPQHTIETYYROOQOQOHLOKHLA 360
DB 301 SPDELLIYLPVRGRETYEMLIKESLELMQYLPQHTIETYYROOQOQOHLOKHLA 360
QY 361 CFENELVEPRRETPKQSDVFFRHSKPP 387
DB 361 CFENELVEPRRETPKQSDVFFRHSKPP 387
QY 356 -----QTSMSQSSSYGNSSP 371
DB 356 -----QTSMSQSSSYGNSSP 371

RESULT 15
Q99J06 PRELIMINARY; PRT; 461 AA.
AC Q99J06;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DN KET beta protein.

GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Mistral; TISSUE=Tongue;
RC MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
RT variants.";
RT FBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AJ277453; CAC37105.1; -;
DR HSSP: P04637; 1YCS.
DR Interpro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51398 MW; B5F898EBE7E4F97A CRC64;

Query Match 90.0%; Score 1873; DB 11; Length 461;
Best Local Similarity 92.5%; Pred. No. 2.5e-159;
Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;
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DB 61 TFDALSPSPAIIPSNNTDYPGPHSFDVSFOQSTAKSATWTSTELKLYCOIACTCPQIK 120
QY 121 VMTPPPGAVIRAMPYKKAHEVTEYVKRCPNHELSEFNEGQIAPSHLIRVGNHQAQ 180
DB 121 VMTPPPGAVIRAMPYKKAHEVTEYVKRCPNHELSEFNEGQIAPSHLIRVGNHQAQ 180
QY 181 YVEDPITGRQSVLVPEPPQVGTETTVLYNFMCNSSCVGGMNRRPILITVLETRDGY 240
DB 181 YVEDPITGRQSVLVPEPPQVGTETTVLYNFMCNSSCVGGMNRRPILITVLETRDGY 240
QY 241 LGRRCFEARICACPGDRKADSDSIRKQVSDSKNGDGTKRPFROTHGIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKADSDSIRKQVSDSKNGDGTKRPFROTHGIOMTSIKRR 300
QY 301 SPDELLIYLPVRGRETYEMLIKESLELMQYLPQHTIETYYROOQOQOHLOKHLA 360
DB 301 SPDELLIYLPVRGRETYEMLIKESLELMQYLPQHTIETYYROOQOQOHLOKHLA 360
QY 361 CFENELVEPRRETPKQSDVFFRHSKPP 387
DB 361 CFENELVEPRRETPKQSDVFFRHSKPP 387
QY 356 -----QTSMSQSSSYGNSSP 371
DB 356 -----QTSMSQSSSYGNSSP 371

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